GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:15:31 ; Search time 87.4 Seconds
(without alignments)
3712.721 Million cell updates/sec

Title: US-09-396-985B-2
Perfect score: 4355
Sequence: 1 MMSASRLAGTLIPAMAFLSC.....SWNPEGTVGTGCNWQEATSI 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4355	100.0	839	6	ABU04773	Abu04773 Human exp
2	4355	100.0	839	6	ABU04774	Abu04774 Human exp
3	4355	100.0	839	6	ABU04775	Abu04775 Human exp
4	4355	100.0	839	7	ADC78785	Adc78785 Human PRO
5	4355	100.0	839	7	ADD48826	Add48826 Human Pro
6	4335.5	99.6	837	2	AAW86361	Aaw86361 Human DNA
7	4335.5	99.6	837	5	AAE16102	Aae16102 Human DNA
8	4335.5	99.6	837	6	ABU04776	Abu04776 Human exp
9	4328.5	99.4	837	5	AAE16116	Aae16116 Human DNA
10	4178	95.9	808	8	ADO57782	Ado57782 Chimpanze
11	4167	95.7	808	8	ADO57785	Ado57785 Gorilla t
12	4164	95.6	808	8	ADO57803	Ado57803 Chimpanze
13	4141	95.1	799	2	AAW86352	Aaw86352 Human DNA
14	4141	95.1	799	5	AAE16093	Aae16093 Human DNA
15	4141	95.1	799	5	ABB83162	Abb83162 Human Tol
16	4141	95.1	799	6	ABR42963	Abr42963 Human Tol
17	4141	95.1	799	7	ADB39121	Adb39121 Human tol
18	4141	95.1	799	8	ADP56656	Adp56656 Human Tol
19	4141	95.1	799	8	ADP48597	Adp48597 Human Tol
20	4040	92.8	801	8	ADO57788	Ado57788 Gibbon to
21	3918	90.0	795	8	ADO57791	Ado57791 Rhesus mo
22	3892	89.4	795	8	ADO57800	Ado57800 Hamadryas
23	3819	87.7	801	8	ADO57797	Ado57797 Squirrel
24	3683.5	84.6	738	8	ADP29455	Adp29455 Human sec
25	3501	80.4	745	8	ADO57794	Ado57794 White-fac
26	1090	25.0	208	3	AAY88059	Aay88059 Human Tol
27	919	21.1	178	8	ADN12270	Adn12270 IL-1R/TLR
28	785	18.0	179	7	ADC42707	Adc42707 Murine To
29	629.5	14.5	661	2	AAW28510	Aaw28510 Product o
30	629.5	14.5	661	2	AAW87556	Aaw87556 B cell su
31	629.5	14.5	661	7	ADC38652	Adc38652 Human sec
32	629.5	14.5	661	7	ADF69098	Adf69098 Human MP5
33	628.5	14.4	650	3	AAY82527	Aay82527 Human RP1
34	615.5	14.1	661	2	AAW47274	Aaw47274 Human B-c
35	603.5	13.9	784	2	AAW86350	Aaw86350 Human DNA
36	603.5	13.9	784	5	AAE16091	Aae16091 Human DNA
37	603.5	13.9	784	5	ABB83161	Abb83161 Human Tol
38	603.5	13.9	784	8	ADN02005	Adn02005 Human inf
39	602.5	13.8	784	2	AAY05869	Aay05869 Human Tol
40	602.5	13.8	784	6	ABU61956	Abu61956 Human Tol
41	602.5	13.8	784	7	ADL15005	Adl15005 Human Tol
42	602.5	13.8	784	8	ADP56652	Adp56652 Human Tol
43	602.5	13.8	784	8	ADP48593	Adp48593 Human Tol
44	602.5	13.8	784	8	ADP23787	Adp23787 PRO polyp
45	602.5	13.8	784	8	ADQ39727	Adq39727 Human myo

ALIGNMENTS

RESULT 1
ABU04773
ID ABU04773 standard; protein; 839 AA.
XX
AC ABU04773;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1439.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1439; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a

CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 839 AA;

Query Match 100.0%; Score 4355; DB 6; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660

Qy        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720

Qy        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780

Qy        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
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RESULT 2
ABU04774
ID ABU04774 standard; protein; 839 AA.
XX
AC ABU04774;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1440.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1440; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 839 AA;

Query Match 100.0%; Score 4355; DB 6; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60
```

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Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180
Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480
Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540
Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660
Db        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660

Qy        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720
Db        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720

Qy        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780
Db        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780

Qy        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
Db        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
```

```
RESULT 3
ABU04775
ID   ABU04775 standard; protein; 839 AA.
XX
AC   ABU04775;
XX
DT   29-JAN-2003  (first entry)
XX
DE   Human expressed protein tag (EPT) #1441.
XX
KW   Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW   protease; protease inhibitor; transporter; cytoskeletal protein;
KW   receptor; transcription factor; cancer; MHC;
KW   major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW   adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200278524-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US009671.
XX
PR   28-MAR-2001; 2001US-0279495P.
PR   21-MAY-2001; 2001US-0292544P.
PR   08-AUG-2001; 2001US-0310801P.
PR   01-OCT-2001; 2001US-0326370P.
PR   04-DEC-2001; 2001US-0336780P.
PR   20-FEB-2002; 2002US-0358985P.
XX
PA   (ZYCO-) ZYCOS INC.
XX
PI   Chicz RM,  Tomlinson AJ,  Urban RG;
XX
DR   WPI; 2003-040607/03.
XX
PT   New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT   cytoskeletal proteins, receptors or transcription factors), useful for
PT   treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT   leukemia.
XX
PS   Example 2; SEQ ID NO 1441; 134pp; English.
XX
CC   The invention describes a purified polypeptide, which comprises a
CC   fragment of a kinase, phosphatase, protease, protease inhibitor,
CC   transporter, cytoskeletal protein, receptor or transcription factor. The
CC   polypeptide is useful as an immunogenic composition for eliciting in a
CC   mammal an immunogenic response directed against any of the purified
CC   polypeptide. The purified polypeptide, or the antibody that binds to this
CC   polypeptide, is useful for treating cancer. The polypeptide is also
CC   useful for identifying compounds that binds to a naturally processed
CC   class I or class II MHC-binding polypeptide. The polypeptides and
CC   polynucleotides are particularly useful for treating or preventing
CC   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC   lymphoma or leukaemia. These are also useful for screening agents for
CC   treating the above mentioned diseases. This sequence represents an
CC   expressed protein tag (EPT) isolated from human tissue for translational
CC   profiling. Note: This sequence does not appear in the printed
CC   specification but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 839 AA;

  Query Match           100.0%;  Score 4355;  DB 6;  Length 839;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60
Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180
Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360
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Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660

Qy        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720

Qy        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780

Qy        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
```

RESULT 4
ADC78785
ID ADC78785 standard; protein; 839 AA.
XX
AC ADC78785;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human PRO protein #7.
XX
KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease.
XX
OS Homo sapiens.
XX
PN WO2003034984-A2.
XX
PD 01-MAY-2003.
XX
PF 15-OCT-2002; 2002WO-US033070.
XX
PR 19-OCT-2001; 2001US-0340083P.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Gurney AL;
XX
DR WPI; 2003-481990/45.
DR N-PSDB; ADC78784.
XX
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
PT medicament for diagnosing or treating cancer or inflammatory bowel
PT disorder e.g., ulcerative colitis or Crohn's disease.
XX
PS Claim 12; SEQ ID NO 14; 327pp; English.
XX
CC The invention comprises the amino acid and coding sequences of human PRO
CC proteins. The DNA and protein sequences of the invention are useful for
CC the diagnosis and treatment of cancer and inflammatory bowel disease
CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
CC sequence represents a human PRO protein of the invention.
XX
SQ Sequence 839 AA;

```
  Query Match             100.0%;  Score 4355;  DB 7;  Length 839;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660

Qy        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720

Qy        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780

Qy        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
```

RESULT 5
ADD48826
ID ADD48826 standard; protein; 839 AA.
XX
AC ADD48826;
XX

```
DT   02-DEC-2004  (revised)
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein AAF05316, SEQ ID NO 14536.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; AAF05316.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Example 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (described in Table 3
CC   of the specification) which is differentially expressed during pain.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 839 AA;

  Query Match             100.0%;  Score 4355;  DB 7;  Length 839;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660

Qy        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720

Qy        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780

Qy        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839


RESULT 6
AAW86361
ID   AAW86361 standard; protein; 837 AA.
XX
AC   AAW86361;
XX
DT   15-MAR-1999  (first entry)
XX
DE   Human DNAX toll-like receptor DTLR4.
XX
KW   DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KW   interleukin 1 receptor; phosphate metabolism; innate immunity response;
KW   modulate inflammatory function; morphological effect;
KW   immunological disorder.
XX
OS   Homo sapiens.
XX
PN   WO9850547-A2.
XX
PD   12-NOV-1998.
```

```
XX
PF   07-MAY-1998;   98WO-US008979.
XX
PR   07-MAY-1997;   97US-0044293P.
PR   22-JAN-1998;   98US-0072212P.
PR   05-MAR-1998;   98US-0076947P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Hardiman GT,  Rock FL,  Bazan JF,  Kastelein RA;
XX
DR   WPI; 1999-059670/05.
DR   N-PSDB; AAV80675.
XX
PT   Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
PT   metabolism, modulate inflammatory function or innate immunity responses.
XX
PS   Claim 3; Page 147-149; 171pp; English.
XX
CC   The present invention specifically describes human DNAX toll-like
CC   receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
CC   in the present invention. Also described are: (1) a fusion protein
CC   comprising a DTLR protein or peptide; (2) a binding compound, preferably
CC   an antibody or antibody fragment which specifically binds to a DTLR
CC   protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
CC   ; (4) an expression vector comprising the nucleic acid of (3); and (5) a
CC   host cell comprising the vector of (4). The host cell of (5) can be used
CC   to produce the DTLR proteins. The DTLR proteins can be used to alter
CC   phosphate metabolism, to modulate inflammatory function, innate immunity
CC   responses or morphological effects. The DTLR proteins can be used in the
CC   treatment of conditions exhibiting abnormal expression of the receptors
CC   of their ligands. These abnormalities are typically manifested by
CC   immunological disorders
XX
SQ   Sequence 837 AA;

  Query Match             99.6%;  Score 4335.5;  DB 2;  Length 837;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  837;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 MSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDL 61
              ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db          1 MSASRLAGTLIPAMAFLSCVRPESWEPCVE-VPNITYQCMELNFYKIPDNLPFSTKNLDL 59

Qy         62 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 119

Qy        122 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 179

Qy        182 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 239

Qy        242 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 299

Qy        302 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 359

Qy        362 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 419

Qy        422 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 479

Qy        482 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 539

Qy        542 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 599

Qy        602 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 659

Qy        662 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 719

Qy        722 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 779

Qy        782 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 837


RESULT 7
AAE16102
ID   AAE16102 standard; protein; 837 AA.
XX
AC   AAE16102;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human DNAX Toll like receptor (DTLR) 4 #2.
XX
KW   Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW   interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS   Homo sapiens.
XX
PN   WO200190151-A2.
XX
PD   29-NOV-2001.
XX
PF   23-MAY-2001; 2001WO-US016766.
XX
PR   25-MAY-2000; 2000US-0207558P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Hardiman GT,  Rock FL,  Bazan JF,  Kastelein RA,  Ho SWK,  Liu Y;
XX
DR   WPI; 2002-083085/11.
DR   N-PSDB; AAD26292.
XX
PT   New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT   conditions exhibiting abnormal expression of the receptors of their
PT   ligands, particularly abnormalities manifested by immunological
PT   disorders.
XX
PS   Claim 3; Page 41; 297pp; English.
XX
CC   The invention relates to mammalian receptor proteins, e.g., primate,
CC   human DNAX Toll like receptor (DTLR) protein and their corresponding
CC   nucleic acids. The DTLR is useful for treating conditions exhibiting
CC   abnormal expression of the receptors of their ligands. Such abnormality
CC   is manifested by immunological disorders. In particular, the DTLR is
CC   useful for treating various disease or disorders associated with abnormal
CC   expression or abnormal triggering of response to a ligand. The DTLR is
CC   also useful as an immunogen for the production of antisera or antibodies
CC   specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC   receptor family members, for the DTLR or its various fragments. The
CC   purified DTLR can be used to screen monoclonal antibodies or antigen-
CC   binding fragments. The antibodies are useful for screening expression
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CC   libraries for particular expression products. These are useful for
CC   detecting or diagnosing various immunological conditions related to
CC   expression of DTLR or cells that express it. The present sequence is
CC   human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33.
CC   Note: The present sequence SEQ ID NO 26 is stated to be similar to the
CC   sequence shown in page 240-243 (AAE16116). However these sequences differ
CC   at several locations
XX
SQ   Sequence 837 AA;

  Query Match             99.6%;  Score 4335.5;  DB 5;  Length 837;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  837;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 MSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDL 61
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 MSASRLAGTLIPAMAFLSCVRPESWEPCVE-VPNITYQCMELNFYKIPDNLPFSTKNLDL 59

Qy         62 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 119

Qy        122 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 179

Qy        182 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 239

Qy        242 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 299

Qy        302 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 359

Qy        362 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 419

Qy        422 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 479

Qy        482 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 539

Qy        542 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 599

Qy        602 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 659

Qy        662 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 719

Qy        722 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 779

Qy        782 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 837


RESULT 8
ABU04776
ID   ABU04776 standard; protein; 837 AA.
XX
AC   ABU04776;
XX
DT   29-JAN-2003  (first entry)
XX
DE   Human expressed protein tag (EPT) #1442.
XX
KW   Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW   protease; protease inhibitor; transporter; cytoskeletal protein;
KW   receptor; transcription factor; cancer; MHC;
KW   major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW   adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200278524-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US009671.
XX
PR   28-MAR-2001; 2001US-0279495P.
PR   21-MAY-2001; 2001US-0292544P.
PR   08-AUG-2001; 2001US-0310801P.
PR   01-OCT-2001; 2001US-0326370P.
PR   04-DEC-2001; 2001US-0336780P.
PR   20-FEB-2002; 2002US-0358985P.
XX
PA   (ZYCO-) ZYCOS INC.
XX
PI   Chicz RM,  Tomlinson AJ,  Urban RG;
XX
DR   WPI; 2003-040607/03.
XX
PT   New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT   cytoskeletal proteins, receptors or transcription factors), useful for
PT   treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT   leukemia.
XX
PS   Example 2; SEQ ID NO 1442; 134pp; English.
XX
CC   The invention describes a purified polypeptide, which comprises a
CC   fragment of a kinase, phosphatase, protease, protease inhibitor,
CC   transporter, cytoskeletal protein, receptor or transcription factor. The
CC   polypeptide is useful as an immunogenic composition for eliciting in a
CC   mammal an immunogenic response directed against any of the purified
CC   polypeptide. The purified polypeptide, or the antibody that binds to this
CC   polypeptide, is useful for treating cancer. The polypeptide is also
CC   useful for identifying compounds that binds to a naturally processed
CC   class I or class II MHC-binding polypeptide. The polypeptides and
CC   polynucleotides are particularly useful for treating or preventing
CC   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC   lymphoma or leukaemia. These are also useful for screening agents for
CC   treating the above mentioned diseases. This sequence represents an
CC   expressed protein tag (EPT) isolated from human tissue for translational
CC   profiling. Note: This sequence does not appear in the printed
CC   specification but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 837 AA;

  Query Match             99.6%;  Score 4335.5;  DB 6;  Length 837;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  837;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 MSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDL 61
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 MSASRLAGTLIPAMAFLSCVRPESWEPCVE-VPNITYQCMELNFYKIPDNLPFSTKNLDL 59

Qy         62 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 119
```

```
Qy        122 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 179

Qy        182 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 239

Qy        242 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 299

Qy        302 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 359

Qy        362 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 419

Qy        422 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 479

Qy        482 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 539

Qy        542 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 599

Qy        602 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 659

Qy        662 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 719

Qy        722 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 779

Qy        782 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 837


RESULT 9
AAE16116
ID   AAE16116 standard; protein; 837 AA.
XX
AC   AAE16116;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human DNAX Toll like receptor (DTLR) 4 #2, alternative version.
XX
KW   Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW   interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 211
FT                   /label= Unknown
FT                   /note= "Encoded by AAY"
XX
PN   WO200190151-A2.
XX
PD   29-NOV-2001.
XX
PF   23-MAY-2001; 2001WO-US016766.
XX
PR   25-MAY-2000; 2000US-0207558P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Hardiman GT,  Rock FL,  Bazan JF,  Kastelein RA,  Ho SWK,  Liu Y;
XX
DR   WPI; 2002-083085/11.
DR   N-PSDB; AAD26306.
XX
PT   New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT   conditions exhibiting abnormal expression of the receptors of their
PT   ligands, particularly abnormalities manifested by immunological
PT   disorders.
XX
PS   Claim 3; Page 240-243; 297pp; English.
XX
CC   The invention relates to mammalian receptor proteins, e.g., primate,
CC   human DNAX Toll like receptor (DTLR) protein and their corresponding
CC   nucleic acids. The DTLR is useful for treating conditions exhibiting
CC   abnormal expression of the receptors of their ligands. Such abnormality
CC   is manifested by immunological disorders. In particular, the DTLR is
CC   useful for treating various disease or disorders associated with abnormal
CC   expression or abnormal triggering of response to a ligand. The DTLR is
CC   also useful as an immunogen for the production of antisera or antibodies
CC   specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC   receptor family members, for the DTLR or its various fragments. The
CC   purified DTLR can be used to screen monoclonal antibodies or antigen-
CC   binding fragments. The antibodies are useful for screening expression
CC   libraries for particular expression products. These are useful for
CC   detecting or diagnosing various immunological conditions related to
CC   expression of DTLR or cells that express it. The present sequence is
CC   human DTLR4 protein, alternative version. The DTLR4 gene is located on
CC   chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
CC   be similar to the sequence shown in page 41 (AAE16102). However these
CC   sequences differ at several locations
XX
SQ   Sequence 837 AA;

  Query Match           99.4%;  Score 4328.5;  DB 5;  Length 837;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches  836;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          2 MSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDL 61
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 MSASRLAGTLIPAMAFLSCVRPESWEPCVE-VPNITYQCMELNFYKIPDNLPFSTKNLDL 59

Qy         62 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 119

Qy        122 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 179

Qy        182 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 241
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        180 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLXPMNFIQPGAFKEIRLHKLTLRNNFDSLN 239

Qy        242 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 299

Qy        302 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 359

Qy        362 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 419
```

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Qy        422 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 479

Qy        482 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 539

Qy        542 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 599

Qy        602 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 659

Qy        662 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 719

Qy        722 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 779

Qy        782 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 837


RESULT 10
ADO57782
ID   ADO57782 standard; protein; 808 AA.
XX
AC   ADO57782;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Chimpanzee toll-like receptor 4 SEQ ID NO:3.
XX
KW   toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW   immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW   sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS   Pan troglodytes.
XX
PN   WO2004042365-A2.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-US036247.
XX
PR   01-NOV-2002; 2002US-0423113P.
XX
PA   (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI   Messier W;
XX
DR   WPI; 2004-400726/37.
DR   N-PSDB; ADO57780, ADO57781.
XX
PT   Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT   in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT   sequence of the Old World monkey with that of a human.
XX
PS   Example 1; SEQ ID NO 3; 111pp; English.
XX
CC   The invention relates to a novel method for identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an old world monkey
CC   comprising comparing the TLR4 polynucleotide sequence of the Old World
CC   monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC   method of the invention has antibacterial, immunosuppressive, and
CC   antiasthmatic activity. The method is useful in identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC   change may be associated with reduced sensitivity to Gram-negative
CC   bacterial infection. The methods, agents and composition are useful in
CC   treating sepsis, severe sepsis or septic shock and asthma. The present
CC   sequence represents chimpanzee TLR4.
XX
SQ   Sequence 808 AA;

  Query Match             95.9%;  Score 4178;  DB 8;  Length 808;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches  805;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 60

Qy         92 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        152 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 180

Qy        212 LNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEK 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEK 240

Qy        272 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFG 331
              |||||||||||||||||||||||||||||||||||||||||||||||||: |||||||||
Db        241 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIKSVKDFSYNFG 300

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        392 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 420

Qy        452 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 480

Qy        512 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 540

Qy        572 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNK 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNK 600

Qy        632 TIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNE 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNE 660

Qy        692 LVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEY 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEY 720

Qy        752 EIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRL 811
              |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        721 EIAQTWQFLSSRAGIIFIVLQKVEKTLLRRQVELYRLLSRNTYLEWEDSVLGRHIFWRRL 780

Qy        812 RKALLDGKSWNPEGTVGTGCNWQEATSI 839
              ||||||||||||||||||||||||||||
Db        781 RKALLDGKSWNPEGTVGTGCNWQEATSI 808


RESULT 11
ADO57785
ID   ADO57785 standard; protein; 808 AA.
XX
AC   ADO57785;
```

XX
DT 12-AUG-2004 (first entry)
XX
DE Gorilla toll-like receptor 4 SEQ ID NO:6.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; gorilla.
XX
OS Gorilla gorilla.
XX
PN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
DR WPI; 2004-400726/37.
DR N-PSDB; ADO57783, ADO57784.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Example 1; SEQ ID NO 6; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents gorilla TLR4.
XX
SQ Sequence 808 AA;

Query Match 95.7%; Score 4167; DB 8; Length 808;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 803; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Qy         32 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 91
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 60

Qy         92 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 151
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        152 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 211
               |||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEYLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 180

Qy        212 LNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEK 271
               |||| ||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        181 LNPMTFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVRRLVLGEFRNEGNLEK 240

Qy        272 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFG 331
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFG 300

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 391
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        392 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 451
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 420

Qy        452 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 511
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 480

Qy        512 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 571
               ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        481 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLRVLDYSLNHIMTSKKQELQHFPSSL 540

Qy        572 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNK 631
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNK 600

Qy        632 TIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNE 691
               ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        601 TIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENVYDAFVIYSSQDEDWVRNE 660

Qy        692 LVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEY 751
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEY 720

Qy        752 EIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRL 811
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 EIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRL 780

Qy        812 RKALLDGKSWNPEGTVGTGCNWQEATSI 839
               ||||||||||||||||||||||||||||
Db        781 RKALLDGKSWNPEGTVGTGCNWQEATSI 808
```

RESULT 12
ADO57803
ID ADO57803 standard; protein; 808 AA.
XX
AC ADO57803;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimpanzee toll-like receptor 4 SEQ ID NO:24.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS Pan troglodytes.
XX
PN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
DR WPI; 2004-400726/37.
DR N-PSDB; ADO57801, ADO57802.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Disclosure; SEQ ID NO 24; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey

CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents chimpanzee TLR4.
XX
SQ Sequence 808 AA;

Query Match 95.6%; Score 4164; DB 8; Length 808;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 803; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy         32 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 91
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 60

Qy         92 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 151
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        152 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 211
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 180

Qy        212 LNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEK 271
               |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        181 LNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEENLEK 240

Qy        272 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFG 331
               |||||||||||||||||||||||||||||||||||||||||||||||||: |||||||||
Db        241 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIKSVKDFSYNFG 300

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 391
               ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WQHLELVKCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        392 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 451
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 420

Qy        452 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 511
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 480

Qy        512 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 571
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 540

Qy        572 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNK 631
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNK 600

Qy        632 TIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNE 691
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNE 660

Qy        692 LVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEY 751
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEY 720

Qy        752 EIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRL 811
               ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        721 EIAQTWQFLSSRAGIIFIVLQKVEKTLLRRQVELYRLLSRNTYLEWEDSVLGRHIFWRRL 780

Qy        812 RKALLDGKSWNPEGTVGTGCNWQEATSI 839
               ||||||||||||||||||||||||||||
Db        781 RKALLDGKSWNPEGTVGTGCNWQEATSI 808
```

RESULT 13
AAW86352
ID AAW86352 standard; protein; 799 AA.
XX
AC AAW86352;
XX
DT 15-MAR-1999 (first entry)
XX
DE Human DNAX toll-like receptor DTLR4.
XX
KW DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KW interleukin 1 receptor; phosphate metabolism; innate immunity response;
KW modulate inflammatory function; morphological effect;
KW immunological disorder.
XX
OS Homo sapiens.
XX
PN WO9850547-A2.
XX
PD 12-NOV-1998.
XX
PF 07-MAY-1998; 98WO-US008979.
XX
PR 07-MAY-1997; 97US-0044293P.
PR 22-JAN-1998; 98US-0072212P.
PR 05-MAR-1998; 98US-0076947P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
XX
DR WPI; 1999-059670/05.
DR N-PSDB; AAV80666.
XX
PT Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
PT metabolism, modulate inflammatory function or innate immunity responses.
XX
PS Example; Page 115-117; 171pp; English.
XX
CC The present invention specifically describes human DNAX toll-like
CC receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
CC in the present invention. Also described are: (1) a fusion protein
CC comprising a DTLR protein or peptide; (2) a binding compound, preferably
CC an antibody or antibody fragment which specifically binds to a DTLR
CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
CC ; (4) an expression vector comprising the nucleic acid of (3); and (5) a
CC host cell comprising the vector of (4). The host cell of (5) can be used
CC to produce the DTLR proteins. The DTLR proteins can be used to alter
CC phosphate metabolism, to modulate inflammatory function, innate immunity
CC responses or morphological effects. The DTLR proteins can be used in the
CC treatment of conditions exhibiting abnormal expression of the receptors
CC of their ligands. These abnormalities are typically manifested by
CC immunological disorders
XX
SQ Sequence 799 AA;

Query Match 95.1%; Score 4141; DB 2; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         41 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy        101 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        161 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        221 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 280
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        281 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        341 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        401 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        461 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 520
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        521 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 580
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        581 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 640
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600

Qy        641 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 700
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

Qy        701 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 760
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720

Qy        761 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 820
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Qy        821 WNPEGTVGTGCNWQEATSI 839
                |||||||||||||||||||
Db        781 WNPEGTVGTGCNWQEATSI 799
```

```
RESULT 14
AAE16093
ID   AAE16093 standard; protein; 799 AA.
XX
AC   AAE16093;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human DNAX Toll like receptor (DTLR) 4 #1.
XX
KW   Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW   interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS   Homo sapiens.
XX
PN   WO200190151-A2.
XX
PD   29-NOV-2001.
XX
PF   23-MAY-2001; 2001WO-US016766.
XX
PR   25-MAY-2000; 2000US-0207558P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Hardiman GT,  Rock FL,  Bazan JF,  Kastelein RA,  Ho SWK,  Liu Y;
XX
DR   WPI; 2002-083085/11.
DR   N-PSDB; AAD26283.
XX
PT   New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT   conditions exhibiting abnormal expression of the receptors of their
PT   ligands, particularly abnormalities manifested by immunological
PT   disorders.
XX
PS   Claim 1; Page 35; 297pp; English.
XX
CC   The invention relates to mammalian receptor proteins, e.g., primate,
CC   human DNAX Toll like receptor (DTLR) protein and their corresponding
CC   nucleic acids. The DTLR is useful for treating conditions exhibiting
CC   abnormal expression of the receptors of their ligands. Such abnormality
CC   is manifested by immunological disorders. In particular, the DTLR is
CC   useful for treating various disease or disorders associated with abnormal
CC   expression or abnormal triggering of response to a ligand. The DTLR is
CC   also useful as an immunogen for the production of antisera or antibodies
CC   specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC   receptor family members, for the DTLR or its various fragments. The
CC   purified DTLR can be used to screen monoclonal antibodies or antigen-
CC   binding fragments. The antibodies are useful for screening expression
CC   libraries for particular expression products. These are useful for
CC   detecting or diagnosing various immunological conditions related to
CC   expression of DTLR or cells that express it. The present sequence is
CC   human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33
XX
SQ   Sequence 799 AA;
```

```
  Query Match             95.1%;  Score 4141;  DB 5;  Length 799;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  799;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         41 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy        101 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        161 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        221 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        281 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        341 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 400
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Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        401 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 460
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Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        461 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        521 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        581 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600

Qy        641 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 700
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Db        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

Qy        701 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 760
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Db        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720

Qy        761 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Qy        821 WNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||
Db        781 WNPEGTVGTGCNWQEATSI 799


RESULT 15
ABB83162
ID   ABB83162 standard; protein; 799 AA.
XX
AC   ABB83162;
XX
DT   09-AUG-2002  (first entry)
XX
DE   Human Toll-like receptor-4, Tlr4.
XX
KW   Human; virucide; antibacterial; fungicide; parasiticide; receptor;
KW   cytostatic; immunostimulatory; scavenger receptor; Toll receptor;
KW   respiratory tract infection; Toll-like receptor; Tlr4.
XX
OS   Homo sapiens.
XX
PN   WO200235236-A1.
XX
PD   02-MAY-2002.
XX
PF   26-OCT-2001; 2001WO-FR003352.
XX
PR   27-OCT-2000; 2000FR-00013883.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
PI   Jeannin P,  Magistrelli G,  Herbault N,  Bonnefoy J;
XX
DR   WPI; 2002-383586/41.
DR   N-PSDB; ABN83318.
XX
PT   Identifying agent that binds to scavenger receptors and signals through a
PT   Toll receptor, useful as carrier or adjuvant in vaccines, promotes a
PT   cytotoxic T cell response.
XX
PS   Disclosure; Page 58-60; 71pp; French.
XX
CC   The present invention relates to a method for identifying new therapeutic
CC   compounds (I) by selecting molecules that bind to scavenger receptors and
CC   signal through a Toll receptor. The present sequence is the protein
CC   sequence for human Toll-like receptor-4, Tlr4, which was used to
CC   illustrate the method of the invention. (I) are useful as carriers and/or
CC   adjuvants in prophylactic or therapeutic vaccines, particularly where the
CC   antigen is derived from a virus, bacterium, yeast, fungus, parasite or
CC   tumour cell, especially a pathogen that causes respiratory tract
CC   infection, also more generally for inducing an immune response. (I) can
CC   also be used for specific targeting of active agents (antigens etc.) to
CC   antigen-presenting cells (especially immature dendritic cells), for
CC   subsequent internalisation by these cells
XX
SQ   Sequence 799 AA;

  Query Match           95.1%;  Score 4141;  DB 5;  Length 799;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  799;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         41 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 100
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Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy        101 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        161 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        221 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        281 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        341 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        401 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        461 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        521 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        581 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600

Qy        641 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

Qy        701 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720

Qy        761 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Qy        821 WNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||
Db        781 WNPEGTVGTGCNWQEATSI 799


Search completed: March 12, 2005, 19:54:56
Job time : 97.4 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:46 ; Search time 23.0639 Seconds
(without alignments)
2715.523 Million cell updates/sec

Title: US-09-396-985B-2
Perfect score: 4355
Sequence: 1 MMSASRLAGTLIPAMAFLSC.....SWNPEGTVGTGCNWQEATSI 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4197	96.4	844	4	US-09-949-016-9438	Sequence 9438, Ap
2	629.5	14.5	661	1	US-08-514-014-4	Sequence 4, Appli
3	629.5	14.5	661	2	US-08-833-823-4	Sequence 4, Appli
4	599.5	13.8	784	4	US-09-982-308B-23	Sequence 23, Appl
5	539	12.4	775	4	US-09-949-016-8799	Sequence 8799, Ap
6	316	7.3	605	3	US-09-063-950-5	Sequence 5, Appli
7	305	7.0	623	4	US-09-949-016-10995	Sequence 10995, A
8	303	7.0	605	1	US-08-190-802A-49	Sequence 49, Appl
9	303	7.0	605	3	US-08-477-346-49	Sequence 49, Appl
10	303	7.0	605	3	US-08-473-089-49	Sequence 49, Appl
11	303	7.0	605	4	US-08-487-072A-49	Sequence 49, Appl
12	303	7.0	605	4	US-09-538-092-1087	Sequence 1087, Ap
13	299.5	6.9	662	4	US-09-538-092-1325	Sequence 1325, Ap
14	299.5	6.9	662	4	US-09-949-016-6619	Sequence 6619, Ap
15	299.5	6.9	665	4	US-09-949-016-10710	Sequence 10710, A
16	299	6.9	1525	3	US-09-191-647-2	Sequence 2, Appli
17	299	6.9	1525	3	US-09-540-245A-2	Sequence 2, Appli
18	299	6.9	1525	3	US-09-540-153-2	Sequence 2, Appli
19	296	6.8	603	1	US-08-190-802A-50	Sequence 50, Appl
20	296	6.8	603	3	US-08-477-346-50	Sequence 50, Appl
21	296	6.8	603	3	US-08-473-089-50	Sequence 50, Appl
22	296	6.8	603	4	US-08-487-072A-50	Sequence 50, Appl
23	292.5	6.7	907	4	US-09-170-496D-264	Sequence 264, App
24	292.5	6.7	907	4	US-09-170-496D-278	Sequence 278, App
25	289.5	6.6	1112	3	US-09-353-585-3	Sequence 3, Appli
26	289	6.6	1529	4	US-09-312-283C-396	Sequence 396, App
27	286	6.6	1112	3	US-09-353-585-2	Sequence 2, Appli
28	285	6.5	1523	3	US-09-182-024A-2	Sequence 2, Appli
29	283.5	6.5	1166	4	US-10-101-464A-900	Sequence 900, App
30	281	6.5	1101	3	US-08-986-485-2	Sequence 2, Appli
31	278	6.4	1091	3	US-08-986-485-5	Sequence 5, Appli
32	275	6.3	620	4	US-09-907-794A-73	Sequence 73, Appl
33	275	6.3	620	4	US-09-905-125A-73	Sequence 73, Appl
34	275	6.3	620	4	US-09-902-775A-73	Sequence 73, Appl
35	275	6.3	620	4	US-09-906-700-73	Sequence 73, Appl
36	275	6.3	620	4	US-09-903-603A-73	Sequence 73, Appl
37	275	6.3	620	4	US-09-904-920A-73	Sequence 73, Appl
38	275	6.3	620	4	US-09-909-064-73	Sequence 73, Appl
39	275	6.3	620	4	US-09-905-381A-73	Sequence 73, Appl
40	275	6.3	620	4	US-09-906-618-73	Sequence 73, Appl
41	272	6.2	1480	3	US-09-191-647-7	Sequence 7, Appli
42	272	6.2	1480	3	US-09-540-245A-7	Sequence 7, Appli
43	272	6.2	1480	3	US-09-540-153-7	Sequence 7, Appli
44	272	6.2	1480	5	PCT-US91-09055-2	Sequence 2, Appli
45	271	6.2	1139	4	US-09-513-505-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9438

Query Match 96.4%; Score 4197; DB 4; Length 844;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          31 EVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEI 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          36 EVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEI 95

Qy          91 QTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLK 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         151 TLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDL 210
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Qy         211 SLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLE 270
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         216 SLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLE 275

Qy         271 KFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNF 330
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         276 KFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNF 335

Qy         331 GWQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGC 390
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Db        336 GWQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGC 395

Qy        391 CSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLI 450

Db        396 CSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLI 455

Qy        451 YLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQ 510

Db        456 YLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQ 515

Qy        511 LSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSS 570

Db        516 LSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSS 575

Qy        571 LAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMN 630

Db        576 LAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMN 635

Qy        631 KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRN 690

Db        636 KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRN 695

Qy        691 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 750

Db        696 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 755

Qy        751 YEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRR 810

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Qy        811 LRKALLDGKSWNPEGTVGTGCNWQEATSI 839

Db        816 LRKALLDGKSWNPEGTVGTGCNWQEATSI 844
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RESULT 2
US-08-514-014-4
; Sequence 4, Application US/08514014
; Patent No. 5707829
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  Kelleher, Kerry
;    APPLICANT:  Carlin, McKeough
;    TITLE OF INVENTION:  DNA SEQUENCES AND SECRETED PROTEINS
;    TITLE OF INVENTION:  ENCODED THEREBY
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc. -- Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/514,014
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI6000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  661 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-514-014-4

  Query Match             14.5%;  Score 629.5;  DB 1;  Length 661;
  Best Local Similarity   29.7%;  Pred. No. 5.3e-49;
  Matches  199;  Conservative  109;  Mismatches  274;  Indels   89;  Gaps   24;

Qy         25 SWEP-CVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVL 83

Db         23 SWDQMCIEKEANKTYNCENLGLSEIPDTLPNTTEFLEFSFNFLPTIHNRTFSRLMNLTFL 82

Qy         84 DLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLEN 143

Db         83 DLTRCQINWIHEDTFQSHHQLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEF 142

Qy        144 FPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPL 203

Db        143 IPVHNLENLESLYLGSNHISSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--A 199

Qy        204 LNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEF 263

Db        200 INLSLNFNGNNVKGIELGAFDSTVFQSL----NFGGTPNLSVIFNGLQNSTTQSLWLGTF 255

Qy        264 RNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIID-LFNCLTNVSSFSLVSVTIER 322

Db        256 EDIDD-EDISSAMLKGLCEMSVESLNLQ--EHRFSDISSTTFQCFTQLQELDLTATHLKG 312

Qy        323 VKDFSYNFGWQHLELVN-----------CKF--GQFPTL-------KLKSLKRLTFTSN 361

Db        313 LPS-----GMKGLNLLKKLVLSVNHFDQLCQISAANFPSLTHLYIRGNVKKLHLGVGCLE 367

Qy        362 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSN-FLG 420

Db        368 KLGN---------LQTLDLSHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKE 418

Qy        421 LEQLEHLDFQ----HSNLKQMSEFS--VFLSLRNLIY--LDISHTHTRVAFNGIFNGLSS 472

Db        419 CPQLELLDLAFTRLHINAPQ-SPFQNLHFLQVLNLTYCFLDTSNQH-------LLAGLPV 470

Qy        473 LEVLKMAGNSFQENFL--PDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHN 530

Db        471 LRHLNLKGNHFQDGTITKTNLLQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHN 530

Qy        531 NFF--SLDTFPY-------KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDF 581

Db        531 SLTCDSIDSLSHLKGIYLNLAANSINIISPRLLPIL----------SQQSTINLSHNPL 579

Qy        582 ACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSV 641

Db        580 DCTCSNIHFLTWYKENLHKLEGSEETTCANPPSLRGVKLSDVKLSCGI--TAIGIFFLIV 637

Qy        642 LVVSVVAVLVY 652

Db        638 FLL-LLAILLF 647
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RESULT 3
US-08-833-823-4
; Sequence 4, Application US/08833823
; Patent No. 5969093
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  Kelleher, Kerry
;    APPLICANT:  Carlin, McKeough
;    TITLE OF INVENTION:  DNA SEQUENCES AND SECRETED PROTEINS
;    TITLE OF INVENTION:  ENCODED THEREBY
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc. -- Legal Affairs
```

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;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/833,823
;      FILING DATE:  10-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/514,014
;      FILING DATE:  11-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI6000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  661 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-833-823-4

  Query Match             14.5%;  Score 629.5;  DB 2;  Length 661;
  Best Local Similarity   29.7%;  Pred. No. 5.3e-49;
  Matches  199;  Conservative  109;  Mismatches  274;  Indels   89;  Gaps   24;

Qy         25 SWEP-CVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVL 83
              ||:  |:|   | || |  |   :||| || :|: |: ||| |  : : :|     |  |
Db         23 SWDQMCIEKEANKTYNCENLGLSEIPDTLPNTTEFLEFSFNFLPTIHNRTFSRLMNLTFL 82

Qy         84 DLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLEN 143
              ||:||:|  | :  :||   ||||:|||||:  :|  : :|   ||: |  ::| :::||
Db         83 DLTRCQINWIHEDTFQSHHQLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEF 142

Qy        144 FPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPL 203
               |: :|: |: | :  | | | | |: |    ||: ||  :| |  |   |:| | |
Db        143 IPVHNLENLESLYLGSNHISSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--A 199

Qy        204 LNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEF 263
              :||||: : | :  |: |||       |    ||     :     ||       | || |
Db        200 INLSLNFNGNNVKGIELGAFDSTVFQSL----NFGGTPNLSVIFNGLQNSTTQSLWLGTF 255

Qy        264 RNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIID-LFNCLTNVSSFSLVSVTIER 322
               :  : |    : |:||| :::|   |   ::   ||    | | | :    | :  ::
Db        256 EDIDD-EDISSAMLKGLCEMSVESLNLQ--EHRFSDISSTTFQCFTQLQELDLTATHLKG 312

Qy        323 VKDFSYNFGWQHLELVN-----------CKF--GQFPTL-------KLKSLKRLTFTSN 361
              :       | : | |:           |:     ||:|        :| |
Db        313 LPS-----GMKGLNLLKKLVLSVNHFDQLCQISAANFPSLTHLYIRGNVKKLHLGVGCLE 367

Qy        362 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSN-FLG 420
              | ||          |: |||| | :    |||       : |: |:|| |  : : |  |
Db        368 KLGN---------LQTLDLSHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKE 418

Qy        421 LEQLEHLDFQ----HSNLKQMSEFS--VFLSLRNLIY--LDISHTHTRVAFNGIFNGLSS 472
               |||  ||      | |  | | |    || : || |  || |: |       :  ||
Db        419 CPQLELLDLAFTRLHINAPQ-SPFQNLHFLQVLNLTYCFLDTSNQH-------LLAGLPV 470

Qy        473 LEVLKMAGNSFQENFL--PDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHN 530
              |  | : || ||:  :   ::   : :|  | || | |  :    ||:||  :  :::|||
Db        471 LRHLNLKGNHFQDGTITKTNLLQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHN 530

Qy        531 NFF--SLDTFPY-------KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDF 581
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             :    |:|:  :          ||: ::   |  |:          |  : :||: |
Db        531 SLTCDSIDSLSHLKGIYLNLAANSINIISPRLLPIL----------SQQSTINLSHNPL 579

Qy        582 ACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSV 641
              |||:  || | |:    |   |  || |   :|: :  : ::| :  | ||:  | |
Db        580 DCTCSNIHFLTWYKENLHKLEGSEETTCANPPSLRGVKLSDVKLSCGI--TAIGIFFLIV 637

Qy        642 LVVSVVAVLVY 652
               :: ::|:|::
Db        638 FLL-LLAILLF 647


RESULT 4
US-09-982-308B-23
; Sequence 23, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
;  APPLICANT: Dalie, Barbara
;  APPLICANT:  Fan, Xuedong
;  APPLICANT:  Lundell, Daniel
;  APPLICANT:  Lunn, Charles A.
;  APPLICANT:  Tan, Jimmy C.
;  APPLICANT:  Zavodny, Paul J.
;  TITLE OF INVENTION: Mammalian TNF-alpha Convertases
;  FILE REFERENCE: JB0601QC
;  CURRENT APPLICATION NUMBER: US/09/982,308B
;  CURRENT FILING DATE:  2001-10-17
;  PRIOR APPLICATION NUMBER: 09/156,163
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 08/889,909
;  PRIOR FILING DATE: 1997-07-10
;  PRIOR APPLICATION NUMBER: 60/021,710
;  PRIOR FILING DATE: 1996-07-12
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;   LENGTH: 784
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-982-308B-23

  Query Match             13.8%;  Score 599.5;  DB 4;  Length 784;
  Best Local Similarity   27.0%;  Pred. No. 4.1e-46;
  Matches  233;  Conservative  128;  Mismatches  282;  Indels  219;  Gaps   38;

Qy         48 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 107
              ||  |  : |:|||| | : :: :          || | |:   | |||: :: ||  |  |
Db         46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 105

Qy        108 ILTGNPIQSLALGAFSGLSSLQKL-----------VAVETNLASLENFPIGHLKT---- 151
               |: | : :|:   |  ||||  |              :: ::|  |:   :|:: |
Db        106 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 165

Qy        152 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK----------IQSI 190
                       |:|| :  : :||:: |:   :: |: || |   :            |:
Db        166 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 224

Qy        191 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 244
              | :||              |  |:  :|  :  |    : : | | ||     :|| |||
Db        225 ECLELR-----------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 271

Qy        245 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 297
              |  ||  ||      |   | ||   |    :|    |||    :   || |
Db        272 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 326

Qy        298 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 357
              |:  |::    |       :|:|  | |          || |   |
Db        327 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------ 357

Qy        358 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 412
                          | |||:|||| |       |     |    :    ||: | | |
Db        358 ------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 397
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Qy        413 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 472
Db        398 -------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 422

Qy        473 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 529
Db        423 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 466

Qy        530 N--NFFSLD---------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 571
Db        467 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 525

Qy        572 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 626
Db        526 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 581

Qy        627 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 674
Db        582 VSECHRIALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 641

Qy        675 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 734
Db        642 DAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 700

Qy        735 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQ-VELYRLLSRNT 793
Db        701 FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKT 760

Qy        794 YLEWEDSVLGRHIFWRRLRKAL 815
Db        761 YLEWPMDEAQREGFWVNLRAAI 782
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RESULT 5
US-09-949-016-8799
; Sequence 8799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8799

Query Match 12.4%; Score 539; DB 4; Length 775;
Best Local Similarity 26.6%; Pred. No. 1.6e-40;
Matches 218; Conservative 120; Mismatches 264; Indels 218; Gaps 37;

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Qy         48 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 107
Db         81 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 140

Qy        108 ILTGNPIQSLALGAFSGLSSLQKL------------VAVETNLASLENFPIGHLKT---- 151
Db        141 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 200

Qy        152 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK-----------IQSI 190
Db        201 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 259

Qy        191 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 244
Db        260 ECLELR------------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 306

Qy        245 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 297
Db        307 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 361

Qy        298 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 357
Db        362 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------- 392

Qy        358 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 412
Db        393 -------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 432

Qy        413 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 472
Db        433 -------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 457

Qy        473 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 529
Db        458 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 501

Qy        530 N--NFFSLD---------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 571
Db        502 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 560

Qy        572 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 626
Db        561 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 616

Qy        627 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 674
Db        617 VSECHRTALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 676

Qy        675 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 734
Db        677 DAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 735

Qy        735 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKV 774
Db        736 FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPI 775
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RESULT 6
US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-09-063-950-5

Query Match 7.3%; Score 316; DB 3; Length 605;
Best Local Similarity 24.4%; Pred. No. 4.1e-20;
Matches 157; Conservative 94; Mismatches 242; Indels 150; Gaps 23;

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Qy         33 VPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQT 92
Db         53 VNELSVFCSSRNLTRLPDGIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGS 112
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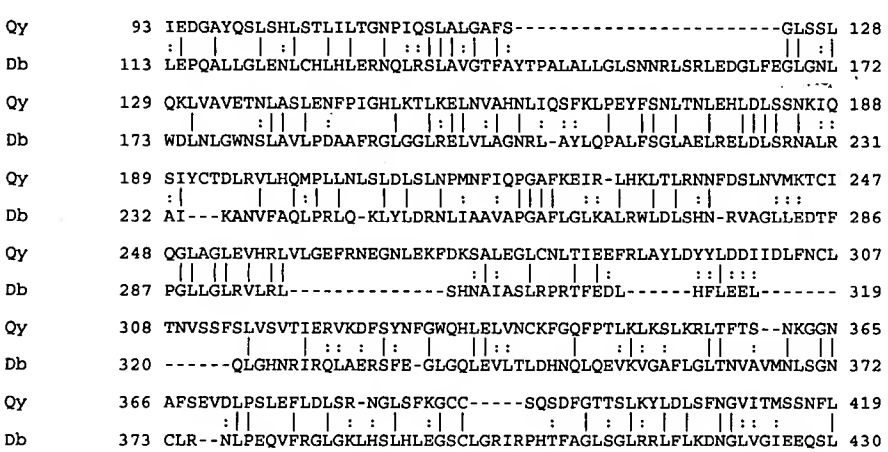
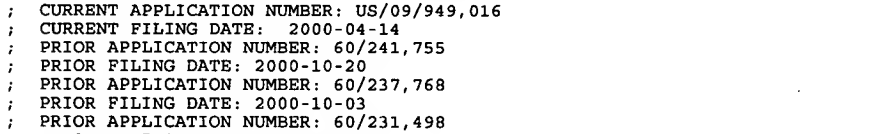


RESULT 7
US-09-949-016-10995
; Sequence 10995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10995
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10995

Query Match 7.0%; Score 305; DB 4; Length 623;
Best Local Similarity 24.3%; Pred. No. 4.4e-19;
Matches 171; Conservative 96; Mismatches 260; Indels 178; Gaps 28;



RESULT 8
US-08-190-802A-49
; Sequence 49, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:

```
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  8600-0139
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-190-802A-49

  Query Match             7.0%;  Score 303;  DB 1;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 6.4e-19;
  Matches  157;  Conservative   91;  Mismatches  243;  Indels  152;  Gaps   24;

Qy         40 CMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQ 99
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy        100 SLSHLSTLILTGNPIQSLALGAFS----------------------GLSSLQKLVAVE 135
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        136 TNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDL 195
Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KA 235

Qy        196 RVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLE 254
Db        236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLR 293

Qy        255 VHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFS 314
Db        294 VLRL--------------SHNAIASLRPRTFKDL------HFLEEL------------Q 320

Qy        315 LVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDL 372
Db        321 LGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NL 377

Qy        373 PSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLE 425
Db        378 PEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELL 437

Qy        426 HLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQE 485
Db        438 ELDLTSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE 472

Qy        486 NFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLN 544
Db        473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ--- 524

Qy        545 SLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD-------- 596
Db        525 ----------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSA 557

Qy        597 -QRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 638
Db        558 VPRFVQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594


RESULT 9
US-08-477-346-49
; Sequence 49, Application US/08477346
; Patent No. 6262023
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,346
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/487,072
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-477-346-49

  Query Match             7.0%;  Score 303;  DB 3;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 6.4e-19;
  Matches  157;  Conservative   91;  Mismatches  243;  Indels  152;  Gaps   24;

Qy         40 CMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQ 99
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy        100 SLSHLSTLILTGNPIQSLALGAFS----------------------GLSSLQKLVAVE 135
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        136 TNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDL 195
Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KA 235

Qy        196 RVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLE 254
Db        236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLR 293

Qy        255 VHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFS 314
Db        294 VLRL--------------SHNAIASLRPRTFKDL------HFLEEL------------Q 320

Qy        315 LVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDL 372
Db        321 LGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NL 377

Qy        373 PSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLE 425
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Db        378 PEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELL 437

Qy        426 HLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQE 485

Db        438 ELDLTSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE 472

Qy        486 NFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLN 544

Db        473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ--- 524

Qy        545 SLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD-------- 596

Db        525 ----------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSA 557

Qy        597 -QRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 638

Db        558 VPRFVQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594


RESULT 10
US-08-473-089-49
; Sequence 49, Application US/08473089
; Patent No. 6342368
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/473,089
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-473-089-49

  Query Match             7.0%;  Score 303;  DB 3;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 6.4e-19;
  Matches  157;  Conservative   91;  Mismatches  243;  Indels  152;  Gaps   24;

Qy         40 CMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQ 99

Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy        100 SLSHLSTLILTGNPIQSLALGAFS----------------------GLSSLQKLVAVE 135

Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        136 TNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDL 195

Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KA 235

Qy        196 RVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLE 254

Db        236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLR 293

Qy        255 VHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFS 314

Db        294 VLRL--------------SHNAIASLRPRTFKDL------HFLEEL-------------Q 320

Qy        315 LVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDL 372

Db        321 LGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NL 377

Qy        373 PSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLE 425

Db        378 PEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELL 437

Qy        426 HLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQE 485

Db        438 ELDLTSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE 472

Qy        486 NFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLN 544

Db        473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ--- 524

Qy        545 SLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD-------- 596

Db        525 ----------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSA 557

Qy        597 -QRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 638

Db        558 VPRFVQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594


RESULT 11
US-08-487-072A-49
; Sequence 49, Application US/08487072A
; Patent No. 6423684
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,072A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.20
;    TELECOMMUNICATION INFORMATION:
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;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-487-072A-49

  Query Match             7.0%;  Score 303;  DB 4;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 6.4e-19;
  Matches  157;  Conservative   91;  Mismatches  243;  Indels  152;  Gaps   24;

Qy         40 CMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQ 99
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy        100 SLSHLSTLILTGNPIQSLALGAFS-----------------------GLSSLQKLVAVE 135
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        136 TNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDL 195
Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KA 235

Qy        196 RVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLE 254
Db        236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLR 293

Qy        255 VHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFS 314
Db        294 VLRL--------------SHNAIASLRPRTFKDL------HFLEEL-------------Q 320

Qy        315 LVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDL 372
Db        321 LGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NL 377

Qy        373 PSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLE 425
Db        378 PEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELL 437

Qy        426 HLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQE 485
Db        438 ELDLTSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE 472

Qy        486 NFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLN 544
Db        473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ--- 524

Qy        545 SLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD-------- 596
Db        525 ----------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSA 557

Qy        597 -QRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 638
Db        558 VPRFVQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594


RESULT 12
US-09-538-092-1087
; Sequence 1087, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1087
;   LENGTH: 605
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number P35858
US-09-538-092-1087

  Query Match             7.0%;  Score 303;  DB 4;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 6.4e-19;
  Matches  157;  Conservative   91;  Mismatches  243;  Indels  152;  Gaps   24;

Qy         40 CMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQ 99
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy        100 SLSHLSTLILTGNPIQSLALGAFS-----------------------GLSSLQKLVAVE 135
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        136 TNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDL 195
Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KA 235

Qy        196 RVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLE 254
Db        236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLR 293

Qy        255 VHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFS 314
Db        294 VLRL--------------SHNAIASLRPRTFKDL------HFLEEL-------------Q 320

Qy        315 LVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDL 372
Db        321 LGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NL 377

Qy        373 PSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLE 425
Db        378 PEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELL 437

Qy        426 HLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQE 485
Db        438 ELDLTSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE 472

Qy        486 NFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLN 544
Db        473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ--- 524

Qy        545 SLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD-------- 596
Db        525 ----------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSA 557

Qy        597 -QRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 638
Db        558 VPRFVQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594


RESULT 13
US-09-538-092-1325
; Sequence 1325, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
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;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1325
;   LENGTH: 662
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number Q14392
US-09-538-092-1325

  Query Match             6.9%;  Score 299.5;  DB 4;  Length 662;
  Best Local Similarity   25.9%;  Pred. No. 1.6e-18;
  Matches  187;  Conservative   94;  Mismatches  259;  Indels  181;  Gaps   35;

Qy         28 PCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSR 87
              ||  |   ::  |  |   ::|  ||  |: |||| | || : :     :  |: ||||
Db         25 PCKMVDKKVS--CQVLGLLQVPSVLPPDTETLDLSGNQLRSILASPLGFYTALRHLDLST 82

Qy         88 CEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLAS-----LE 142
               ||  :: ||:|:|:||  | |  | :      :  ||  | :: ::: :  |     ||
Db         83 NEISFLQPGAFQALTHLEHLSLAHNRLAMATALSAGGLGPLPRVTSLDLSGNSLYSGLLE 142

Qy        143 NFPIGHLKTLKELNVAHNLIQSFKLPEY-FSNLTNLEHLDLSSNKIQSIYCTDLRVLHQM 201
              :|   :|  |::| | :   :|  : | ::  || ||| || :  |       | ::
Db        143 RL-LGEAPSLHTLSLAENSLT--RLTRHTFRDMPALEQLDLHSNVLMDIEDGAFEGLPRL 199

Qy        202 PLLNLS-----------------LDLSLNPMNFI----QPGAFKEIRLHKLTLRNN---- 236
              ||||                 ||||  | :       || |  | :|  | || |
Db        200 THLNLSRNSLTCISDFSLQQLRVLDLSCNSIEAFQTASQPQA--EFQLTWLDLRENKLLH 257

Qy        237 FDSLNVMKTCIQGLAGLEVHRLVLGEFRN------------------EGNLEKFDKSAL 277
              |  |  :   |     : ||  |  ::                  ||      | |
Db        258 FPDLAALPRLIYLNLSNNLIRLPTGPPQDSKGIHAPSEGWSALPLSAPSGNASGRPLSQL 317

Qy        278 EGLCNLTIEEFRLAYLDYYLDDIIDLF------NCLTNVSSFSLVSVTIERVKDFSYNFG 331
              | :|:  |  |    | :|: : |       |||    :  | |:    : | |:|
Db        318 LNL-DLSYNEIEL-IPDSFLEHLTSLCFLNLSRNCLRTFEARRLGSLPCLMLLDLSHN-A 374

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEV------DLPSLEFLDLSRNGL 385
              : |||      |   || |:             |||  ::      :| ||: |:|  | :
Db        375 LETLELGARALGSLRTLLLQ-----------GNALRDLPPYTFANLASLQRLNLQGNRV 422

Qy        386 S---------FKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQ 436
              |          || : |  | |||: | |  | :          | |    | |: | :
Db        423 SPCGGPDEPGPSGCVAFS--GITSLRSLSLVDNEI----------ELLRAGAFLHTPLTE 470

Qy        437 MSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGL-SSLEVLKMAGNSFQ--ENFLPDIFT 493
                          ||:|          |   || :|||| : ||     :  ||
Db        471 --------------LDLSSNPGLEVATGALGGLEASLEVLALQGNGLMVLQVDLPCFIC 515

Qy        494 ELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSL 553
                |  |:|:: :|  |   |:    ||:||::  || |||   |   :  |:
Db        516 ----LKRLNLAENRLSHL--PAWTQAVSLEVLDL-RNNSFSL--LPGSAMGGLE------ 560

Qy        554 NHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQ-RQLLVEVERME---C 609
                          :||  | | |  :| | :       |:  |  |  |:|:  :   |
Db        561 --------------TSLRRLYLQGNPLSC-CGN----GWLAAQLHQGRVDVDATQDLIC 600

Qy        610 ATPSDKQGMPVLSLNIT----CQMN--KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAG 663
              | ::    :||:      |:    | |  : :|: ::|| :          |  ||
Db        601 RFSSQEE----VSLSHVRPEDCEKGGLKNINLIIILTFILVSAIL---------LTTLAA 647

Qy        664 C 664
              |
Db        648 C 648


RESULT 14
US-09-949-016-6619
; Sequence 6619, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6619
;   LENGTH: 662
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-6619

  Query Match             6.9%;  Score 299.5;  DB 4;  Length 662;
  Best Local Similarity   25.9%;  Pred. No. 1.6e-18;
  Matches  187;  Conservative   94;  Mismatches  259;  Indels  181;  Gaps   35;

Qy         28 PCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSR 87
              ||  |   ::  |  |   ::|  ||  |: |||| | || : :     :  |: ||||
Db         25 PCKMVDKKVS--CQVLGLLQVPSVLPPDTETLDLSGNQLRSILASPLGFYTALRHLDLST 82

Qy         88 CEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLAS-----LE 142
               ||  :: ||:|:|:||  | |  | :      :  ||  | :: ::: :  |     ||
Db         83 NEISFLQPGAFQALTHLEHLSLAHNRLAMATALSAGGLGPLPRVTSLDLSGNSLYSGLLE 142

Qy        143 NFPIGHLKTLKELNVAHNLIQSFKLPEY-FSNLTNLEHLDLSSNKIQSIYCTDLRVLHQM 201
              :|   :|  |::| | :   :|  : | ::  || ||| || :  |       | ::
Db        143 RL-LGEAPSLHTLSLAENSLT--RLTRHTFRDMPALEQLDLHSNVLMDIEDGAFEGLPRL 199

Qy        202 PLLNLS-----------------LDLSLNPMNFI----QPGAFKEIRLHKLTLRNN---- 236
              ||||                 ||||  | :       || |  | :|  | || |
Db        200 THLNLSRNSLTCISDFSLQQLRVLDLSCNSIEAFQTASQPQA--EFQLTWLDLRENKLLH 257

Qy        237 FDSLNVMKTCIQGLAGLEVHRLVLGEFRN------------------EGNLEKFDKSAL 277
              |  |  :   |     : ||  |  ::                  ||      | |
Db        258 FPDLAALPRLIYLNLSNNLIRLPTGPPQDSKGIHAPSEGWSALPLSAPSGNASGRPLSQL 317

Qy        278 EGLCNLTIEEFRLAYLDYYLDDIIDLF------NCLTNVSSFSLVSVTIERVKDFSYNFG 331
              | :|:  |  |    | :|: : |       |||    :  | |:    : | |:|
Db        318 LNL-DLSYNEIEL-IPDSFLEHLTSLCFLNLSRNCLRTFEARRLGSLPCLMLLDLSHN-A 374

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEV------DLPSLEFLDLSRNGL 385
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Db        375 LETLELGARALGSLRTLLLQ-----------GNALRDLPPYTFANLASLQRLNLQGNRV 422

Qy        386 S---------FKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQ 436
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Db        423 SPCGGPDEPGPSGCVAFS--GITSLRSLSLVDNEI----------ELLRAGAFLHTPLTE 470

Qy        437 MSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGL-SSLEVLKMAGNSFQ--ENFLPDIFT 493
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Db        471 --------------LDLSSNPGLEVATGALGGLEASLEVLALQGNGLMVLQVDLPCFIC 515

Qy        494 ELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSL 553
                |  |:|:: :|  |   |:    ||:||::  || |||   |   :  |:
Db        516 ----LKRLNLAENRLSHL--PAWTQAVSLEVLDL-RNNSFSL--LPGSAMGGLE------ 560
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Qy        554 NHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQ-RQLLVEVERME---C 609
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Db        561 --------------TSLRRLYLQGNPLSC-CGN----GWLAAQLHQGRVDVDATQDLIC 600

Qy        610 ATPSDKQGMPVLSLNIT----CQMN--KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAG 663
                | ::    :||:      |:    | |  : :|: ::|| :           |  ||
Db        601 RFSSQEE----VSLSHVRPEDCEKGGLKNINLIIILTFILVSAIL---------LTTLAA 647

Qy        664 C 664
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Db        648 C 648


RESULT 15
US-09-949-016-10710
; Sequence 10710, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10710
;   LENGTH: 665
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10710

  Query Match             6.9%;  Score 299.5;  DB 4;  Length 665;
  Best Local Similarity   25.9%;  Pred. No. 1.6e-18;
  Matches  187;  Conservative   94;  Mismatches  259;  Indels  181;  Gaps   35;

Qy         28 PCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSR 87
              ||  |   ::  |  |   ::|  ||  |: |||| | || : :     :  |: ||||
Db         28 PCKMVDKKVS--CQVLGLLQVPSVLPPDTETLDLSGNQLRSILASPLGFYTALRHLDLST 85

Qy         88 CEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLAS-----LE 142
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Db         86 NEISFLQPGAFQALTHLEHLSLAHNRLAMATALSAGGLGPLPRVTSLDLSGNSLYSGLLE 145

Qy        143 NFPIGHLKTLKELNVAHNLIQSFKLPEY-FSNLTNLEHLDLSSNKIQSIYCTDLRVLHQM 201
                :|   :|  |::| | :   :|  : | ::  || ||| || :  |        | ::
Db        146 RL-LGEAPSLHTLSLAENSLT--RLTRHTFRDMPALEQLDLHSNVLMDIEDGAFEGLPRL 202

Qy        202 PLLNLS----------------LDLSLNPMNFI----QPGAFKEIRLHKLTLRNN---- 236
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Db        203 THLNLSRNSLTCISDFSLQQLRVLDLSCNSIEAFQTASQPQA--EFQLTWLDLRENKLLH 260

Qy        237 FDSLNVMKTCIQGLAGLEVHRLVLGEFRN------------------EGNLEKFDKSAL 277
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Db        261 FPDLAALPRLIYLNLSNNLIRLPTGPPQDSKGIHAPSEGWSALPLSAPSGNASGRPLSQL 320

Qy        278 EGLCNLTIEEFRLAYLDYYLDDIIDLF------NCLTNVSSFSLVSVTIERVKDFSYNFG 331
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Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEV------DLPSLEFLDLSRNGL 385
               : |||      |   || |:             |||  ::      :| ||: |:|  | :
Db        378 LETLELGARALGSLRTLLLQ------------GNALRDLPPYTFANLASLQRLNLQGNRV 425

Qy        386 S---------FKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQ 436
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Db        426 SPCGGPDEPGPSGCVAFS--GITSLRSLSLVDNEI----------ELLRAGAFLHTPLTE 473

Qy        437 MSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGL-SSLEVLKMAGNSFQ--ENFLPDIFT 493
                                ||:|          |   || :||||| : ||     :  ||
Db        474 --------------LDLSSNPGLEVATGALGGLEASLEVLALQGNGLMVLQVDLPCFIC 518

Qy        494 ELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSL 553
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Db        519 ----LKRLNLAENRLSHL--PAWTQAVSLEVLDL-RNNSFSL--LPGSAMGGLE------ 563

Qy        554 NHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQ-RQLLVEVERME---C 609
                          :||  | |  |  :| | :     |:  |  |  |:|:  :   |
Db        564 --------------TSLRRLYLQGNPLSC-CGN----GWLAAQLHQGRVDVDATQDLIC 603

Qy        610 ATPSDKQGMPVLSLNIT----CQMN--KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAG 663
                | ::    :||:      |:    | |  : :|: ::|| :           |  ||
Db        604 RFSSQEE----VSLSHVRPEDCEKGGLKNINLIIILTFILVSAIL---------LTTLAA 650

Qy        664 C 664
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Db        651 C 651


Search completed: March 12, 2005, 19:58:48
Job time : 27.0639 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:55:29 ; Search time 74.2496 Seconds
(without alignments)
3727.157 Million cell updates/sec

Title: US-09-396-985B-2
Perfect score: 4355
Sequence: 1 MMSASRLAGTLIPAMAFLSC.....SWNPEGTVGTGCNWQEATSI 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4335.5	99.6	837	10	US-09-950-041-26	Sequence 26, Appl
2	4141	95.1	799	10	US-09-950-041-8	Sequence 8, Appli
3	4141	95.1	799	14	US-10-128-166-7	Sequence 7, Appli
4	4141	95.1	799	16	US-10-732-563-8	Sequence 8, Appli
5	4141	95.1	799	16	US-10-732-796A-8	Sequence 8, Appli
6	663	15.2	661	15	US-10-038-854-135	Sequence 135, App
7	663	15.2	661	15	US-10-037-417-107	Sequence 107, App
8	629.5	14.5	661	13	US-10-114-893-10	Sequence 10, Appl
9	629.5	14.5	661	15	US-10-038-854-134	Sequence 134, App
10	603.5	13.9	784	10	US-09-950-041-4	Sequence 4, Appli
11	603.5	13.9	784	15	US-10-456-947-46	Sequence 46, Appl
12	602.5	13.8	784	14	US-10-095-627-12	Sequence 12, Appl
13	602.5	13.8	784	16	US-10-732-563-4	Sequence 4, Appli
14	602.5	13.8	784	16	US-10-732-796A-4	Sequence 4, Appli
15	602.5	13.8	784	17	US-10-741-600-1390	Sequence 1390, Ap
16	602.5	13.8	784	17	US-10-741-600-1391	Sequence 1391, Ap
17	599.5	13.8	784	13	US-10-145-014-23	Sequence 23, Appl
18	580.5	13.3	1032	10	US-09-954-987B-192	Sequence 192, App
19	580.5	13.3	1032	14	US-10-272-502A-31	Sequence 31, Appl
20	580.5	13.3	1032	15	US-10-407-952-32	Sequence 32, Appl
21	567	13.0	1050	10	US-09-954-987B-175	Sequence 175, App
22	567	13.0	1050	14	US-10-272-502A-22	Sequence 22, Appl
23	567	13.0	1050	15	US-10-407-952-26	Sequence 26, Appl
24	534	12.3	1032	10	US-09-950-041-37	Sequence 37, Appl
25	534	12.3	1040	9	US-09-864-761-38325	Sequence 38325, A
26	534	12.3	1041	10	US-09-954-987B-184	Sequence 184, App
27	534	12.3	1041	10	US-09-954-987B-186	Sequence 186, App
28	534	12.3	1041	14	US-10-272-502A-26	Sequence 26, Appl
29	534	12.3	1041	15	US-10-407-952-28	Sequence 28, Appl
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31	534	12.3	1041	16	US-10-732-796A-16	Sequence 16, Appl
32	533	12.2	1041	9	US-09-168-978-3	Sequence 3, Appli
33	533	12.2	1041	9	US-09-978-295A-498	Sequence 498, App
34	533	12.2	1041	9	US-09-978-697-498	Sequence 498, App
35	533	12.2	1041	9	US-09-978-192A-498	Sequence 498, App
36	533	12.2	1041	9	US-09-999-832A-498	Sequence 498, App
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39	533	12.2	1041	10	US-09-978-585A-498	Sequence 498, App
40	533	12.2	1041	10	US-09-978-191A-498	Sequence 498, App
41	533	12.2	1041	10	US-09-978-403A-498	Sequence 498, App
42	533	12.2	1041	10	US-09-978-564A-498	Sequence 498, App
43	533	12.2	1041	10	US-09-999-833A-498	Sequence 498, App
44	533	12.2	1041	10	US-09-981-915A-498	Sequence 498, App
45	533	12.2	1041	10	US-09-978-824-498	Sequence 498, App

ALIGNMENTS

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RESULT 1
US-09-950-041-26
; Sequence 26, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
;  APPLICANT: Hardiman, Gerard T.
;  APPLICANT:  Rock, Fernando L.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  APPLICANT:  Ho, Stephen W.K.
;  APPLICANT:  Liu, Yong-Jun
;  TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
;  FILE REFERENCE: DX0724XK1
;  CURRENT APPLICATION NUMBER: US/09/950,041
;  CURRENT FILING DATE:  2002-05-06
;  PRIOR APPLICATION NUMBER: 09/728,540
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 60/207,558
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 09/073,363
;  PRIOR FILING DATE: 1999-06-05
;  PRIOR APPLICATION NUMBER: 60/044,293
;  PRIOR FILING DATE: 1997-05-07
;  PRIOR APPLICATION NUMBER: 60/072,212
;  PRIOR FILING DATE: 1998-01-22
;  PRIOR APPLICATION NUMBER: 60/076,947
;  PRIOR FILING DATE: 1998-03-05
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 837
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-950-041-26

  Query Match             99.6%;  Score 4335.5;  DB 10;  Length 837;
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  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  837;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

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Qy         62 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 121
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Qy        122 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 181
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Db        120 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 179

Qy        182 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 239

Qy        242 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 301
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Qy        362 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 421
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Qy        422 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 481
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Db        420 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 479

Qy        482 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 541
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Qy        662 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 721
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Db        660 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 719

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Db        720 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 779

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RESULT 2
US-09-950-041-8
; Sequence 8, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
;  APPLICANT: Hardiman, Gerard T.
;  APPLICANT:  Rock, Fernando L.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  APPLICANT:  Ho, Stephen W.K.
;  APPLICANT:  Liu, Yong-Jun
;  TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
;  FILE REFERENCE: DX0724XK1
;  CURRENT APPLICATION NUMBER: US/09/950,041
;  CURRENT FILING DATE:  2002-05-06
;  PRIOR APPLICATION NUMBER: 09/728,540
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 60/207,558
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 09/073,363
;  PRIOR FILING DATE: 1999-06-05
;  PRIOR APPLICATION NUMBER: 60/044,293
;  PRIOR FILING DATE: 1997-05-07
;  PRIOR APPLICATION NUMBER: 60/072,212
;  PRIOR FILING DATE: 1998-01-22
;  PRIOR APPLICATION NUMBER: 60/076,947
;  PRIOR FILING DATE: 1998-03-05
;  NUMBER OF SEQ ID NOS: 45
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;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-950-041-8

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Qy        101 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        161 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        221 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        281 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        341 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        401 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        461 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        521 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        581 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600

Qy        641 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

Qy        701 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720
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Qy        761 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Qy        821 WNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||
Db        781 WNPEGTVGTGCNWQEATSI 799


RESULT 3
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US20030077279A1
; GENERAL INFORMATION:
;  APPLICANT: ARDITI, MOSHE
;  APPLICANT:  RAJAVASHISTH, TRIPATHI
;  APPLICANT:  SHAH, PREDIMAN K.
;  TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
;  TITLE OF INVENTION:  TOLL-LIKE RECEPTOR-4
;  FILE REFERENCE: 81476-0255398
;  CURRENT APPLICATION NUMBER: US/10/128,166
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-128-166-7

  Query Match             95.1%;  Score 4141;  DB 14;  Length 799;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  799;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         41 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy        101 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        161 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        221 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        281 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        341 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        401 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        461 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        521 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        581 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600

Qy        641 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

Qy        701 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720

Qy        761 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Qy        821 WNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||
Db        781 WNPEGTVGTGCNWQEATSI 799


RESULT 4
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
;  APPLICANT: Gupta, Shalley K.
;  APPLICANT:  Ghosh, Tarun K.
;  APPLICANT:  Fink, Jason R.
;  TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
;  FILE REFERENCE: 58183WO003
;  CURRENT APPLICATION NUMBER: US/10/732,563
;  CURRENT FILING DATE:  2003-12-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-732-563-8

  Query Match             95.1%;  Score 4141;  DB 16;  Length 799;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  799;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         41 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy        101 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        161 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        221 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        281 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        341 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        401 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        461 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 520
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Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        521 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        581 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600

Qy        641 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

Qy        701 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720

Qy        761 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Qy        821 WNPEGTVGTGCNWQEATSI 839
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Db        781 WNPEGTVGTGCNWQEATSI 799
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RESULT 5
US-10-732-796A-8
; Sequence 8, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
; FILE REFERENCE: 58182US004
; CURRENT APPLICATION NUMBER: US/10/732,796A
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-796A-8

Query Match 95.1%; Score 4141; DB 16; Length 799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         41 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy        101 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        161 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        221 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        281 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        341 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        401 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        461 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        521 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        581 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600

Qy        641 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

Qy        701 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720

Qy        761 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Qy        821 WNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||
Db        781 WNPEGTVGTGCNWQEATSI 799
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RESULT 6
US-10-038-854-135
; Sequence 135, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29

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;  PRIOR APPLICATION NUMBER: 60/259,415
;  PRIOR FILING DATE: 2001-01-02
;  PRIOR APPLICATION NUMBER: 60/259,785
;  PRIOR FILING DATE: 2001-01-04
;  PRIOR APPLICATION NUMBER: 60/269,814
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/279,832
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/279,833
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/279,863
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/283,889
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,447
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: 60/286,683
;  PRIOR FILING DATE: 2001-04-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 411
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
;   LENGTH: 661
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-038-854-135

  Query Match             15.2%;  Score 663;  DB 15;  Length 661;
  Best Local Similarity   28.7%;  Pred. No. 4.1e-44;
  Matches  196;  Conservative  116;  Mismatches  289;  Indels   82;  Gaps   16;

Qy         14 AMAFLSC-VRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSY 72
              |:   ||      | : |:|    | || |   |    :||  || ||: |: ||| |  : :
Db         12 ALFLASCRATTSSDQKCIEKEVNKTYNCENLGLNEIPGTLPNSTECLEFSFNVLPTIQNT 71

Qy         73 SFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLV 132
              :|      |  |||:||:|  | :  :||   | ||:|| ||:  :|  | ||  :|: |
Db         72 TFSRLINLTFLDLTRCQIYWIHEDTFQSQHRLDTLVLTANPLIFMAETALSGPKALKHLF 131

Qy        133 AVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYC 192
              ::| ::|::  |: : |||: | :  | | | |||: |     |: ||  :| |  :
Db        132 FIQTGISSIDFIPLHNQKTLESLYLGSNHISSIKLPKGFPT-EKLKVLDFQNNAIHYLSK 190

Qy        193 TDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAG 252
              |:  | |    ||||:|: | :  |:||||       |    ||      :    :||
Db        191 EDMSSLQQ--ATNLSLNLNGNDIAGIEPGAFDSAVFQSL----NFGGTQNLLVIFKGLKN 244

Qy        253 LEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSS 312
              :  | || | :  : |    :  |||| :::|   |     |: :   : |:| :
Db        245 STIQSLWLGTFEDMDD-EDISPAVFEGLCEMSVESINL-QKHYFFNISSNTFHCFS---- 298

Qy        313 FSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPT--LKLKSLKRLTFTSNKGGN--AFS 368
                          | | |:|      : |:  : | :||:|  ::||  |    |
Db        299 -----------------GLQELDLTATHLSELPSGLVGLSTLKKLVLSANKFENLCQIS 340

Qy        369 EVDLPSLEF-----------------------LDLSRNGLSFKGCCSQSDFGTTSLKY 403
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Db        341 ASNFPSLTHLSIKGNTKRLELGTGCLENLENLRELDLSHDDIETSDCCNLQLRNLSHLQS 400

Qy        404 LDLSFNGVITMSSN-FLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVA 462
              |:||:|  ::: :  |    ||| ||   : ||     | | :|  |  |::||:   ::
Db        401 LNLSYNEPLSLKTEAFKECPQLELLDLAFTRLKVKDAQSPFQNLHLLKVLNLSHSLLDIS 460

Qy        463 FNGIFNGLSSLEVLKMAGNSFQENFL--PDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 520
                :|:|| :|: | : || | :  :    |  | || | |  :    || ||
Db        461 SEQLFDGLPALQHLNLQGNHFPKGNIQKTNSLQTLGRLEILVLSFCDLSSIDQHAFTSLK 520

Qy        521 SLQVLNMSHNNFFSLDTFPYKCLNSLQ--VLDYSLNHIMTSKKQELQHFPSSLAFL---- 574
              :  :::|||    | :   : |:|:   |: : |||           || |  |
Db        521 MMNHVDLSHNR---LTSSSIEALSHLKGIYLNLASNHISII-------LPSLLPILSQQR 570

Qy        575 --NLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKT 632
                || ||   ||| :  ||:| |:  | | : |   |  |   :|: :  : ::| |
Db        571 TINLRQNPLDCTCSNIYFLEWYKENMQKLEDTEDTLCENPPLLRGVRLSDVTLSCSMAAV 630

Qy        633 IIGVSVLSVLVVSVVAVLVYKFY 655
                |   :: :|| ::: :   |::
Db        631 GIFFLIVFLLVFAILLIFAVKYF 653


RESULT 7
US-10-037-417-107
; Sequence 107, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
;  APPLICANT: Kekuda, Ramesh
;  APPLICANT:  Alsobrook II, John P
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Li, Li
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Sciore, Paul
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Rothenberg, Mark
;  APPLICANT:  Stone, David J
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Anderson, David W
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Eisen, Andrew J
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-235
;  CURRENT APPLICATION NUMBER: US/10/037,417
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: 60/260,018
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: 60/260,360
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/272,411
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/272,817
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: 60/291,186
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: 60/303,231
;  PRIOR FILING DATE: 2001-07-05
;  PRIOR APPLICATION NUMBER: 60/305,060
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: 60/318,405
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/318,700
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
;   LENGTH: 661
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-037-417-107

  Query Match             15.2%;  Score 663;  DB 15;  Length 661;
  Best Local Similarity   28.7%;  Pred. No. 4.1e-44;
  Matches  196;  Conservative  116;  Mismatches  289;  Indels   82;  Gaps   16;

Qy         14 AMAFLSC-VRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSY 72
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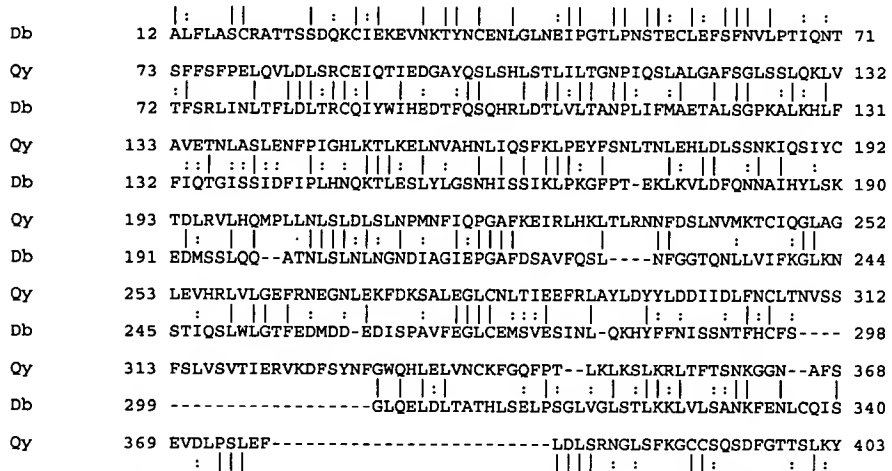
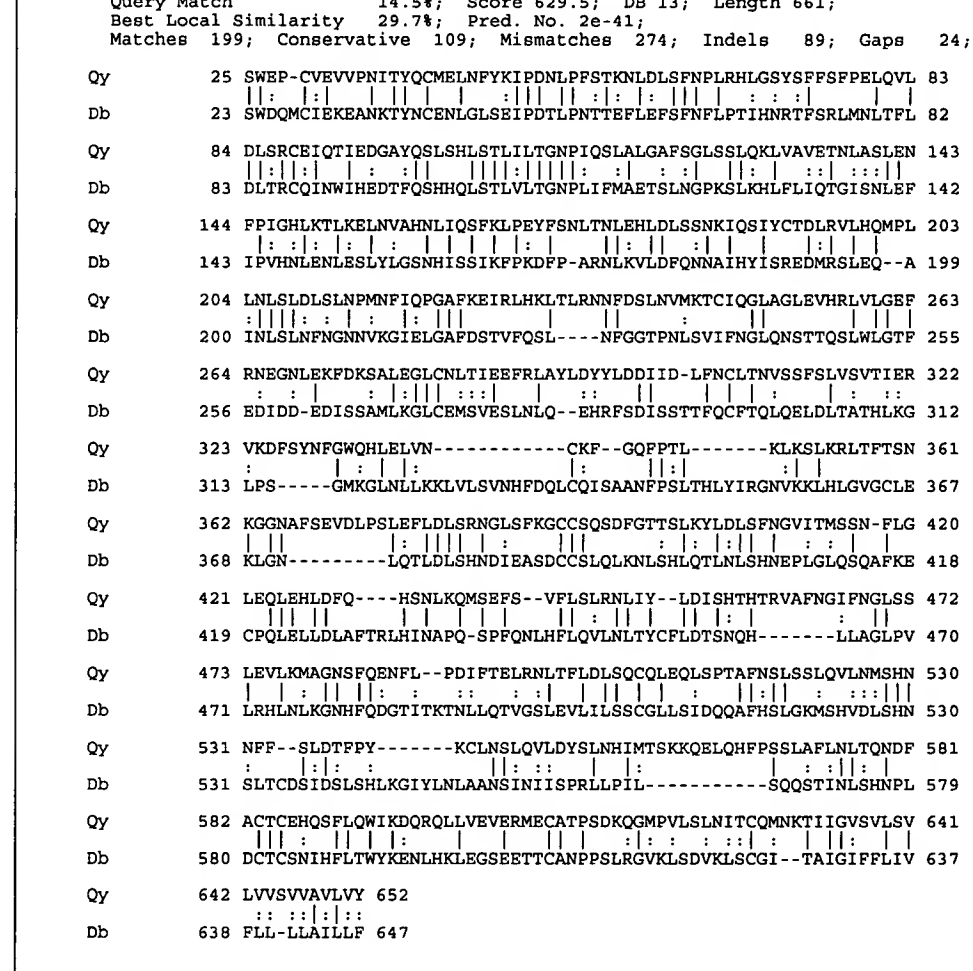


RESULT 8
US-10-114-893-10
; Sequence 10, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; CURRENT FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; EARLIER FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-10

Query Match 14.5%; Score 629.5; DB 13; Length 661;
Best Local Similarity 29.7%; Pred. No. 2e-41;
Matches 199; Conservative 109; Mismatches 274; Indels 89; Gaps 24;



RESULT 9
US-10-038-854-134
; Sequence 134, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar

```
;  APPLICANT:  Spaderna, Steven K
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Gusev, Vladimir Y
;  APPLICANT:  Gangolli, Esha A
;  APPLICANT:  Guo, Xiaojia S
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  MacDougall, John R
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-230
;  CURRENT APPLICATION NUMBER: US/10/038,854
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 60/258,928
;  PRIOR FILING DATE: 2000-12-29
;  PRIOR APPLICATION NUMBER: 60/259,415
;  PRIOR FILING DATE: 2001-01-02
;  PRIOR APPLICATION NUMBER: 60/259,785
;  PRIOR FILING DATE: 2001-01-04
;  PRIOR APPLICATION NUMBER: 60/269,814
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/279,832
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/279,833
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/279,863
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/283,889
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,447
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: 60/286,683
;  PRIOR FILING DATE: 2001-04-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 411
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
;   LENGTH: 661
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-038-854-134

  Query Match            14.5%;  Score 629.5;  DB 15;  Length 661;
  Best Local Similarity   29.7%;  Pred. No. 2e-41;
  Matches  199;  Conservative  109;  Mismatches  274;  Indels   89;  Gaps   24;

Qy         25 SWEP-CVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVL 83
              ||:  |:|   | || |  |   :||| || :|: |: ||| |  : : :|     | |
Db         23 SWDQMCIEKEANKTYNCENLGLSEIPDTLPNTTEFLEFSFNFLPTIHNRTFSRLMNLTFL 82

Qy         84 DLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLEN 143
              ||:||:|  | :  :||   ||||:|||||:  :|  : :|  ||: |  ::| :::||
Db         83 DLTRCQINWIHEDTFQSHHQLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEF 142

Qy        144 FPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPL 203
               |: :|: |: | :  | | | | |: |    ||: ||  :| |  |    |:| | |
Db        143 IPVHNLENLESLYLGSNHISSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--A 199

Qy        204 LNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEF 263
              :||||: : | :  |: |||       |    ||     :     ||       | || |
Db        200 INLSLNFNGNNVKGIELGAFDSTVFQSL----NFGGTPNLSVIFNGLQNSTTQSLWLGTF 255

Qy        264 RNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIID-LFNCLTNVSSFSLVSVTIER 322
               :  : |    : |:||| :::|   |   ::   ||    | | | :    | :  ::

Db        256 EDIDD-EDISSAMLKGLCEMSVESLNLQ--EHRFSDISSTTFQCFTQLQELDLTATHLKG 312

Qy        323 VKDFSYNFGWQHLELVN-----------CKF--GQFPTL-------KLKSLKRLTFTSN 361
              :       | : | |:             |:     ||:|        :| |
Db        313 LPS-----GMKGLNLLKKLVLSVNHFDQLCQISAANFPSLTHLYIRGNVKKLHLGVGCLE 367

Qy        362 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSN-FLG 420
              | ||         |: |||| | :    |||      : |: |:|| |  : : |  |
Db        368 KLGN---------LQTLDLSHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKE 418

Qy        421 LEQLEHLDFQ----HSNLKQMSEFS--VFLSLRNLIY--LDISHTHTRVAFNGIFNGLSS 472
              |||  ||      | |  | | |    || : || |  || |: |       :  ||
Db        419 CPQLELLDLAFTRLHINAPQ-SPFQNLHFLQVLNLTYCFLDTSNQH-------LLAGLPV 470

Qy        473 LEVLKMAGNSFQENFL--PDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHN 530
              |  | : || ||:  :   ::   : :|  | || | |  :   ||:||  :  :::|||
Db        471 LRHLNLKGNHFQDGTITKTNLLQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHN 530

Qy        531 NFF--SLDTFPY-------KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDF 581
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Db        531 SLTCDSIDSLSHLKGIYLNLAANSINIISPRLLPIL----------SQQSTINLSHNPL 579

Qy        582 ACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSV 641
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Db        580 DCTCSNIHFLTWYKENLHKLEGSEETTCANPPSLRGVKLSDVKLSCGI--TAIGIFFLIV 637

Qy        642 LVVSVVAVLVY 652
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Db        638 FLL-LLAILLF 647


RESULT 10
US-09-950-041-4
; Sequence 4, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
;  APPLICANT: Hardiman, Gerard T.
;  APPLICANT:  Rock, Fernando L.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  APPLICANT:  Ho, Stephen W.K.
;  APPLICANT:  Liu, Yong-Jun
;  TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
;  FILE REFERENCE: DX0724XK1
;  CURRENT APPLICATION NUMBER: US/09/950,041
;  CURRENT FILING DATE:  2002-05-06
;  PRIOR APPLICATION NUMBER: 09/728,540
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 60/207,558
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 09/073,363
;  PRIOR FILING DATE: 1999-06-05
;  PRIOR APPLICATION NUMBER: 60/044,293
;  PRIOR FILING DATE: 1997-05-07
;  PRIOR APPLICATION NUMBER: 60/072,212
;  PRIOR FILING DATE: 1998-01-22
;  PRIOR APPLICATION NUMBER: 60/076,947
;  PRIOR FILING DATE: 1998-03-05
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 784
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-950-041-4

  Query Match            13.9%;  Score 603.5;  DB 10;  Length 784;
  Best Local Similarity   27.0%;  Pred. No. 3.1e-39;
  Matches  233;  Conservative  128;  Mismatches  282;  Indels  219;  Gaps   38;

Qy         48 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 107
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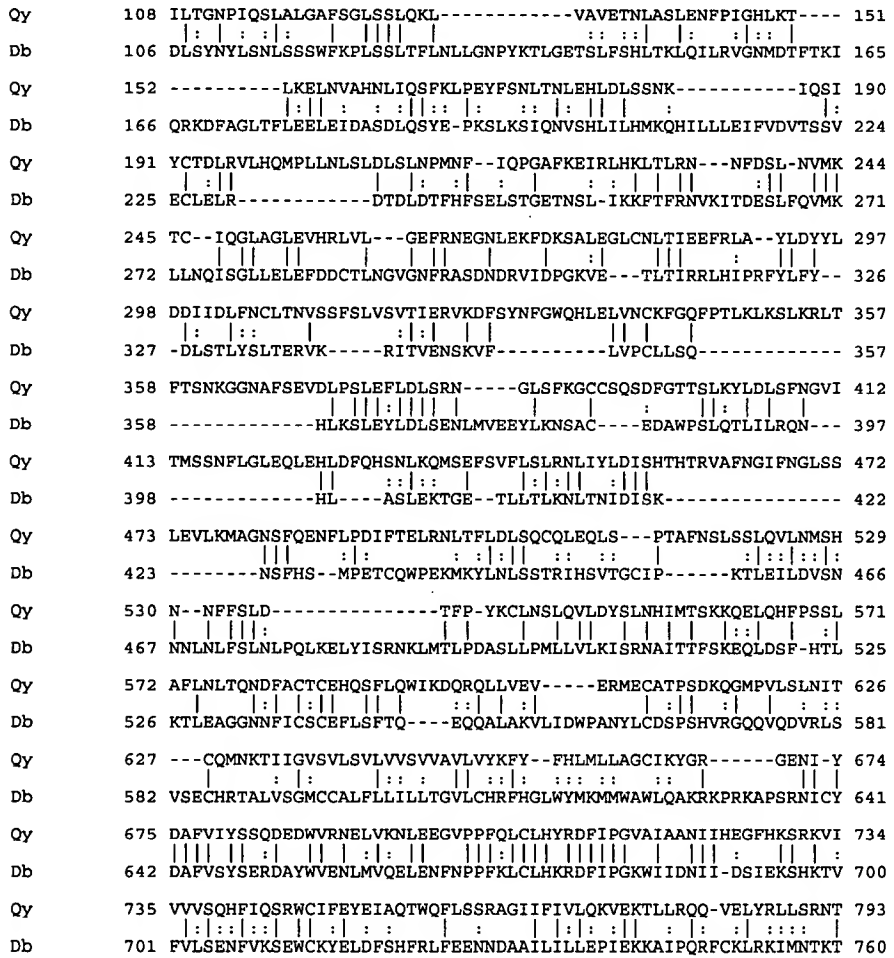
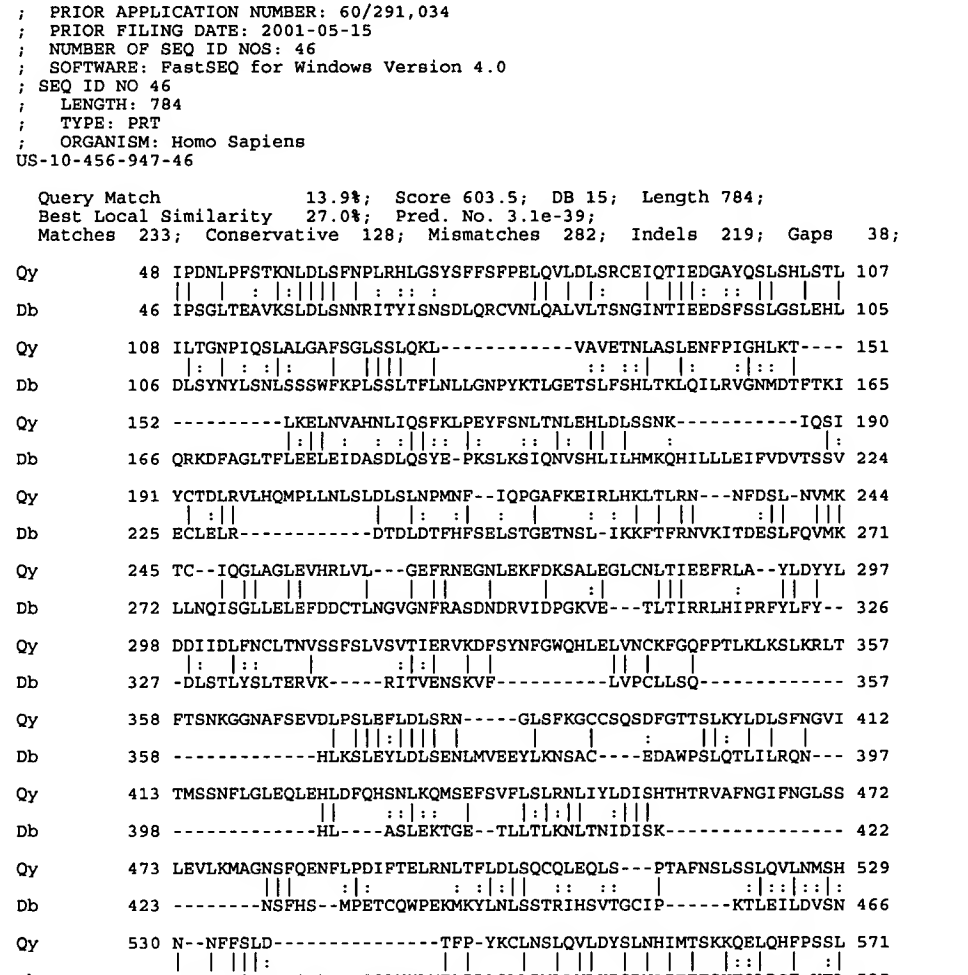


RESULT 11
US-10-456-947-46
; Sequence 46, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
; TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
; FILE REFERENCE: 3268.1001-007
; CURRENT APPLICATION NUMBER: US/10/456,947
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-456-947-46

Query Match 13.9%; Score 603.5; DB 15; Length 784;
Best Local Similarity 27.0%; Pred. No. 3.1e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;



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RESULT 12
US-10-095-627-12
; Sequence 12, Application US/10095627
; Publication No. US20030027260A1
;   GENERAL INFORMATION:
;        APPLICANT: Goddard, Audrey
;                   Godowski, Paul J.
;                   Gurney, Austin
;                   Mark, Melanie
;                   Yang, Ruey-Bing
;        TITLE OF INVENTION: Human Toll Homologues
;        NUMBER OF SEQUENCES: 32
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/095,627
;             FILING DATE: 11-Mar-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/105,413A
;             FILING DATE: 26-Jun-1998
;             APPLICATION NUMBER: 60/083322
;             FILING DATE: 28-APR-1998
;             APPLICATION NUMBER: 60/065311
;             FILING DATE: 13-NOV-1997
;             APPLICATION NUMBER: 60/062250
;             FILING DATE: 17-OCT-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Marschang, Diane L.
;             REGISTRATION NUMBER: 35,600
;             REFERENCE/DOCKET NUMBER: P1154-2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-5416
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 784 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-095-627-12

  Query Match             13.8%;  Score 602.5;  DB 14;  Length 784;
  Best Local Similarity   27.0%;  Pred. No. 3.7e-39;
  Matches  233;  Conservative  128;  Mismatches  282;  Indels  219;  Gaps   38;

Qy          48 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 107
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Db          46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 105

Qy         108 ILTGNPIQSLALGAFSGLSSLQKL----------VAVETNLASLENFPIGHLKT---- 151
                |: | : :|:   |  ||||  |             :: ::|  |:   :|:: |
Db         106 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 165

Qy         152 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK----------IQSI 190
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Db         166 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 224

Qy         191 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 244
                | :||             |  |:  :|  :  |     : : | | ||     :||  |||
Db         225 ECLELR-----------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 271

Qy         245 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 297
               | ||  ||      |   | ||   |   |   :|    |||    :   || |
Db         272 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 326

Qy         298 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 357
                |:  |::    |       :|:|  | |           || |   |
Db         327 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------- 357

Qy         358 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 412
                         | |||:|||| |       |    |    :    ||: | |  |
Db         358 ------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 397

Qy         413 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 472
                        ||    ::|::  |    |:|:||  :|||
Db         398 ------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 422

Qy         473 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 529
                      |||    :|:       : :|:||  ::  ::   |       :|::|::|:
Db         423 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 466

Qy         530 N--NFFSLD---------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 571
               |  | |||:               | |    |  | ||  | | | |  |::|  |  :|
Db         467 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 525

Qy         572 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 626
                  |    |:| |:||  || |    ::| | :|         | :||  :|  |  : ::
Db         526 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 581

Qy         627 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 674
                  |    : |:      |:: :  || ::|:  ::: ::   ::  |         || |
Db         582 VSECHRTALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 641

Qy         675 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 734
               |||| || :|  || | :|: ||   |||:|||| ||||||  |  ||| :   || | :
Db         642 DAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 700

Qy         735 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQ-VELYRLLSRNT 793
                |:|::|::| || :| : :    |  :    | |:|: :||  : |:  :| :::: |
Db         701 FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKT 760

Qy         794 YLEWEDSVLGRHIFWRRLRKAL 815
               ||||      |  ||  || |:
Db         761 YLEWPMDEAQREGFWVNLRAAI 782


RESULT 13
US-10-732-563-4
; Sequence 4, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
;  APPLICANT: Gupta, Shalley K.
;  APPLICANT:  Ghosh, Tarun K.
;  APPLICANT:  Fink, Jason R.
;  TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
;  FILE REFERENCE: 58183WO003
;  CURRENT APPLICATION NUMBER: US/10/732,563
;  CURRENT FILING DATE:  2003-12-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 784
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-732-563-4

  Query Match             13.8%;  Score 602.5;  DB 16;  Length 784;
  Best Local Similarity   27.0%;  Pred. No. 3.7e-39;
  Matches  233;  Conservative  128;  Mismatches  282;  Indels  219;  Gaps   38;

Qy          48 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 107
               ||  |  : |:|||| | : :: :        || | |:   | |||: :: ||  |  |
Db          46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 105
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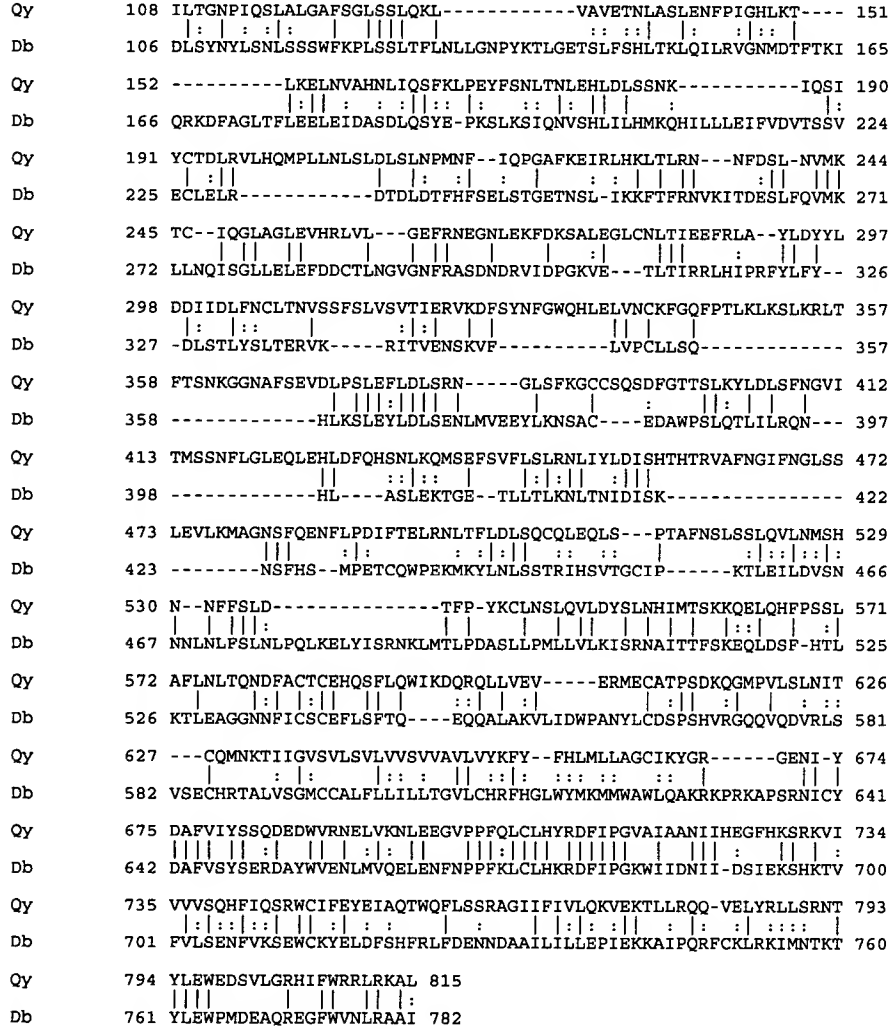
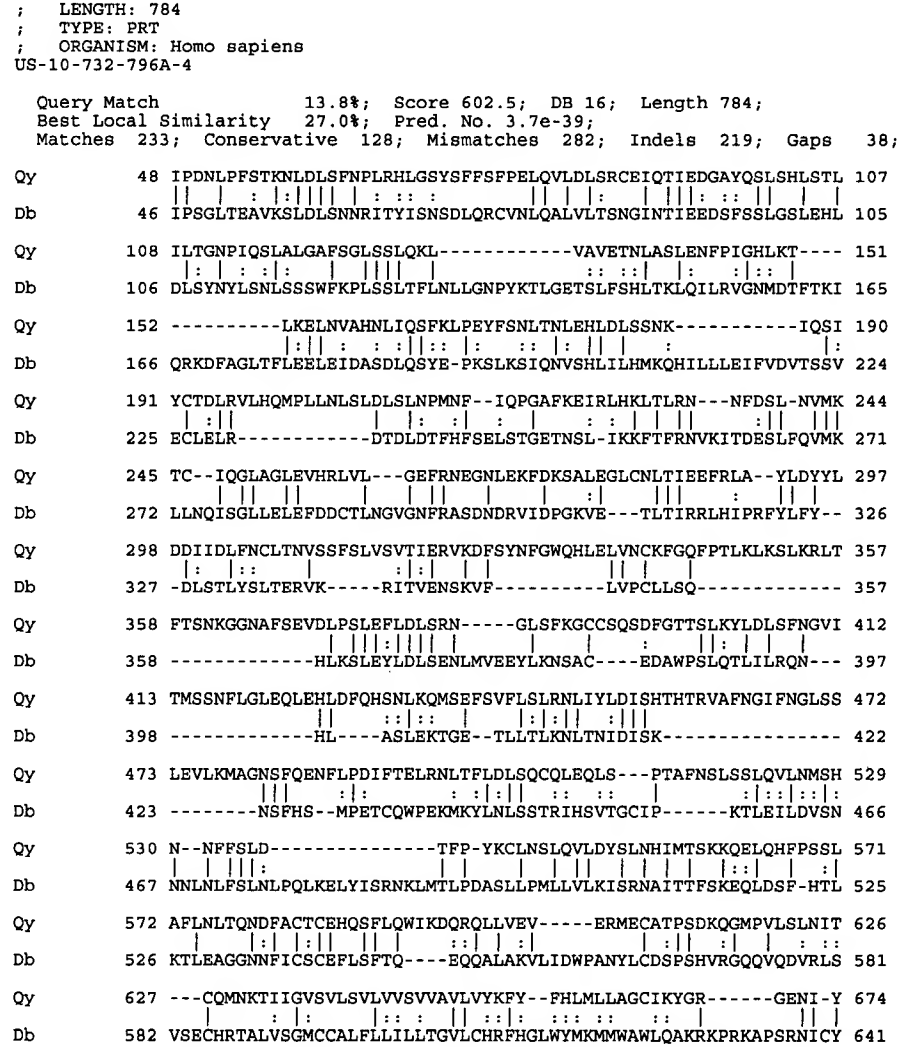


RESULT 14
US-10-732-796A-4
; Sequence 4, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
; FILE REFERENCE: 58182US004
; CURRENT APPLICATION NUMBER: US/10/732,796A
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4

; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-796A-4

Query Match 13.8%; Score 602.5; DB 16; Length 784;
Best Local Similarity 27.0%; Pred. No. 3.7e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;



RESULT 15
US-10-741-600-1390
; Sequence 1390, Application US/10741600

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; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1390
;   LENGTH: 784
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-600-1390

  Query Match             13.8%;  Score 602.5;  DB 17;  Length 784;
  Best Local Similarity   27.0%;  Pred. No. 3.7e-39;
  Matches  233;  Conservative  128;  Mismatches  282;  Indels  219;  Gaps   38;

Qy         48 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 107
              ||  |  : |:|||| | : :: :         || | |:   | |||: :: ||  |  |
Db         46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 105

Qy        108 ILTGNPIQSLALGAFSGLSSLQKL-----------VAVETNLASLENFPIGHLKT---- 151
              |: | : :|:   |  ||||  |           :: ::|  |:   :|:: |
Db        106 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 165

Qy        152 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK----------IQSI 190
                     |:|| :  : :||:: |:   :: |: || |   :             |:
Db        166 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 224

Qy        191 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 244
              | :||           |  |:  :|  :  |    : : | | ||     :||  |||
Db        225 ECLELR-----------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 271

Qy        245 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 297
              | ||  ||    |   | ||  |   |  :|   |||   :   || |
Db        272 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 326

Qy        298 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 357
              |:  |::    |       :|:|  | |           || |   |
Db        327 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------ 357

Qy        358 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 412
                     | |||:|||| |       |     |    :    ||: | |  |
Db        358 ------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 397

Qy        413 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 472
                    ||    ::|::  |    |:|:||  :|||
Db        398 ------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 422

Qy        473 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 529
                 |||    :|:       : :|:||  ::  ::   |       :|::|::|:
Db        423 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 466

Qy        530 N--NFFSLD--------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 571
              |  | |||:              | |    |  | ||  | | | |  |::|  |  :|
Db        467 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 525

Qy        572 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 626
              |    |:| |:||  || |    ::| | :|         | :||  :|  |  : ::
Db        526 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 581

Qy        627 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 674
                 |      : |:     |:: :  || ::|:  ::: ::   ::  |         || |
Db        582 VSECHRTALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 641

Qy        675 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 734
              |||| || :|  || | :|: ||   |||:|||| ||||||  |  ||| :   || | :
Db        642 DAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 700

Qy        735 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQ-VELYRLLSRNT 793
                    |:|::|::| || :| : :    |  :    | |:|: :||  : |:  :| ::::  |
Db        701 FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILLLLEPIEKKAIPQRFCKLRKIMNTKT 760

Qy        794 YLEWEDSVLGRHIFWRRLRKAL 815
              ||||      |  ||  || |:
Db        761 YLEWPMDEAQREGFWVNLRAAI 782


Search completed: March 12, 2005, 20:27:48
Job time : 78.2496 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:01 ; Search time 21.6477 Seconds
(without alignments)
3729.074 Million cell updates/sec

Title: US-09-396-985B-2
Perfect score: 4355
Sequence: 1 MMSASRLAGTLIPAMAFLSC.....SWNPEGTVGTGCNWQEATSI 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	663	15.2	661	2	I56258	RP105 - mouse
2	474	10.9	786	2	T08664	Toll protein-like
3	454	10.4	1097	2	A29943	Toll protein precu
4	433	9.9	1389	2	T13852	gene wheeler prote
5	421	9.7	1385	2	T13887	tlr protein - frui
6	396	9.1	1066	2	T15864	hypothetical prote
7	333.5	7.7	1134	1	A29944	chaoptin precursor
8	316	7.3	605	2	JC5239	insulin-like growt
9	305	7.0	853	2	T17461	disease resistance
10	303	7.0	605	2	A41915	insulin-like growt
11	299.5	6.9	662	2	S42799	garp precursor - h
12	299.5	6.9	1531	2	T42218	slit-1 protein hom
13	296.5	6.8	994	2	H96510	probable disease r
14	296	6.8	603	2	JC1282	insulin-like growt
15	295	6.8	907	2	JG0193	G protein-coupled
16	294	6.8	845	2	T07039	Hcr9-0 protein - t
17	292.5	6.7	603	2	T24315	hypothetical prote
18	292.5	6.7	907	2	JE0176	orphan G protein-c
19	290	6.7	603	2	JC6128	insulin-like growt
20	290	6.7	855	2	T07015	Cf-4A protein - to
21	289.5	6.6	1112	2	T10504	disease resistance
22	289	6.6	855	2	T17460	disease resistance
23	284.5	6.5	1134	2	T04587	hypothetical prote
24	281.5	6.5	622	2	JC7973	synleurin - human
25	280	6.4	890	2	T00800	disease resistance
26	279	6.4	1027	2	B85089	receptor protein k
27	278.5	6.4	1019	2	C96519	probable disease r
28	278	6.4	1091	2	A58532	glial cell membran
29	276.5	6.3	768	2	T17462	disease resistance
30	276	6.3	983	2	G84524	probable disease r
31	275	6.3	1523	2	T13953	MEGF5 protein - ra
32	272	6.2	1469	2	B36665	slit protein 2 pre
33	272	6.2	1480	2	A36665	slit protein 1 pre
34	270	6.2	1143	2	T10636	hypothetical prote
35	268	6.2	910	2	G84648	probable disease r
36	267	6.1	766	2	T01817	hypothetical prote
37	267	6.1	1784	2	C96615	hypothetical prote
38	266	6.1	863	2	A55173	cf-9 protein precu
39	263.5	6.1	967	2	T48210	hypothetical prote
40	262.5	6.0	1109	2	T18536	receptor-like prot
41	261.5	6.0	1051	2	T13174	gp150 protein - fr
42	260	6.0	1064	2	B86465	probable Protein k
43	259	5.9	1029	2	T00712	protein kinase hom
44	257.5	5.9	738	2	T19938	hypothetical prote
45	256	5.9	771	2	T02565	disease resistance

ALIGNMENTS

RESULT 1
I56258
RP105 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56258
R;Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995
A;Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a mc
A;Reference number: I56258; MUID:95204928; PMID:7897216
A;Accession: I56258
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-661 <RES>
A;Cross-references: UNIPROT:Q62192; GB:D37797; NID:g761711; PIDN:BAA07043.1; PID:g761712

Query Match 15.2%; Score 663; DB 2; Length 661;
Best Local Similarity 28.7%; Pred. No. 1.4e-33;
Matches 196; Conservative 116; Mismatches 289; Indels 82; Gaps 16;

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Qy         14 AMAFLSC-VRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSY 72
              |:   ||     | : |:|   | || |  |   :||  || ||: |: ||| |  : :
Db         12 ALFLASCRATTSSDQKCIEKEVNKTYNCENLGLNEIPGTLPNSTECLEFSFNVLPTIQNT 71

Qy         73 SFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLV 132
              :|     | |||:||:|  | :  :||   | ||:|| ||:  :|  | ||  :|: |
Db         72 TFSRLINLTFLDLTRCQIYWIHEDTFQSQHRLDTLVLTANPLIFMAETALSGPKALKHLF 131

Qy        133 AVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYC 192
              ::| ::|::  |: : |||: | :  | | | |||: |     |: || :| | :
Db        132 FIQTGISSIDFIPLHNQKTLESLYLGSNHISSIKLPKGFPT-EKLKVLDFQNNAIHYLSK 190

Qy        193 TDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAG 252
              |:  | |    ||||:|: | :  |:||||        |    ||     :    :||
Db        191 EDMSSLQQ--ATNLSLNLNGNDIAGIEPGAFDSAVFQSL----NFGGTQNLLVIFKGLKN 244

Qy        253 LEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSS 312
              :  | || | :  : |    :  |||| :::|   |    |: :   : |:| :
Db        245 STIQSLWLGTFEDMDD-EDISPAVFEGLCEMSVESINL-QKHYFFNISSNTFHCFS---- 298

Qy        313 FSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPT--LKLKSLKRLTFTSNKGGN--AFS 368
                                 | | |:|      : |:  :  | :||:|  ::||  |    |
Db        299 -----------------GLQELDLTATHLSELPSGLVGLSTLKKLVLSANKFENLCQIS 340

Qy        369 EVDLPSLEF-----------------------LDLSRNGLSFKGCCSQSDFGTTSLKY 403
              : |||                          ||||  : :    ||:      : |:
Db        341 ASNFPSLTHLSIKGNTKRLELGTGCLENLENLRELDLSHDDIETSDCCNLQLRNLSHLQS 400

Qy        404 LDLSFNGVITMSSN-FLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVA 462
              |:||:|  ::: :  |   ||| ||   : ||     | | :|  |  |::||:   ::
Db        401 LNLSYNEPLSLKTEAFKECPQLELLDLAFTRLKVKDAQSPFQNLHLLKVLNLSHSLLDIS 460
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Qy        463 FNGIFNGLSSLEVLKMAGNSFQENFL--PDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 520
Db        461 SEQLFDGLPALQHLNLQGNHFPKGNIQKTNSLQTLGRLEILVLSFCDLSSIDQHAFTSLK 520

Qy        521 SLQVLNMSHNNFFSLDTFPYKCLNSLQ--VLDYSLNHIMTSKKQELQHFPSSLAFL---- 574
Db        521 MMNHVDLSHNR---LTSSSIEALSHLKGIYLNLASNHISII-------LPSLLPILSQQR 570

Qy        575 --NLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKT 632
Db        571 TINLRQNPLDCTCSNIYFLEWYKENMQKLEDTEDTLCENPPLLRGVRLSDVTLSCSMAAV 630

Qy        633 IIGVSVLSVLVVSVVAVLVYKFY 655
Db        631 GIFFLIVFLLVFAILLIFAVKYF 653


RESULT 2
T08664
Toll protein-like receptor DKFZp547I0610.1 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08664
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16466
A;Accession: T08664
A;Molecule type: mRNA
A;Residues: 1-786 <POU>
A;Cross-references: UNIPROT:Q15399; EMBL:AL050262
A;Experimental source: fetal brain; clone DKFZp547I0610
C;Genetics:
A;Note: DKFZp547I0610.1

  Query Match             10.9%;  Score 474;  DB 2;  Length 786;
  Best Local Similarity   25.5%;  Pred. No. 9.6e-22;
  Matches  204;  Conservative  130;  Mismatches  303;  Indels  162;  Gaps   32;

Qy        123 SGLSSLQKLVAVETNLASLENFPIGHLKT--------LKELNVAHNLIQSFKLPEYFSNL 174
Db         34 NGLIHVPKDLSQKTTILNISQNYISELWTSDILSLSKLRILIISHNRIQYLDISVFKFN- 92

Qy        175 TNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLS-LDLSLNPMNFI----QPGAFKEIRLH 229
Db         93 QELEYLDLSHNKLVKISC--------HPTVNLKHLDLSFNAFDALPICKEFGNMSQLKFL 144

Qy        230 KLTLRNNFDSLNVMKTCIQGLAGLEVHRLVL------GEFRNEGNLEKFDKSALEGLCNL 283
Db        145 GLS------TTHLEKSSVLPIAHLNISKVLLVLGETYGEKEDPGGLQDFNTESLHIVFPT 198

Qy        284 TIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFG 343
Db        199 NKE----------------FHFILDVSVKTVANLELSNIKCVLEDSKCSYFLSILAKLQ 241

Qy        344 QFPTLKLKSLKRLTFTSNK------------GGNAFSEVDLP-SLEFLDLSRNGLSFKG 389
Db        242 TNPKLSSLTLNNIETTWNSFIRILQLVWHTTVWYSSISNVKLQGQLDFRDFDYSGTSLKA 301

Qy        390 CCSQ---SD------------FGTTSLK--------------------YLDLSFNGVI-- 412
Db        302 LSIHQVVSDVFGFPQSYIYEIFSNMNIKNFTVSGTRMVHMLCPSKISPFLHLDFSNNLLT 361

Qy        413 -TMSSNFLGLEQLEHLDFQHSNLKQMSEFS-VFLSLRNLIYLDISHTHTRVAFN---GIF 467
Db        362 DTVFENCGHLTELETLILQMNQLKELSKIAEMTTQMKSLQQLDIS--QNSVSYDEKKGDC 419

Qy        468 NGLSSLEVLKMAGNSFQENF---LPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQV 524
Db        420 SWTKSLLSLNMSSNILTDTIFRCLPP------RIKVLDLHSNKIKSI-PKQVVKLEALQE 472

Qy        525 LNMSHNNFFSLDTFP----YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 580
Db        473 LNVAFN---SLTDLPGCGSFSSLSVLIIDHNSVSHPSADFFQSCQKMRS----IKAGDNP 525

Qy        581 FACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQG-------MPVLSLNITCQ 628
Db        526 FQCTCELGEF---VKNIDQVSSEVLEGWPDSYKCDYPESYRGTLLKDFHMSELSCNITLL 582

Qy        629 MNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENI----------YDAFV 678
Db        583 IVTIVATMLVLAVTVTSLCIYLDLPWYLR-MVCQWTQTRRRARNIPLEELQRNLQFHAFI 641

Qy        679 IYSSQDEDWVRNELVKNLE-EGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVV 737
Db        642 SYSGHDSFWVKNELLPNLEKEGM---QICLHERNFVPGKSIVENII-TCIEKSYKSIFVL 697

Qy        738 SQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKV-EKTLLRQQVELYRLLSRNTYLE 796
Db        698 SPNFVQSEWCHYELYFAHHNLFHEGSNSLILILLEPIPQYSIPSSYHKLKSLMARRTYLE 757

Qy        797 WEDSVLGRHIFWRRLRKAL 815
Db        758 WPKEKSKRGLFWANLRAAI 776


RESULT 3
A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A29943
R;Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A;Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, ap
A;Reference number: A29943; MUID:88135760; PMID:2449285
A;Accession: A29943
A;Molecule type: DNA
A;Residues: 1-1097 <HAS>
A;Cross-references: UNIPROT:P08953; GB:M19969; GB:J02682; NID:g158640; PIDN:AAA28941.1;
C;Genetics:
A;Gene: FlyBase:Tl
A;Cross-references: FlyBase:FBgn0003717
C;Keywords: transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-1097/Product: Toll protein #status predicted <MAT>

  Query Match             10.4%;  Score 454;  DB 2;  Length 1097;
  Best Local Similarity   24.5%;  Pred. No. 2.6e-20;
  Matches  219;  Conservative  129;  Mismatches  291;  Indels  254;  Gaps   43;

Qy         35 NITYQCMELNFYK-IPDNLPFSTKNLD---LSFN--PLRHLGSYSFFSFPELQVLDLSRC 88
Db        270 NVTDINLSANLFRSLPQGLFDHNKHLNEVRLMNNRVPLATLPSRLFANQPELQILRL-RA 328

Qy         89 EIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGH 148
Db        329 ELQSLPGDLFEHSTQITNISLGDNLLKTLPATLLEHQVNLLSLDLSNNRLTHLPDSLFAH 388

Qy        149 LKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSI------YCTDLRVLH--- 199
Db        389 TTNLTDLRLEDNLLTGIS-GDIFSNLGNLVTLVMSRNRLRTIDSRAFVSTNGLRHLHLDH 447

Qy        200 -----QMPLLNLSLDLSLN-PMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGL 253
Db        448 NDIDLQQPLLDIMLQTQINSPFGYMH-------GLLTLNLRNN----SII---------- 486

Qy        254 EVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSF 313
Db        487 ----FVYNDWKN---------------TMLQLRELDLSY---------------NNISSL 512

Qy        314 SL------------VSVTIERVKDFS----------YNFGWQHLEL------VNCKFGQF 345
Db        513 GYEDLAFLSQNRLHVNMTHNKIRRIALPEDVHLGEGYNNNLVHVDLNDNPLVCDCTILWF 572

Qy        346 PTL------------KLKSLKRLTFTSN-KGGNAFSEVD----LPSLEFLDLSRNGLSF 387
```

```
Db        573 IQLVRGVHKPQYSRQFKLRTDRLVCSQPNVLEGTPVRQIEPQTLICPLDFSDDPRERKCP 632

Qy        388 KGC-CSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSL 446
              :|| |    :      | | :: :    | |   : :| :|   | |:: |      | |
Db        633 RGCNCHVRTYD----KALVINCH-----SGNLTHVPRLPNL---HKNMQLME-----LHL 675

Qy        447 RNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQC 506
              |   | :   :|          |  |:  | :|||               ||| :|: |
Db        676 ENNTLLRLPSANT--------PGYESVTSLHLAGN--------------NLTSIDVDQL 712

Qy        507 QLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQH 566
                  ||          |::|              || | ||:     | |
Db        713 ------PT----------NLTH-----------------LDISWNHL-----QMLN- 730

Qy        567 FPSSLAFLN---------LTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQG 617
              : | |||           |: | : | |  :  | : :|  : : :   | |
Db        731 -ATVLGFLNRTMKWRSVKLSGNPWMCDCTAKPLLLFTQDNFERIGDRNEMMCVNAEMPTR 789

Qy        618 MPVLSLNITCQMNKTI-IGVSV---LSVLVVSVVAVLVYKF--------YFHLMLLAGCI 665
              |  || | |   | : | ::|    |: |:    |  | |||          | | :||
Db        790 MVELSTNDICPAEKGVFIALAVVIALTGLLAGFTAALYYKFQTEIKIWLYAHNLLL---- 845

Qy        666 KYGRGENI-----YDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720
              :   |::     :|||: || :|: :: : ||  || |   ||||:| ||:: |  |
Db        846 WFVTEEDLDKDKKFDAFISYSHKDQSFIEDYLVPQLEHGPQKFQLCVHERDWLVGGHIPE 905

Qy        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIV---LQKVEKT 777
              ||:      ||: |:|:||:||:| |    |:  |         |: || |:   :  |||
Db        906 NIM-RSVADSRRTIIVLSQNFIKSEWARLEFRAAHRSALNEGRSRIIVIIYSDIGDVEK- 963

Qy        778 LLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTG 830
              | :::: |  |  ||||:| |       || :|| ||   :   |  | :| |
Db        964 -LDEELKAY--LKMNTYLKWGDP-----WFWDKLRFALPHRR---PVGNIGNG 1005
```

RESULT 4
T13852
gene wheeler protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13852
R;Eldon, E.; Kooyer, S.; D'evelyn, D.; Duman, M.; Lawinger, P.; Botas, J.; Bellen, H.
Development 120, 885-899, 1994
A;Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simila
A;Reference number: Z17796; MUID:95324375; PMID:7600965
A;Accession: T13852
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1389 <ELD>
A;Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:g415682; PID:g1019104; PIDN:AAA7920
C;Genetics:
A;Gene: wheeler
A;Cross-references: FlyBase:FBgn0004364

  Query Match   9.9%; Score 433; DB 2; Length 1389;
  Best Local Similarity   24.4%; Pred. No. 7.2e-19;
  Matches 217; Conservative 138; Mismatches 356; Indels 178; Gaps   34;

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Qy         59 LDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLA 118
              |:|| | |  :|| :|     ||:||:    |  ||:||:  | :| || |  | : :|
Db        338 LNLSNNALTRIGSKTFKELYFLQILDMRNNSIGHIEEGAFLPLYNLHTLNLAENRLHTLD 397

Qy        119 LGAFSGLSSLQKLVAVETNLASL-ENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNL 177
                 |:||  | ||  :  || |: |:    :   ||||::: |  |  ::||   :|: |
Db        398 NRIFNGLYVLTKL-TLNNNLVSIVESQAFRNCSDLKELDLSSN--QLTEVPEAVQDLSML 454

Qy        178 EHLDLSSNKIQSIYCTDLRVLHQMPLLNL-------------------SLDLSLNPMNF 217
              : |||  |:|         | |:|:  | |                  |:|: | :
Db        455 KTLDLGENQISEFKNNTFRNLNQLTGLRLIDNRIGNITVGMFQDLPRLSVLNLAKNRIQS 514

Qy        218 IQPGAF-KEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEPFRNE---------- 266
              |: ||| |   :  : |  ||       | | |:       | |    |
Db        515 IERGAFDKNTEIEAIRLDKNF------LTDINGIFATLASLLWLNLSENHLVWFDYAFIP 568

Qy        267 GNLEKFD--KSALEGLCNL--TIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIER 322
              ||:  |   : :| | |      || |:  ||   : | ::   ::  :|  |: :
Db        569 SNLKWLDIHGNYIEALGNYYKLQEEIRVTTLDASHNRITEI-GAMSVPNSIELLFINNNI 627

Qy        323 VKDFSYN--FGWQHLELVNCKFGQFPTLKLKSLKRLTFTSNK-------GGNAFS----- 368
              :      |          | |:        : | :|:    ::  |        ||| |
Db        628 IGQIQANTFVDKTRLARVDLYANVLSKISLNALRVAPVSAEKPVPEFYLGGNPFECDCSM 687

Qy        369 ---------------EVDLPSLEFL-------------DLSRNGLSFK---------GC 390
                            ||| ::| |              || :    |           |
Db        688 EWLQRINNLTTRQHPHVVDLGNIECLMPHSRSAPLRPLASLSASDFVCKYESHCPPTCHC 747

Qy        391 CSQSDFGTTSLKYLDLSFNGVITMSSNFL--GLEQLEHLDFQHSNLKQMSEFSVFLSLRN 448
              |          :   : |      | ::| :  | :  |  |      |          ::|   |
Db        748 CEYEQCECEVICPGNCSCFHDATWATNIVDCGRQDLAAL----PNRIPQDVSDLYLDGNN 803

Qy        449 LIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQL 508
              :  |:: |   |      ::   |:|  |:                  :| || | |   :|
Db        804 MPELEVGHLTGRRNLRALYLNASNLMTLQNGS-----------LAQLVNLRVLHLENNKL 852

Qy        509 EQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFP 568
              |  | | ||  |: | : :|    :    :: | ||:||    | : :    : :|
Db        853 TALEGTEFRSLGLLRELYLHNNMLTHISNATFEPLVSLEVLRLDNNRLSSLPHLQYRH-- 910

Qy        569 SSLAFLNLTQNDFACTCEH-QSFLQWIKDQRQLLVEVERMECATPSDKQGMPVL------ 621
              ||  | | :| ::| |:  :   |:: |   :: :   : |      |: : ::
Db        911 -SLQGLTLGRNAWSCRCQQLRELAQFVSDNAMVVRDAHDIYCLDAGIKRELELIGNLANG 969

Qy        622 ----------SLNITCQMNKT-IIG------VSVLSVLVVSVVAVLVYKFYFHLMLLAGC 664
                       : ||:   :    ||       | ||  ||| :: | | ::     : | |
Db        970 PDCSDLLDASASNISSSQDLAGAIGCPCWPAVLVLIFLVVVLIIVFVFRESVRMWLFA-- 1027

Qy        665 IKYG------RGEN---IYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPG 715
                ||       | |:   :|||  :::| :| ::|   :    || | |||:||:  || :|
Db       1028 -HYGVRVCEPRFEDAGKLYDAIILHSEKDYEFVCRNIAAELEHGRPPFRLCIQQRD-LPP 1085

Qy        716 VAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQK-- 773
              |     :: ||   |||:|:|:::: : : |   |:  |     | |  |:      ||
Db       1086 QASHLQLV-EGARASRKIILVLTRNLLATEWNRIEFRNA----FHESLRGL----AQKLV 1136

Qy        774 -VEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHI------FWRRLRKAL 815
              :|:| : : |     ||   ||:   ||    :       || :|| |:
Db       1137 IIEETSVSAEAEDVAELS--PYLK---SVPSNRLLTCDRYFWEKLRYAI 1180
```

RESULT 5
T13887
tlr protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13887
R;Chiang, C.; Beachy, P.A.
Mech. Dev. 47, 225-239, 1994
A;Title: Expression of a novel Toll-like gene spans the parasegment boundary and contrib
A;Reference number: Z17805; MUID:95151581; PMID:7848870
A;Accession: T13887
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1385 <CHI>
A;Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PIDN:AAB33383
C;Genetics:
A;Cross-references: FlyBase:FBgn0004364
A;Note: tlr

  Query Match   9.7%; Score 421; DB 2; Length 1385;
  Best Local Similarity   24.0%; Pred. No. 4e-18;
  Matches 213; Conservative 139; Mismatches 359; Indels 178; Gaps   33;

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Qy         59 LDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLA 118
              |:|| | |  :|| :|     ||:||:    |  ||:||:  | :| || |  | : :|
Db        338 LNLSNNALTRIGSKTFKELYFLQILDMRNNSIGHIEEGAFLPLYNLHTLNLAENRLHTLD 397
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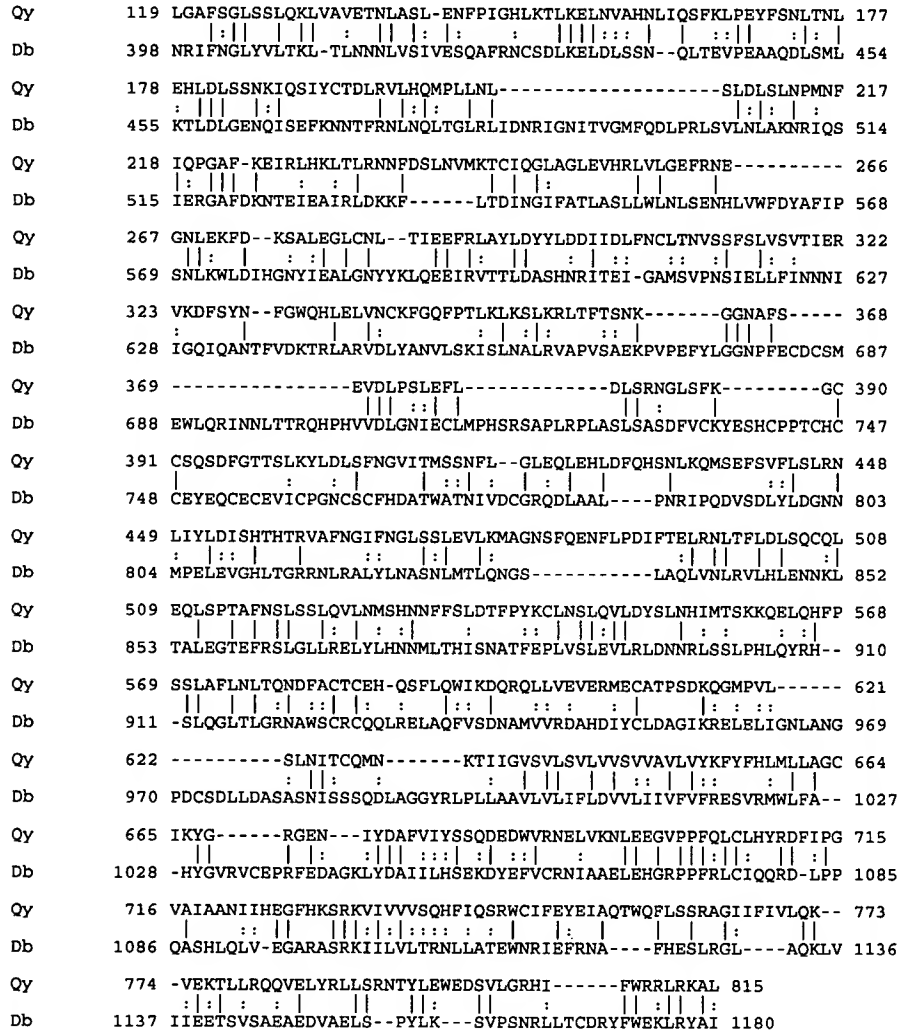
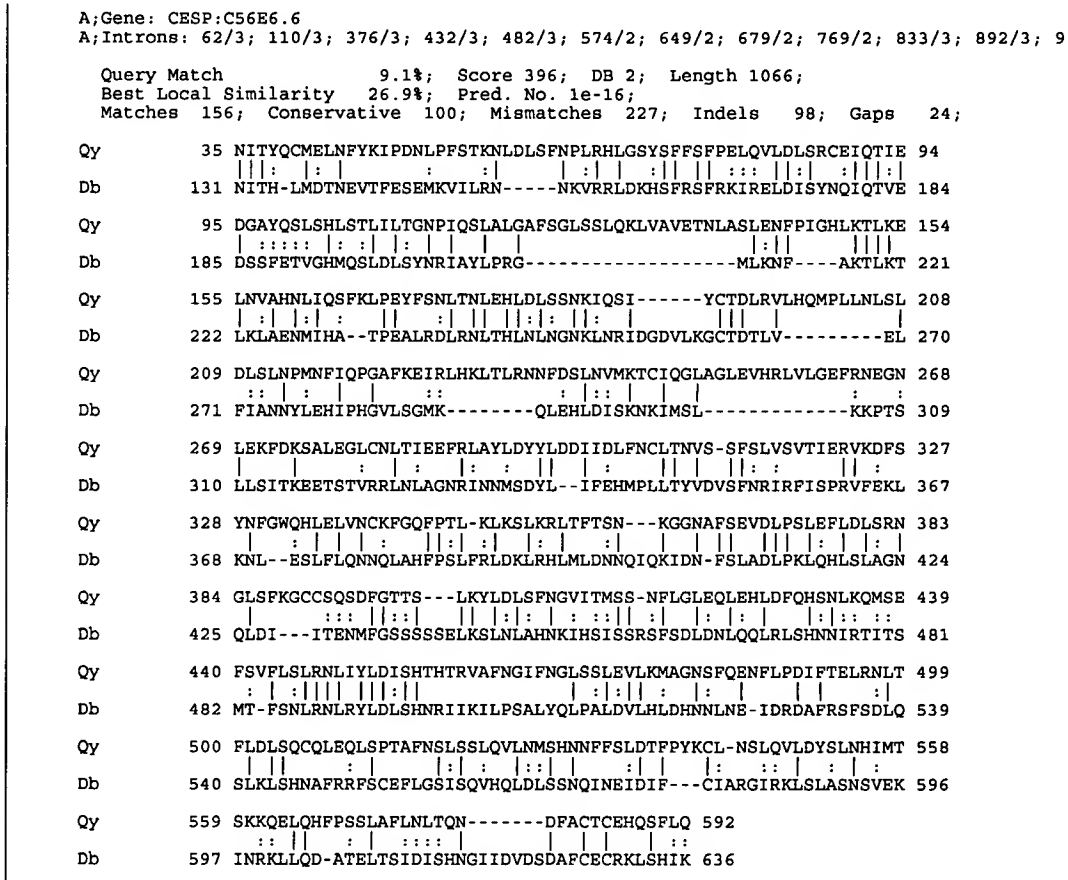


RESULT 6
T15864
hypothetical protein C56E6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15864
R;Fulton, L.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C56E6.
A;Reference number: S69019
A;Accession: T15864
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1066 <FUL>
A;Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:g1055114; PID:g1055120; PIDN:AAA81(
C;Genetics:



A;Gene: CESP:C56E6.6
A;Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3; 9

Query Match 9.1%; Score 396; DB 2; Length 1066;
Best Local Similarity 26.9%; Pred. No. 1e-16;
Matches 156; Conservative 100; Mismatches 227; Indels 98; Gaps 24;

RESULT 7
A29944
chaoptin precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: photoreceptor cell-specific membrane protein
C;Species: Drosophila melanogaster
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29944; A21123
R;Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
Cell 52, 291-301, 1988
A;Title: Chaoptin, a cell surface glycoprotein required for Drosophila photoreceptor cell
A;Reference number: A29944; MUID:88135762; PMID:3124963
A;Accession: A29944
A;Molecule type: DNA
A;Residues: 1-1134 <REI>
A;Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M1901
R;Zipursky, S.L.; Venkatesh, T.R.; Teplow, D.B.; Benzer, S.
Cell 36, 15-26, 1984
A;Title: Neuronal development in the Drosophila retina: monoclonal antibodies as molecula
A;Reference number: A21123; MUID:84106810; PMID:6420071
A;Accession: A21123
A;Molecule type: protein
A;Residues: 31-43,'HX',46-49,'H' <ZIP>
C;Genetics:
A;Gene: FlyBase:chp
A;Cross-references: FlyBase:FBgn0000313

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A;Introns: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
C;Superfamily: chaoptin; leucine-rich alpha-2-glycoprotein repeat homology
C;Keywords: cell adhesion; glycoprotein; membrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-1134/Product: chaoptin #status predicted <MAT>
F;80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR
F;103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;303-325/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F;551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
F;577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
F;601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>
F;625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR23>
F;649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>
F;673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR25>
F;708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>
F;733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR27>
F;757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR28>
F;781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>
F;805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR30>
F;828-851/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR31>
F;854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
F;879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
F;903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
F;928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F;949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
F;973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
F;996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
F;1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
F;1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

  Query Match             7.7%;  Score 333.5;  DB 1;  Length 1134;
  Best Local Similarity   23.0%;  Pred. No. 8.4e-13;
  Matches  177;  Conservative  114;  Mismatches  249;  Indels  231;  Gaps   30;

Qy          50 DNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQV-------------------------L 83
               |:|  | : ||||  |  |    |  :|  |:|                         |
Db         346 DSLVNSLQILDLSGNNLTKLHHKLFNNFDVLRVISMRDNKIKIQKPTETFNAVHYTLLKL 405

Qy          84 DLS-----RCEIQTIEDGA----YQSLS-------------------HLSTLILTGNPIQ 115
               |||          :||: :       :|||                 | | :|   :
Db         406 DLSGDRNDPTNLQTLRNMTRMRNMRSLSISRLGSSSVGPEDFKDFGVELEDLQITRASLS 465

Qy         116 SLALGAFSGLSSLQKLVAVETNLASLEN---FPIGHLKTLKELNVAHNLIQSFKLPEYFS 172
                :   ||  :  |::|    |  ::|:||     |||  :|  | ::|     |    |
Db         466 GIQSHAFKHVRGLKRLDFSENGISSIENDAFHEIGH--SLISLKMSHGYSGSALPAEPLR 523

Qy         173 NLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFK---EIRLH 229
               :||:|: || |:| | |:  |    |  : |    |:|  | :  :  | |:     :| |
Db         524 HLTSLQELDFSNNHISSMSDTSFHFLKNLRL----LELHDNRIEQVLKGTFQGDIHSKLE 579

Qy         230 KLTLRNN---------FDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEG- 279
               :::|| |         |  |  ::        |: :::   | |   ||:: :  :| |
Db         580 EISLRFNHLTSISQHTFFDLEALRK-----LHLDDNKIDKIERRAFMNLDELEYLSLRGN 634

Qy         280 -LCNLTIEEF----RLAYLDYYLDDI----IDLFNCLTNVSSFSLVSVTIERVKDFSYNF 330
                : ||  | |    :|  ||   : :      | |: :  :|: : |:|:  :::   ||
Db         635 KINNLADESFQNLPKLEILDMAFNQLPNFNFDYFDQVGTLSNLN-VNVSHNQIRQLMYNS 693

Qy         331 GWQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSF--K 388
               |                                 | |    :   ::: |||| | :|
Db         694 SW----------------------------SGRNEHGGMYHSNIKILDLSHNNISIIHP 724

Qy         389 GCCSQSDFGTT--------------------SLKYLDLSFNGVITMSSN-FLGLEQLEH 426
               |    ::   |                    |::||||:| :  :  : |   :||:
Db         725 GYFRPAEISLTHLHLGYNSLMNTTRDVFGNMPHLQWLDLSYNWIHELDFDAFKNTKQLQL 784

Qy         427 LDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR-VAFNGIFNG---------------- 469
               : | |: |  : :  :|  :: |  :| || | | :  |  :||
Db         785 VFFGHNYLSDIPQ-DIFKPVQGLRIVDFSHNHLRGLPDNLFYNGGMEKLDVSHNMMLKIP 843

Qy         470 ---LSSLEVLKMAGNSFQENFLP-----DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSS 521
                  ||||  | :       ||:      |:  : |:| :||:|   | ::    | ::
Db         844 SSSLSSLAALTLCELHLSNNFISTIHSMDLSNKFRSLRYLDISYNYLLRIDDAVFATMPK 903

Qy         522 LQVLNMSHN--------NFF--------------SLDTFPYKCLNSLQVLDYSLNHIMTS 559
               | ||::|||         :|              || | |   |  |:       | : |
Db         904 LAVLDLSHNRDLKVMDKSFMGLENSLIKLGLENVSLSTVPEIRLKYLREFRLGYNE-LPS 962

Qy         560 KKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQ--- 616
                 ||| |  |:|  |:|: ||                    |  |  |  | | ::
Db         963 IPQELAHNMSNLRMLDLSNND-------------------LTNVPLMTQALPHLRRLML 1002

Qy         617 -GMPVLSLNITCQMNKTIIGVSV-LSVLVVSVVAVLVYKFYFHLMLLAGCI 665
                | |: |||     | :  ||:  | :| :|   :  :::        ||:
Db        1003 SGNPITSLN-----NNSFDGVNEDLEMLDISNFRLHYFEY--------GCL 1040


RESULT 8
JC5239
insulin-like growth factor acid-labile chain - baboon
C;Species: Papio sp. (baboon)
C;Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C;Accession: JC5239
R;Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-lik
A;Reference number: JC5239; MUID:97040714; PMID:8886027
A;Contents: liver
A;Accession: JC5239
A;Molecule type: mRNA
A;Residues: 1-605 <DEL>
C;Comment: This factor is structurally related to proinsulin and have insuline-like meta

  Query Match             7.3%;  Score 316;  DB 2;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 4.5e-12;
  Matches  157;  Conservative   94;  Mismatches  242;  Indels  150;  Gaps   23;

Qy          33 VPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQT 92
               |  ::   |   |  ::|| :|  |: | |  | |  :   :| :   |  |:|  :: :
Db          53 VNELSVFCSSRNLTRLPDGIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGS 112

Qy          93 IEDGAYQSLSHLSTLILTGNPIQSLALGAFS----------------------GLSSL 128
               :|  |   | :|  | |  | ::|||:| |:                      || :|
Db         113 LEPQALLGLENLCHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLEDGLFEGLGNL 172

Qy         129 QKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQ 188
               |      :|| | :      |  |:|| :| | : ::  |  || |  |  ||||  | ::
Db         173 WDLNLGWNSLAVLPDAAFRGLGGLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALR 231

Qy         189 SIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCI 247
               :|       |  |:| |   | |  |  :  : ||||  ::  |  | | :|     :::
Db         232 AI---KANVFAQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTF 286

Qy         248 QGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCL 307
               || || | ||                :|:  |   | |:       ::|:::
Db         287 PGLLGLRVLRL--------------SHNAIASLRPRTFEDL------HFLEEL------- 319

Qy         308 TNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGN 365
                     |    | :: : |:  |   ||::     |   :|: :   ||  :  |  ||
Db         320 ------QLGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKVGAFLGLTNVAVMNLSGN 372
```

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Qy        366 AFSEVDLPSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL 419
Db        373 CLR--NLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFAGLSGLRRLFLKDNGLVGIEEQSL 430

Qy        420 -GLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKM 478
Db        431 WGLAELLELDLTSNQL----------------------THLP---HQLFQGLGKLEYLLL 465

Qy        479 AGNSFQENFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDT 537
Db        466 SHNRLAE--LPADALGPLQRAFWLDVSHNRLEALPGSLLASLGRLRYLNLRNN---SLRT 520

Qy        538 FPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQS-------- 589
Db        521 FTPQ------------------------PPGLERLWLEGNPWDCSCPLKALRDFALQN 554

Qy        590 ------FLQWI---KDQRQLLVEVERMECATPSDKQGMPVLSL 623
Db        555 PSAVPRFVQAICEGDDCQPPVYTYNNITCASPPEVAGLDLRDL 597
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RESULT 9
T17461
disease resistance protein D - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17461
R;Parniske, M.; Jones, J.D.
Proc. Natl. Acad. Sci. U.S.A. 96, 5850-5855, 1999
A;Title: Recombination between diverged clusters of the tomato Cf-9 plant disease resist
A;Reference number: Z18801; MUID:99254130; PMID:10318973
A;Accession: T17461
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-853 <PAR>
A;Cross-references: UNIPROT:Q9ZS82; EMBL:AF119040; NID:g4235640; PID:g4235641; PIDN:AAD1
C;Genetics:
A;Gene: NL0D

  Query Match 7.0%; Score 305; DB 2; Length 853;
  Best Local Similarity 24.5%; Pred. No. 3.4e-11;
  Matches 192; Conservative 106; Mismatches 291; Indels 194; Gaps 35;

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Qy         35 NITYQCMELNFY------KIPDNLPF----STKNLDLSFN-----PLRHLGSYSFFSFPE 79
Db         79 NTTGQVIELDLRCSQLQGKLHSNSSLFQLSNLKRLDLSYNDFTGSPI----SPKFGEFSN 134

Qy         80 LQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG------AFSGLSSLQKLVA 133
Db        135 LTHLDLFDSNFTGIIPSEISHLSKLYVLRTSTDYPYGLSLGPHNFELLLKNLTQLRELNL 194

Qy        134 VETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCT 193
Db        195 YDVNLSS--TIPSNFSSHLTNLRLAYTELRGI-LPERFFHLSNLESLDLSFNPQLTVRFP 251

Qy        194 DLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGL 253
Db        252 TTKWNSSASLVNLYL-AGVNIADRI-PESFSHL------------------------T 283

Qy        254 EVHRLVLGEFRNEGNLEKFDKSALEGLCNLT-IEEFRLAYLDY-YLDDIIDLFNCLTNVS 311
Db        284 ALHKLHMGYTNLSGPIPK-------PLWNLTHIESL---FLDYNHLEGPISHFTIFEKLK 333

Qy        312 SFSLVSVTIE-RVKDFSYNFGWQHLELV----NCKFGQFPT--LKLKSLKRLTFTSNK-G 363
Db        334 SLSLGNNNFDGRLEFLSFNRSWMKLERLDFSSNFLTGPIPSNVSGLQNLQQLILSSNHLN 393

Qy        364 GNAFSEV-DLPSLEFLDLSRNGLSFK-------------------GCCSQSDFGTTSLK 402
Db        394 GTIPSWIFSLPSLTVLNLSDNTLSGKIQEFKSKTLYFVSLEQNKLEGPIPRSLLNQQFLQ 453

Qy        403 YLDLSFNGVI-TMSSNFLGLEQLEHLDFQHSNLK--------QMSEFSVFLSLRNLIYLD 453
Db        454 ALLLSHNNISGHISSAICNLKTFILLNLKSNNLEGTIPQCLGEMSELQV---------LD 504

Qy        454 ISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSP 513
Db        505 LSNNSLSGTMNTTFSIGNPLHIIKLDWNKLQGKVPPSLI-NCKKLELLDLSNNELNDTFP 563

Qy        514 TAFNSLSSLQVLNMSHN----------------------NFFSLDTFPYKCLNSLQVL-- 549
Db        564 KWLGDLPNLQVLNFRSNKLYGPIRTNNLFAKIRVVDLSSNGFSGD-LPVSFFENFEAMKI 622

Qy        550 ---------------DYSLNHIMTSKK---QELQHFPSSLAFLNLTQNDFACTCEH-QS 589
Db        623 NGENNGTRKYVADLYSDYYKNYLIVTTKGLDQELSRVLTTQIIIDLSKNKFE---GHIPN 679

Qy        590 FLQWIKDQRQLLVEVERMECATPSDKQGMPVL------SLNITCQMNKTIIGVSVLSVLV 643
Db        680 IIGDLIGLRTLNLSHNVLEGHIPASFQNLSVLESLDLSSNKISGAIPQQLASLTFLEVLN 739

Qy        644 VSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPF 703
Db        740 LS---------HNHLV---GCIPKGKQ---FDSFENSSYLGNDGLR---------GLPPS 775

Qy        704 QLC 706
Db        776 RDC 778
```

RESULT 10
A41915
insulin-like growth factor-binding complex acid-labile chain precursor - human
N;Alternate names: Acid-Labile Subunit (ALS)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A41915
R;Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
Mol. Endocrinol. 6, 870-876, 1992
A;Title: Structure and functional expression of the acid-labile subunit of the insulin-l
A;Reference number: A41915; MUID:92357025; PMID:1379671
A;Accession: A41915
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-605 <LEO>
A;Cross-references: UNIPROT:P35858; GB:M86826; NID:g184807; PIDN:AAA36047.1; PID:g184808
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:110171)
F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

  Query Match 7.0%; Score 303; DB 2; Length 605;
  Best Local Similarity 24.4%; Pred. No. 2.9e-11;
  Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

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Qy         40 CMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQ 99
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119
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Qy        100 SLSHLSTLILTGNPIQSLALGAFS-----------------------GLSSLQKLVAVE 135
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        136 TNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDL 195
Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KA 235

Qy        196 RVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLE 254
Db        236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLR 293

Qy        255 VHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFS 314
Db        294 VLRL--------------SHNAIASLRPRTFKDL------HFLEEL-------------Q 320

Qy        315 LVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDL 372
Db        321 LGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NL 377

Qy        373 PSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLE 425
Db        378 PEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELL 437

Qy        426 HLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQE 485
Db        438 ELDLTSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE 472

Qy        486 NFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLN 544
Db        473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ--- 524

Qy        545 SLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD-------- 596
Db        525 ----------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSA 557

Qy        597 -QRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 638
Db        558 VPRFVQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594
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RESULT 11
S42799
garp precursor - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S42799; I37407
R;Birnbaum, D.
submitted to the EMBL Data Library, July 1993
A;Reference number: S42799
A;Accession: S42799
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-662 <BIR>
A;Cross-references: UNIPROT:Q14392
R;Ollendorff, V.; Noguchi, T.; deLapeyriere, O.; Birnbaum, D.
Cell Growth Differ. 5, 213-219, 1994
A;Title: The GARP gene encodes a new member of the family of leucine-rich repeat-contain
A;Reference number: I37407; MUID:94235567; PMID:8180135
A;Accession: I37407
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-662 <RES>
A;Cross-references: EMBL:Z24680; NID:g439295; PIDN:CAA80847.1; PID:g439296
C;Genetics:
A;Gene: GDB:GARP; D11S833E
A;Cross-references: GDB:433911
A;Map position: 11q13.5-11q14
F;50-73/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;74-97/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;98-121/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;150-173/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;174-197/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;198-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;244-265/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;266-289/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;316-339/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;340-363/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;364-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;411-433/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;444-466/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;467-490/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;492-514/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;515-536/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F;537-560/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>

  Query Match             6.9%;  Score 299.5;  DB 2;  Length 662;
  Best Local Similarity   25.9%;  Pred. No. 5.3e-11;
  Matches  187;  Conservative   94;  Mismatches  259;  Indels  181;  Gaps   35;
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Qy         28 PCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSR 87
Db         25 PCKMVDKKVS--CQVLGLLQVPSVLPPDTETLDLSGNQLRSILASPLGFYTALRHLDLST 82

Qy         88 CEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLAS-----LE 142
Db         83 NEISFLQPGAFQALTHLEHLSLAHNRLAMATALSAGGLGPLPRVTSLDLSGNSLYSGLLE 142

Qy        143 NFPIGHLKTLKELNVAHNLIQSFKLPEY-FSNLTNLEHLDLSSNKIQSIYCTDLRVLHQM 201
Db        143 RL-LGEAPSLHTLSLAENSLT--RLTRHTFRDMPALEQLDLHSNVLMDIEDGAFEGLPRL 199

Qy        202 PLLNLS-----------------LDLSLNPMNFI----QPGAFKEIRLHKLTLRNN---- 236
Db        200 THLNLSRNSLTCISDFSLQQLRVLDLSCNSIEAFQTASQPQA--EFQLTWLDLRENKLLH 257

Qy        237 FDSLNVMKTCIQGLAGLEVHRLVLGEFRN-------------------EGNLEKFDKSAL 277
Db        258 FPDLAALPRLIYLNLSNNLIRLPTGPPQDSKGIHAPSEGWSALPLSAPSGNASGRPLSQL 317

Qy        278 EGLCNLTIEEFRLAYLDYYLDDIIDLF------NCLTNVSSFSLVSVTIERVKDFSYNFG 331
Db        318 LNL-DLSYNEIEL-IPDSFLEHLTSLCFLNLSRNCLRTFEARRLGSLPCLMLLDLSHN-A 374

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEV------DLPSLEFLDLSRNGL 385
Db        375 LETLELGARALGSLRTLLLQ-----------GNALRDLPPYTFANLASLQRLNLQGNRV 422

Qy        386 S---------FKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQ 436
Db        423 SPCGGPDEPGPSGCVAFS--GITSLRSLSLVDNEI----------ELLRAGAFLHTPLTE 470

Qy        437 MSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGL-SSLEVLKMAGNSFQ--ENFLPDIFT 493
Db        471 ---------------LDLSSNPGLEVATGALGGLEASLEVLALQGNGLMVLQVDLPCFIC 515

Qy        494 ELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSL 553
Db        516 ----LKRLNLAENRLSHL--PAWTQAVSLEVLDL-RNNSFSL--LPGSAMGGLE------ 560

Qy        554 NHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQ-RQLLVEVERME---C 609
Db        561 ---------------TSLRRLYLQGNPLSC-CGN----GWLAAQLHQGRVDVDATQDLIC 600

Qy        610 ATPSDKQGMPVLSLNIT----CQMN--KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAG 663
Db        601 RFSSQEE----VSLSHVRPEDCEKGGLKNINLIIIILTFILVSAIL---------LTTLAA 647

Qy        664 C 664
Db        648 C 648
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```
RESULT 12
T42218
slit-1 protein homolog - rat
N;Alternate names: MEGF4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42218
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T42218
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1531 <NAK>
A;Cross-references: UNIPROT:O88279; EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF4
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r

  Query Match             6.9%;  Score 299.5;  DB 2;  Length 1531;
  Best Local Similarity   22.1%;  Pred. No. 1.6e-10;
  Matches  167;  Conservative   95;  Mismatches  260;  Indels  233;  Gaps   27;

Qy          4 ASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSF 63
              |  |:    |||   ||                |     |        || ||| :   : |
Db        274 ACTLSSGSCPAMC--SC------------SNGIVDCRGKGLTAIPANLPETMTEIRLEL 318

Qy         64 NPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFS 123
              | :: :   :|  : :|: :|||  :|  |    |:| |  |::|:| || |  |  | |
Db        319 NGIKSIPPGAFSPYRKLRRIDLSNNQIAEIAPDAFQGLRSLNSLVLYGNKITDLPRGVFG 378

Qy        124 GLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLS 183
              || :|| |:                        ||   | |   : |: | :| ||  | |
Db        379 GLYTLQLLL---------------------LNA--NKINCIR-PDAFQDLQNLSLLSLY 413

Qy        184 SNKIQSI---YCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240
              |||||:     | || :        :| |: ||  ||     | :        :|
Db        414 DNKIQSLAKGTFTSLRAIQ-------TLHLAQNP--FICDCNLKWLA--------DFLRT 456

Qy        241 NVMKTCIQGLAGLEVHRLV---LGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYL 297
              | ::|   |          ||    :|: ::    :||  || |       : |     ||:|
Db        457 NPIET--TGARCASPRRLANKRIGQIKS----KKFRCSAKE-------QYFIPGTEDYHL 503

Qy        298 D-----DIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKF------GQFP 346
              :     |:     |    |       : : :: :         | | | :       | |
Db        504 NSECTSDVACPHKCRCEASVVECSGLKLSKIPE-RIPQSTTELRLNNNEISILEATGLFK 562

Qy        347 TLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDL 406
              ||  ||::  ::||      ||::  : |                       | ||:  | |
Db        563 --KLSHLKKINLSNNK----VSEIEDGTFE-------------------GATSVSELHL 596

Qy        407 SFNGVITMSSN-FLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNG 465
              : | : :: |  | ||: |  |  ::: :  :    | |  |||:  | :   |       |
Db        597 TANQLESVRSGMFRGLDGLRTLMLRNNRISCIHNDS-FTGLRNVRLLSLYDNHITTISPG 655

Qy        466 IFNGLSSLEVLKMAGNSFQENF----------------------------------- 487
              |: | :|  | :  | | |
Db        656 AFDTLQALSTLNLLANPFNCNCQLAWLGDWLRKRKIVTGNPRCQNPDFLRQIPLQDVAFP 715

Qy        488 ------------------------------------------LPDIFTEL--------- 495
                                                       :|   |||
Db        716 DFRCEEGQEEVGCLPRPQCPQECACLDTVVRCSNKHLQALPKGIPKNVTELYLDGNQFTL 775

Qy        496 --------RNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQ 547
                     : |  :|||  ::  || ::|  ::|  |  | :|:|    :    ::  | ||:
Db        776 VPGQLSTFKYLQLVDLSNNKISSLSNSSFTNMSQLTTLILSYNALQCIPPLAFQGLRSLR 835

Qy        548 VLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERM 607
              :|    | : | ::       :||: | :  |  | |  :    |:|   :   |
Db        836 LLSLHGNDVSTLQEGIFADV-TSLSHLAIGANPLYCDCHLRWLSSWVKTGYK---EPGIA 891

Qy        608 ECA-----------TPSDK---QGMPVLSLNITC 627
              ||            ||: |   || | |::   |
Db        892 RCAGPPEMEGKLLLTTPAKKFECQGPPSLAVQAKC 926


RESULT 13
H96510
probable disease resistance protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H96510
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96510
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-994 <STO>
A;Cross-references: UNIPROT:Q9C637; GB:AE005173; NID:g11321768; PIDN:AAG34245.1; GSPDB:GI
C;Genetics:
A;Gene: F2G19.6
A;Map position: 1

  Query Match             6.8%;  Score 296.5;  DB 2;  Length 994;
  Best Local Similarity   23.0%;  Pred. No. 1.4e-10;
  Matches  161;  Conservative   102;  Mismatches  271;  Indels  167;  Gaps   31;

Qy          2 MSASRLAGTLIPAMAFLSCVRPESWEPC---------VEVVPNITYQCMELNFYKIPDNL 52
              ||:  ::  :    :::  :|  : : |         | ::||:    :: |      ||
Db        213 MSSVDISSAIPIEFSYMWSLRSLTLKGCNLLGRFPNSVLLIPNLESISLDHNL-----NL 267

Qy         53 PFSTKNLDLSFNPLRHLGSY----------SFFSFPELQVLDLSRCEIQTIEDGAYQSLS 102
                |  |  |  | |  |  |              |  :   |  | | :         : :|||
Db        268 EGSLPNF-LRNNSLLKLSIYNTSFSGTIPNSISNLKHLTSLKLQQSAFSGRIPSSLRSLS 326

Qy        103 HLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFP--IGHLKTLKELNVAHN 160
              ||| |:|: |         : | |  |       : ||    |||  : :|  |: :::  |
Db        327 HLSNLVLSENNFVGEIPSSVSNLKQLTLFDVSDNNLNG--NFPSSLLNLNQLRYIDICSN 384

Qy        161 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMP--LLNLS----LDLSLNP 214
                | ||   | |:|||      |                :|  | |:|    | || |
Db        385 HFTGF-LPPTISQLSNLEFFSACDNSFTG----------SIPSSLFNISSLTTLGLSYNQ 433

Qy        215 MNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDK 274
              :|                      |: |:                        :|   |    :
Db        434 LN--------------------DTTNI--------------------KNISLLHNLQR 451

Qy        275 SALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSV---TIERVKDFSYNFG 331
                |:          |: : :|      :|:|  |  : | :|  :   |      |  ::
Db        452 LLLDN------NNFKASQVD------LDVFLSLKRLVSLALSGIPLSTTNITSDSEFSSH 499

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVD-----LPSLEFLDLSRNGL- 385
              ::|||  |   :||   ::: : |:       |   :|      || |  :||| | |
Db        500 LEYLELSGCNIIEFPEF-IRNQRNLSSIDLSNNNIKGQVPNWLWRLPELSTVDLSNNSLI 558

Qy        386 SFKGCCSQSDFGTTSLKYLDLSFNGVITMSSN------FLGLEQLEHLDFQHSNLKQMSE 439
              | |          |||  |  |   :: :|||       |:    :::    ::|
Db        559 GFNG----------SLKALSGSKIVMLDLSSNAFQGPLFMPPRGIQYFLGSYNNFTGYIP 608

Qy        440 FSVFLSLRNLIYLDISHTHTRVAFNGIFNGL---------SSLEVLKMAGNSFQENFLPD 490
              |:    | | : ||:|        |    :||          ||| || :  ||  :  ||:
Db        609 PSI-CGLANPLILDLS--------NNNLHGLIPRCLEAQMSSLSVLNLRNNSL-DGSLPN 658

Qy        491 IFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY--KCLNSLQV 548
```

```
                ||   : |: ||:|   ||   | :    |:|::||:  ||    ||||:    |  |||
Db        659 IFMNAKVLSSLDVSHNTLEGKLPASLAGCSALEILNVESNNI--NDTFPFWLNSLPKLQV 716

Qy        549 LDYSLNHIMTSKKQELQH-------FPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 601
              |    |:      : | :        ||  |   ::: |||  |     |: |   :
Db        717 LVLRSNNF----RGTLHNVDGVWFGFP-LLRITDVSHNDFVGTLPSDYFMNWTAISKS-- 769

Qy        602 VEVERMECATPSD---KQGMPVLSLNITCQMNKTIIGVSVL 639
                | |      | |       : :::  :: :| : :   :|:
Db        770 -ETELQYIGDPEDYGYYTSLVLMNKGVSMEMQRILTKYTVI 809


RESULT 14
JC1282
insulin-like growth factor-binding protein acid labile chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1282
R;Dai, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A;Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A;Reference number: JC1282; MUID:93038676; PMID:1384485
A;Accession: JC1282
A;Molecule type: mRNA
A;Residues: 1-603 <DAI>
A;Cross-references: UNIPROT:P35859; GB:S46785; NID:g258002; PIDN:AAB23770.2; PID:g570593
A;Experimental source: liver
A;Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

  Query Match             6.8%;  Score 296;  DB 2;  Length 603;
  Best Local Similarity   24.1%;  Pred. No. 7.8e-11;
  Matches  155;  Conservative   84;  Mismatches  243;  Indels  162;  Gaps   24;

Qy         40 CMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQ 99
              |   |   :||::| ||: | |  | |  : | :| :   |  |:|    ::::|  |
Db         60 CSSKNLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALL 119

Qy        100 SLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVA- 158
              | :|  | |  | :::||:| |:   ||  |       |  ||       |  | :||:
Db        120 GLQNLYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGW 179

Qy        159 -----------------HNLI-----QSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLR 196
                              | |:       ::  |  |  |  |  |||| | ::|:
Db        180 NSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSV---KAN 236

Qy        197 VLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEV 255
              |   :| |   | |  | :  : ||||  :: |  | | :|     :|:    || || |
Db        237 VFVHLPRLQ-KLYLDRNLITAVAPGAFLGMKALRWLDLSHN-RVAGLMEDTFPGLLGLHV 294

Qy        256 HRLV-----------------LGEFR-NEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYL 297
                ||                  | | :     : :  :   |||  | :    |   | :
Db        295 LRLAHNAIASLRPRTFKDLHFLEELQLGHNRIRQLGERTFEGLGQLEV----LTLNDNQI 350

Qy        298 DDI-IDLFNCLTNVSSFSLVSVTI----ERV---KDFSYNFGWQHLELVNCKFGQFPTLK 349
              :: :  |: | ||:  :|    :    |||    |  ::   :|  | : :   |
Db        351 TEVRVGAFSGLFNVAVMNLSGNCLRSLPERVFQGLDKLHSLHLEHSCLGHVRLHTF--AG 408

Qy        350 LKSLKRLTFTSNKGGNAFSEVD------LPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKY 403
              |  |:||        |: | ::       |  |  |||: | |:       |   |   |:|
Db        409 LSGLRRLFLRD----NSISSIEEQSLAGLSELLELDLTTNRLTH--LPRQLFQGLGHLEY 462

Qy        404 LDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAF 463
              | ||:| : |:|:  ||                          |:   :|||| |
Db        463 LLLSYNQLTTLSAEVLG-----------------------PLQRAFWLDISHNHLETLA 498

Qy        464 NGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQ 523
              |:|: |  :  | :  || |  | |              |  ||:|
Db        499 EGLFSSLGRVRYLSLRNNSLQ-TFSP--------------QPGLERL------------ 530

Qy        524 VLNMSHNNFFSLDTFPYKCLNSLQVL-DYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFA 582
                  ||  |: |   |: | |::| :             |  :     |
Db        531 ----------WLDANPWDCSCPLKALRDFALQN------------PGVVPRFVQT----- 563

Qy        583 CTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNIT 626
                ||        |  | :     : || |::  |: :  :: |
Db        564 -VCE--------GDDCQPVYTYNNITCAGPANVSGLDLRDVSET 598


RESULT 15
JG0193
G protein-coupled receptor FEX - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C;Accession: JG0193
R;Hermey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.
Biochem. Biophys. Res. Commun. 254, 273-279, 1999
A;Title: Identification of a novel seven-transmembrane receptor with homology to glycopr
A;Reference number: JG0193; MUID:99121227; PMID:9920770
A;Accession: JG0193
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-907 <HER>

  Query Match             6.8%;  Score 295;  DB 2;  Length 907;
  Best Local Similarity   23.0%;  Pred. No. 1.5e-10;
  Matches  167;  Conservative  110;  Mismatches  243;  Indels  206;  Gaps   32;

Qy         11 LIPAMAFLSCVRPESWEPCVEVVPN--------------ITYQCMELNFYKIPDNLPFS 55
              |:  :| |  |   |  |  : :|                :   | :|   ::| ||
Db          9 LLSLLALLQLVAAGS-SPGPDAIPRGCPSHCHCELDGRMLLRVDCSDLGLSELPSNLSVF 67

Qy         56 TKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH----LSTLILTG 111
              |  |||| | :  | :                                 || |    |  | | |
Db         68 TSYLDLSMNNISQLPA---------------------------SLLHRLCFLEELRLAG 99

Qy        112 NPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYF 171
              | :  :  |||:|| ||: |:      |  :    : :|::|: | :  | | |:  |  |
Db        100 NALTHIPKGAFTGLHSLKVLMLQNNQLRKVPEEALQNLRSLQSLRLDANHI-SYVPPSCF 158

Qy        172 SNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEI-RLHK 230
              | | :| || |  | :  :      | | :    :: |:|| :: |    ||  :  |
Db        159 SGLHSLRHLWLDDNALTDVPVQAFRSLSALQ----AMTLALNKIHHIADYAFGNLSSLVV 214

Qy        231 LTLRNN-FDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFR 289
              | | ||   ||   | |  ||  ||    |       |  ||::|  :|:: | |
Db        215 LHLHNNRIHSLG--KKCFDGLHSLETLDL------NYNNLDEF-PTAIKTLSN------- 258

Qy        290 LAYLDYYLDDIIDL----FNCLTNVSSFSLVSVTI-ERVKDFSYNFGWQHLELVNCKFGQ 344
              |  | :: ::|  :    |     | : ||:::  :    |     :|||         :
Db        259 LKELGFHSNNIRSIPERAF-----VGNPSLITIHFYDNPIQFVGVSAFQHLP-------E 306

Qy        345 FPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSF--KGCCSQSDFGTTSLK 402
              || |      :|  :  | |        :|| | |:   :|   :  | |      :|:
Db        307 LRTLTLNGASHITEFPHLTGTA-------TLESLTLTGAKISSLPQAVCDQ----LPNLQ 355

Qy        403 YLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVA 462
              ||||:| :  :  |    | ::|: :| :|:
Db        356 VLDLSYNLLEDLPS-LSGCQKLQKIDLRHN---------------------------- 384

Qy        463 FNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSL 522
                    |: :: |::||: |          ||  |:|:  ::  : | ||::| ||
Db        385 -----------EIYEIKGSTFQQLF---------NLRSLNLAWNKIAIIHPNAFSTLPSL 424

Qy        523 QVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQ------HFPSSLAFLNL 576
              |::| |    | :||    |       : | |:  :  : ||      :|| |  : :
Db        425 IKLDLSSN---LLSSFPVTGL-------HGLTHLKLTGNRALQSLIPSANFP-ELKIIEM 473

Qy        577 TQNDFACT---CE--HQSFLQWIKDQRQLLVEVERMECA--TPSDKQGMPVLSLNITCQM 629
                    |    ||  ::   || ||    : :: : :       |:: :    |:    :
Db        474 PSAYQCCAFGGCENVYKISNQWNKDDGNSVDDLHKKDAGLFQVQDERDLEDFLLDFEEDL 533

Qy        630 NK----------------------TIIGVSVLSVLVVS---VVAVLVYK---PYFHLM 659
              |                        |||   :|| :|   :||: |::   :   :
```

```
Db        534 NALHSVQCSPSPGPFKPCEHLFGSWLIRIGVWTTAVLTLSCNALVALTVFRTPLYISSIK 593

Qy        660 LLAGCI 665
              || | |
Db        594 LLIGVI 599
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Search completed: March 12, 2005, 19:56:52
Job time : 30.6477 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:46 ; Search time 21.9643 Seconds
(without alignments)
2715.523 Million cell updates/sec

Title: US-09-396-985B-4
Perfect score: 4141
Sequence: 1 MELNFYKIPDNLPFSTKNLD.....SWNPEGTVGTGCNWQEATSI 799

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4141	100.0	844	4	US-09-949-016-9438	Sequence 9438, Ap
2	599.5	14.5	784	4	US-09-982-308B-23	Sequence 23, Appl
3	590	14.2	661	1	US-08-514-014-4	Sequence 4, Appli
4	590	14.2	661	2	US-08-833-823-4	Sequence 4, Appli
5	539	13.0	775	4	US-09-949-016-8799	Sequence 8799, Ap
6	309	7.5	605	3	US-09-063-950-5	Sequence 5, Appli
7	297	7.2	605	1	US-08-190-802A-49	Sequence 49, Appl
8	297	7.2	605	3	US-08-477-346-49	Sequence 49, Appl
9	297	7.2	605	3	US-08-473-089-49	Sequence 49, Appl
10	297	7.2	605	4	US-08-487-072A-49	Sequence 49, Appl
11	297	7.2	605	4	US-09-538-092-1087	Sequence 1087, Ap
12	297	7.2	623	4	US-09-949-016-10995	Sequence 10995, A
13	290	7.0	603	1	US-08-190-802A-50	Sequence 50, Appl
14	290	7.0	603	3	US-08-477-346-50	Sequence 50, Appl
15	290	7.0	603	3	US-08-473-089-50	Sequence 50, Appl
16	290	7.0	603	4	US-08-487-072A-50	Sequence 50, Appl
17	289.5	7.0	1112	3	US-09-353-585-3	Sequence 3, Appli
18	287.5	6.9	662	4	US-09-538-092-1325	Sequence 1325, Ap
19	287.5	6.9	662	4	US-09-949-016-6619	Sequence 6619, Ap
20	287.5	6.9	665	4	US-09-949-016-10710	Sequence 10710, A
21	286.5	6.9	1525	3	US-09-191-647-2	Sequence 2, Appli
22	286.5	6.9	1525	3	US-09-540-245A-2	Sequence 2, Appli
23	286.5	6.9	1525	3	US-09-540-153-2	Sequence 2, Appli
24	286	6.9	1112	3	US-09-353-585-2	Sequence 2, Appli
25	284.5	6.9	907	4	US-09-170-496D-264	Sequence 264, App
26	284.5	6.9	907	4	US-09-170-496D-278	Sequence 278, App
27	283.5	6.8	1166	4	US-10-101-464A-900	Sequence 900, App
28	279.5	6.7	1529	4	US-09-312-283C-396	Sequence 396, App
29	277.5	6.7	1523	3	US-09-182-024A-2	Sequence 2, Appli
30	273	6.6	620	4	US-09-907-794A-73	Sequence 73, Appl
31	273	6.6	620	4	US-09-905-125A-73	Sequence 73, Appl
32	273	6.6	620	4	US-09-902-775A-73	Sequence 73, Appl
33	273	6.6	620	4	US-09-906-700-73	Sequence 73, Appl
34	273	6.6	620	4	US-09-903-603A-73	Sequence 73, Appl
35	273	6.6	620	4	US-09-904-920A-73	Sequence 73, Appl
36	273	6.6	620	4	US-09-909-064-73	Sequence 73, Appl
37	273	6.6	620	4	US-09-905-381A-73	Sequence 73, Appl
38	273	6.6	620	4	US-09-906-618-73	Sequence 73, Appl
39	270	6.5	1101	3	US-08-986-485-2	Sequence 2, Appli
40	266.5	6.4	1091	3	US-08-986-485-5	Sequence 5, Appli
41	265.5	6.4	863	2	US-08-666-271-2	Sequence 2, Appli
42	265.5	6.4	1874	4	US-09-331-403-2	Sequence 2, Appli
43	264	6.4	1480	3	US-09-191-647-7	Sequence 7, Appli
44	264	6.4	1480	3	US-09-540-245A-7	Sequence 7, Appli
45	264	6.4	1480	3	US-09-540-153-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9438

Query Match 100.0%; Score 4141; DB 4; Length 844;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         46 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 105

Qy         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 165

Qy        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 225

Qy        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 285

Qy        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 345

Qy        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360
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Db        346 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 405

Qy        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Db        406 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 465

Qy        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Db        466 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 525

Qy        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Db        526 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 585

Qy        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600

Db        586 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 645

Qy        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

Db        646 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 705

Qy        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720

Db        706 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 765

Qy        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Db        766 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 825

Qy        781 WNPEGTVGTGCNWQEATSI 799

Db        826 WNPEGTVGTGCNWQEATSI 844
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RESULT 2
US-09-982-308B-23
; Sequence 23, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Fan, Xuedong
; APPLICANT: Lundell, Daniel
; APPLICANT: Lunn, Charles A.
; APPLICANT: Tan, Jimmy C.
; APPLICANT: Zavodny, Paul J.
; TITLE OF INVENTION: Mammalian TNF-alpha Convertases
; FILE REFERENCE: JB0601QC
; CURRENT APPLICATION NUMBER: US/09/982,308B
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/156,163
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 08/889,909
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: 60/021,710
; PRIOR FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-308B-23

Query Match 14.5%; Score 599.5; DB 4; Length 784;
Best Local Similarity 27.0%; Pred. No. 2.5e-46;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;

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Qy          8 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 67

Db         46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 105

Qy         68 ILTGNPIQSLALGAFSGLSSLQKL------------VAVETNLASLENFPIGHLKT---- 111

Db        106 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 165

Qy        112 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK-----------IQSI 150

Db        166 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 224

Qy        151 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 204

Db        225 ECLELR------------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 271

Qy        205 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 257

Db        272 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 326

Qy        258 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 317

Db        327 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------- 357

Qy        318 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 372

Db        358 ------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 397

Qy        373 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 432

Db        398 ------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 422

Qy        433 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 489

Db        423 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 466

Qy        490 N--NFFSLD---------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 531

Db        467 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 525

Qy        532 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 586

Db        526 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 581

Qy        587 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 634

Db        582 VSECHRIALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 641

Qy        635 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 694

Db        642 DAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 700

Qy        695 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQ-VELYRLLSRNT 753

Db        701 FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKT 760

Qy        754 YLEWEDSVLGRHIFWRRLRKAL 775

Db        761 YLEWPMDEAQREGFWVNLRAAI 782
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RESULT 3
US-08-514-014-4
; Sequence 4, Application US/08514014
; Patent No. 5707829
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge

```
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/514,014
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI6000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  661 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-514-014-4

  Query Match             14.2%;  Score 590;  DB 1;  Length 661;
  Best Local Similarity   29.3%;  Pred. No. 1.4e-45;
  Matches  191;  Conservative  107;  Mismatches  266;  Indels   88;  Gaps   23;

Qy          3 LNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLS 62
              |   :||| || :|: |: ||| |  : : :|      |  |||:||:|  | :  :||
Db         42 LGLSEIPDTLPNTTEFLEFSFNFLPTIHNRTFSRLMNLTFLDLTRCQINWIHEDTFQSHH 101

Qy         63 HLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLI 122
               ||||:|||||:  :|  : :|  ||: |  ::| :::||  |: :|: |: | :  | |
Db        102 QLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEFIPVHNLENLESLYLGSNHI 161

Qy        123 QSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGA 182
              | | |: |    ||: ||  :| |  |   |:| | |   :|||: : | :  |: ||
Db        162 SSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--AINLSLNFNGNNVKGIELGA 218

Qy        183 FKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCN 242
              |       |    ||     :     ||       | || | :  : |    : |:|||
Db        219 FDSTVFQSL----NFGGTPNLSVIFNGLQNSTTQSLWLGTFEDIDD-EDISSAMLKGLCE 273

Qy        243 LTIEEFRLAYLDYYLDDIID-LFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVN-- 299
              :::|   |   ::   ||    | | | :   | :  :: :       | : | |:
Db        274 MSVESLNLQ--EHRFSDISSTTFQCFTQLQELDLTATHLKGLPS-----GMKGLNLLKKL 326

Qy        300 ----------CKF--GQFPTL-------KLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDL 340
                       |:    ||:|        :| |        | ||          |: |||
Db        327 VLSVNHFDQLCQISAANFPSLTHLYIRGNVKKLHLGVGCLEKLGN---------LQTLDL 377

Qy        341 SRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSN-FLGLEQLEHLDFQ----HSNLK 395
              | | :    |||      : |: |:|| |  : : |  |    ||| ||      | |
Db        378 SHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKECPQLELLDLAFTRLHINAP 437

Qy        396 QMSEFS--VFLSLRNLIY--LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFL--P 449
              | | |    || : || |  || |: |       :  ||  |  | : || ||:  :
Db        438 Q-SPFQNLHFLQVLNLTYCFLDTSNQH-------LLAGLPVLRHLNLKGNHFQDGTITKT 489

Qy        450 DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFF--SLDTFPY------- 500
              ::   : :|  | || | |  :   ||:||  :  :::|||:    |:|:  :
Db        490 NLLQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHNSLTCDSIDSLSHLKGIYLN 549

Qy        501 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 560
                ||: ::   |  |:              |  : :||: |   ||| :  || | |:
Db        550 LAANSINIISPRLLPIL-----------SQQSTINLSHNPLDCTCSNIHFLTWYKENLHK 598

Qy        561 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVY 612
              |   |   || |   :|: :  : ::| :  | ||:  | | :: ::|:|::
Db        599 LEGSEETTCANPPSLRGVKLSDVKLSCGI--TAIGIFFLIVFLL-LLAILLF 647


RESULT 4
US-08-833-823-4
; Sequence 4, Application US/08833823
; Patent No. 5969093
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  Kelleher, Kerry
;    APPLICANT:  Carlin, McKeough
;    TITLE OF INVENTION:  DNA SEQUENCES AND SECRETED PROTEINS
;    TITLE OF INVENTION:  ENCODED THEREBY
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc. -- Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/833,823
;      FILING DATE:  10-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/514,014
;      FILING DATE:  11-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI6000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  661 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-833-823-4

  Query Match             14.2%;  Score 590;  DB 2;  Length 661;
  Best Local Similarity   29.3%;  Pred. No. 1.4e-45;
  Matches  191;  Conservative  107;  Mismatches  266;  Indels   88;  Gaps   23;

Qy          3 LNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLS 62
              |   :||| || :|: |: ||| |  : : :|      |  |||:||:|  | :  :||
Db         42 LGLSEIPDTLPNTTEFLEFSFNFLPTIHNRTFSRLMNLTFLDLTRCQINWIHEDTFQSHH 101

Qy         63 HLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLI 122
               ||||:|||||:  :|  : :|  ||: |  ::| :::||  |: :|: |: | :  | |
Db        102 QLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEFIPVHNLENLESLYLGSNHI 161

Qy        123 QSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGA 182
              | | |: |    ||: ||  :| |  |   |:| | |   :|||: : | :  |: ||
Db        162 SSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--AINLSLNFNGNNVKGIELGA 218

Qy        183 FKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCN 242
              |       |    ||     :     ||       | || | :  : |    : |:|||
Db        219 FDSTVFQSL----NFGGTPNLSVIFNGLQNSTTQSLWLGTFEDIDD-EDISSAMLKGLCE 273

Qy        243 LTIEEFRLAYLDYYLDDIID-LFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVN-- 299
              :::|   |   ::   ||    | | | :   | :  :: :       | : | |:
Db        274 MSVESLNLQ--EHRFSDISSTTFQCFTQLQELDLTATHLKGLPS-----GMKGLNLLKKL 326
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Qy        300 ----------CKF--GQFPTL-------KLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDL 340
                         |:     ||:|         :| |         | ||          |: |||
Db        327 VLSVNHFDQLCQISAANFPSLTHLYIRGNVKKLHLGVGCLEKLGN---------LQTLDL 377

Qy        341 SRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSN-FLGLEQLEHLDFQ----HSNLK 395
              | | :    |||       : |: |:|| |  : : |  |     ||| ||       | |
Db        378 SHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKECPQLELLDLAFTRLHINAP 437

Qy        396 QMSEFS--VFLSLRNLIY--LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFL--P 449
              | | |     || : || |  || |: |        :  ||  |  | : || ||:  :
Db        438 Q-SPFQNLHFLQVLNLTYCFLDTSNQH-------LLAGLPVLRHLNLKGNHFQDGTITKT 489

Qy        450 DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFF--SLDTFPY------- 500
              ::   : :|  | || | |  :   ||:||  :  :::|||:    |:|:  :
Db        490 NLLQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHNSLTCDSIDSLSHLKGIYLN 549

Qy        501 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 560
                ||: ::   |  |:           |  : :||: |   ||| :  || | |:
Db        550 LAANSINIISPRLLPIL----------SQQSTINLSHNPLDCTCSNIHFLTWYKENLHK 598

Qy        561 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVY 612
              |   |   || |   :|: :  : ::| :  | ||:  | | :: ::|:|::
Db        599 LEGSEETTCANPPSLRGVKLSDVKLSCGI--TAIGIFFLIVFLL-LLAILLF 647


RESULT 5
US-09-949-016-8799
; Sequence 8799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8799
;   LENGTH: 775
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-8799

  Query Match             13.0%;  Score 539;  DB 4;  Length 775;
  Best Local Similarity   26.6%;  Pred. No. 9.9e-41;
  Matches  218;  Conservative  120;  Mismatches  264;  Indels  218;  Gaps   37;

Qy          8 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 67
              ||  |  : |:|||| | : :: :       || | |:   | |||: :: ||  |  |
Db         81 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 140

Qy         68 ILTGNPIQSLALGAFSGLSSLQKL------------VAVETNLASLENFPIGHLKT---- 111
                |: | : :|:   |  ||||  |             :: ::|  |:   :|:: |
Db        141 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 200

Qy        112 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK-----------IQSI 150
                       |:|| :  : :||:: |:   :: |: || |   :              |:
Db        201 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 259

Qy        151 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 204
              | :||              |  |:  :|  :  |    : : | | ||     :||  |||
Db        260 ECLELR-----------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 306

Qy        205 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 257
                  | ||  ||      |   | ||   |     |   :|    |||    :   || |
Db        307 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 361
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Qy        258 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 317
              |:  |::    |       :|:|  | |          || |   |
Db        362 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------ 392

Qy        318 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 372
                          | |||:|||| |       |    |    :    ||: | |  |
Db        393 ------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 432

Qy        373 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 432
                          ||    ::|::  |    |:|:||  :|||
Db        433 ------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 457

Qy        433 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 489
                    |||    :|:       : :|:||  ::  ::   |       :|::|::|:
Db        458 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 501

Qy        490 N--NFFSLD--------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 531
              |  | |||:               | |    |  | ||  | | | |  |::|  |  :|
Db        502 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 560

Qy        532 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 586
                |    |:| |:||  || |    ::| | :|         | :||  :|  |  : ::
Db        561 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 616

Qy        587 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 634
                |      : |:      |:: :  || ::|:  ::: ::   ::  |         || |
Db        617 VSECHRTALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 676

Qy        635 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 694
              |||| || :|  || | :|: ||   |||:|||| ||||||  |  ||| :   || | :
Db        677 DAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 735

Qy        695 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKV 734
              |:|::|::| || :| : :    |  :    | |:|: :
Db        736 FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPI 775


RESULT 6
US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
;  APPLICANT: Holtzman, Douglas A.
;  TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION: THEREFOR
;  FILE REFERENCE: MEI-019
;  CURRENT APPLICATION NUMBER: US/09/063,950C
;  CURRENT FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 605
;   TYPE: PRT
;   ORGANISM: Papio hamadryas
US-09-063-950-5

  Query Match             7.5%;  Score 309;  DB 3;  Length 605;
  Best Local Similarity   24.5%;  Pred. No. 1.4e-19;
  Matches  155;  Conservative   92;  Mismatches  235;  Indels  150;  Gaps   23;

Qy          4 NFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH 63
              |  ::|| :|  |: | |  | |  :   :| :   |  |:|   :: ::|  |    | :
Db         64 NLTRLPDGIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGSLEPQALLGLEN 123

Qy         64 LSTLILTGNPIQSLALGAFS----------------------GLSSLQKLVAVETNLA 99
              |  | |  | ::|||:| |:                     || :|  |     :||
Db        124 LCHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLEDGLFEGLGNLWDLNLGWNSLA 183

Qy        100 SLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLH 159
              | :      |  |:|| :| | : ::  |  || |  | ||||  | :::|      |
Db        184 VLPDAAFRGLGGLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KANVFA 239
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Qy        160 QMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEVHRL 218
              |:| |   | |  | :  : ||||  :: |  | | :|     :::     || || | ||
Db        240 QLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRVLRL 297

Qy        219 VLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSV 278
                          :|:  |   | |:       ::|:::              |
Db        298 -------------SHNAIASLRPRTFEDL------HFLEEL------------QLGHN 324

Qy        279 TIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDLPSLE 336
              | :: : |:  |   ||::      |   :|: :   ||  :  |  ||     :||
Db        325 RIRQLAERSFE-GLGQLEVLTLDHNQLQEVKVGAFLGLTNVAVMNLSGNCLR--NLPEQV 381

Qy        337 FLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLEHLDF 389
              |  | : :  :| |       :  | : |: | |  ||:: :    | || :|  ||
Db        382 FRGLGKLHSLHLEGSCLGRIRPHTFAGLSGLRRLFLKDNGLVGIEEQSLWGLAELLELDL 441

Qy        390 QHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLP 449
              : |                        ||     : :| ||  || | :: |   |  ||
Db        442 TSNQL---------------------THLP---HQLFQGLGKLEYLLLSHNRLAE--LP 474

Qy        450 -DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQV 508
               |    |:   :||:|  :|| |  :   ||  |: ||: :|   || ||  :
Db        475 ADALGPLQRAFWLDVSHNRLEALPGSLLASLGRLRYLNLRNN---SLRTFTPQ------- 524

Qy        509 LDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQS-------------FLQWI 554
                                 | |  | |  | : |:|  ::             |:| |
Db        525 -------------------PPGLERLWLEGNPWDCSCPLKALRDFALQNPSAVPRFVQAI 565

Qy        555 ---KDQRQLLVEVERMECATPSDKQGMPVLSL 583
                | :  :     : ||:| :  |: :  |
Db        566 CEGDDCQPPVYTYNNITCASPPEVAGLDLRDL 597
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RESULT 7
US-08-190-802A-49
; Sequence 49, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 605 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor binding
; INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-190-802A-49

Query Match 7.2%; Score 297; DB 1; Length 605;
Best Local Similarity 24.4%; Pred. No. 1.8e-18;
Matches 156; Conservative 91; Mismatches 240; Indels 152; Gaps 24;

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Qy          4 NFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH 63
              |  ::|| :|  |: | |  | |  :  :| :   |  |:|   :: ::|  |   | :
Db         64 NLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALLGLEN 123

Qy         64 LSTLILTGNPIQSLALGAFS-----------------------GLSSLQKLVAVETNLA 99
              |  | |  | ::|||||  |:                     || ||  |     :||
Db        124 LCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGWNSLA 183

Qy        100 SLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLH 159
              | :     | :|:|| :| | : ::  |  || |  |  |||| | :::|     |
Db        184 VLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KANVFV 239

Qy        160 QMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEVHRL 218
              |:| |   | |  | :  : ||||  :: |  | | :|     :::     || || | ||
Db        240 QLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRVLRL 297

Qy        219 VLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSV 278
                          :|:  |   | |:       ::|:::              |
Db        298 -------------SHNAIASLRPRTFKDL------HFLEEL------------QLGHN 324

Qy        279 TIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDLPSLE 336
              | :: : |:  |   ||::      |   :|  :   ||  :  |  ||     :||
Db        325 RIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NLPEQV 381

Qy        337 FLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLEHLDF 389
              |  | : :  :| |       :  | : |: | |  ||:: :    | || :|  ||
Db        382 FRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELLELDL 441

Qy        390 QHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLP 449
              : |                        ||     : :| ||  || | :: |   |  ||
Db        442 TSNQL---------------------THLP---HRLFQGLGKLEYLLLSRNRLAE--LP 474

Qy        450 -DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQV 508
               |    |:   :||:|  :|| |  :   |  |: |:: :|   || ||  :
Db        475 ADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ------- 524

Qy        509 LDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD---------QRQ 559
                                 |  | |  |  | : | |      |: ::|          |
Db        525 -------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSAVPRF 561

Qy        560 LLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 598
              :    |  :|  |:            ||||     ::|: :
Db        562 VQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594
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RESULT 8
US-08-477-346-49
; Sequence 49, Application US/08477346
; Patent No. 6262023
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:

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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/477,346
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/487,072
;       FILING DATE:  07-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MURASHIGE, KATE H.
;       REGISTRATION NUMBER:  29,959
;       REFERENCE/DOCKET NUMBER:  2550-0025.20
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 887-1500
;       TELEFAX:  (202) 887-0763
;   INFORMATION FOR SEQ ID NO:  49:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  605 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;       INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-477-346-49

  Query Match             7.2%;  Score 297;  DB 3;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 1.8e-18;
  Matches  156;  Conservative   91;  Mismatches  240;  Indels  152;  Gaps   24;

Qy          4 NFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH 63
              |  ::|| :|  |: | |  | |  :  :| :   |  |:|   :: ::|  |  |  | :
Db         64 NLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALLGLEN 123

Qy         64 LSTLILTGNPIQSLALGAFS-----------------------GLSSLQKLVAVETNLA 99
              |  | |  | ::||||| |:                      || ||  |     :||
Db        124 LCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGWNSLA 183

Qy        100 SLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLH 159
               | :     | :|:|| :| | : ::  |  || |  |  |||| | :::|      |
Db        184 VLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KANVFV 239

Qy        160 QMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEVHRL 218
              |:| |   | |  | :  : ||||  :: |  | | :|     :::    || || | ||
Db        240 QLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRVLRL 297

Qy        219 VLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSV 278
                        :|:  |   | ::       ::|:::                 |
Db        298 -------------SHNAIASLRPRTFKDL------HFLEEL------------QLGHN 324

Qy        279 TIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDLPSLE 336
               | :: : |:  |   ||::     |   :|  :   ||  :  |  ||     :||
Db        325 RIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NLPEQV 381

Qy        337 FLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLEHLDF 389
              |  | : : |  :| |       :  | : |: | |  ||:: :    | || :|  ||
Db        382 FRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELLELDL 441

Qy        390 QHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLP 449
              : |                          ||     : :| ||  || | :: |    |  ||
Db        442 TSNQL---------------------THLP---HRLFQGLGKLEYLLLSRNRLAE--LP 474

Qy        450 -DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQV 508
               |    |:  :||:|  :|| |  :    |  |: |:: :|   || ||  :
Db        475 ADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ------- 524

Qy        509 LDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD---------QRQ 559
                                  |  |  | |  | : | |     |: ::|          |
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Db        525 -------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSAVPRF 561

Qy        560 LLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 598
               :    |  :|  |:          ||||     ::|: :
Db        562 VQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594


RESULT 9
US-08-473-089-49
; Sequence 49, Application US/08473089
; Patent No. 6342368
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/473,089
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-473-089-49

  Query Match             7.2%;  Score 297;  DB 3;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 1.8e-18;
  Matches  156;  Conservative   91;  Mismatches  240;  Indels  152;  Gaps   24;

Qy          4 NFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH 63
              |  ::|| :|  |: | |  | |  :  :| :   |  |:|   :: ::|  |  |  | :
Db         64 NLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALLGLEN 123

Qy         64 LSTLILTGNPIQSLALGAFS-----------------------GLSSLQKLVAVETNLA 99
              |  | |  | ::||||| |:                      || ||  |     :||
Db        124 LCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGWNSLA 183

Qy        100 SLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLH 159
               | :     | :|:|| :| | : ::  |  || |  |  |||| | :::|      |
Db        184 VLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KANVFV 239

Qy        160 QMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEVHRL 218
              |:| |   | |  | :  : ||||  :: |  | | :|     :::    || || | ||
Db        240 QLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRVLRL 297
```

```
Qy        219 VLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSV 278
Db        298 --------------SHNAIASLRPRTFKDL------HFLEEL-------------QLGHN 324

Qy        279 TIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDLPSLE 336
Db        325 RIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NLPEQV 381

Qy        337 FLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLEHLDF 389
Db        382 FRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELLELDL 441

Qy        390 QHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLP 449
Db        442 TSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE--LP 474

Qy        450 -DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQV 508
Db        475 ADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ------- 524

Qy        509 LDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD---------QRQ 559
Db        525 -------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSAVPRF 561

Qy        560 LLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 598
Db        562 VQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594
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RESULT 10
US-08-487-072A-49
; Sequence 49, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 605 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor binding
; INDIVIDUAL ISOLATE: protein complex, Fig. 32

US-08-487-072A-49

Query Match 7.2%; Score 297; DB 4; Length 605;
Best Local Similarity 24.4%; Pred. No. 1.8e-18;
Matches 156; Conservative 91; Mismatches 240; Indels 152; Gaps 24;

```
Qy          4 NFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH 63
Db         64 NLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALLGLEN 123

Qy         64 LSTLILTGNPIQSLALGAFS----------------------GLSSLQKLVAVETNLA 99
Db        124 LCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGWNSLA 183

Qy        100 SLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLH 159
Db        184 VLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KANVFV 239

Qy        160 QMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEVHRL 218
Db        240 QLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRVLRL 297

Qy        219 VLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSV 278
Db        298 --------------SHNAIASLRPRTFKDL------HFLEEL-------------QLGHN 324

Qy        279 TIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDLPSLE 336
Db        325 RIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NLPEQV 381

Qy        337 FLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLEHLDF 389
Db        382 FRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELLELDL 441

Qy        390 QHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLP 449
Db        442 TSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE--LP 474

Qy        450 -DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQV 508
Db        475 ADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ------- 524

Qy        509 LDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD---------QRQ 559
Db        525 -------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSAVPRF 561

Qy        560 LLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 598
Db        562 VQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594
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RESULT 11
US-09-538-092-1087
; Sequence 1087, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1087
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number P35858
US-09-538-092-1087

  Query Match             7.2%;  Score 297;  DB 4;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 1.8e-18;
  Matches  156;  Conservative   91;  Mismatches  240;  Indels  152;  Gaps   24;

Qy          4 NFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH 63
              |  ::|| :|  |: | |  | |  :  :| :   | |:|   :: ::|  |   | :
Db         64 NLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALLGLEN 123

Qy         64 LSTLILTGNPIQSLALGAFS----------------------GLSSLQKLVAVETNLA 99
              |  | |  | ::||||| |:                      || ||  |     :||
Db        124 LCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGWNSLA 183

Qy        100 SLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLH 159
              | :     | :|:|| :| | : ::  |  || |  |  |||| | :::|      |
Db        184 VLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KANVFV 239

Qy        160 QMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEVHRL 218
              |:| |   | |  | :  : ||||  :: |  | | :|     :::     || || | ||
Db        240 QLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRVLRL 297

Qy        219 VLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSV 278
                        :|:  |   | ::       ::|:::             |
Db        298 -------------SHNAIASLRPRTFKDL------HFLEEL------------QLGHN 324

Qy        279 TIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDLPSLE 336
              | :: : |:  |   ||::     |   :|  :   || :  |  ||     :||
Db        325 RIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NLPEQV 381

Qy        337 FLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLEHLDF 389
              |  | : : |  :| |       :  | : |: | |  ||:: :    | || :|  ||
Db        382 FRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELLELDL 441

Qy        390 QHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLP 449
              : |                      ||     : :| ||  || | :: |   |  ||
Db        442 TSNQL---------------------THLP---HRLFQGLGKLEYLLLSRNRLAE--LP 474

Qy        450 -DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQV 508
               |    |:   :||:|  :|| |  :    |  |: |:: :|   || ||  :
Db        475 ADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ------- 524

Qy        509 LDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD---------QRQ 559
                                |  |  | |  | : | |      |: ::|           |
Db        525 ------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSAVPRF 561

Qy        560 LLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 598
              :    |  :|  |:          ||||     ::|: :
Db        562 VQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594


RESULT 12
US-09-949-016-10995
; Sequence 10995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 10995
;   LENGTH: 623
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10995

  Query Match             7.2%;  Score 297;  DB 4;  Length 623;
  Best Local Similarity   24.4%;  Pred. No. 1.9e-18;
  Matches  156;  Conservative   91;  Mismatches  240;  Indels  152;  Gaps   24;

Qy          4 NFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH 63
              |  ::|| :|  |: | |  | |  :  :| :   | |:|   :: ::|  |   | :
Db         82 NLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALLGLEN 141

Qy         64 LSTLILTGNPIQSLALGAFS----------------------GLSSLQKLVAVETNLA 99
              |  | |  | ::||||| |:                      || ||  |     :||
Db        142 LCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGWNSLA 201

Qy        100 SLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLH 159
              | :     | :|:|| :| | : ::  |  || |  |  |||| | :::|      |
Db        202 VLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KANVFV 257

Qy        160 QMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEVHRL 218
              |:| |   | |  | :  : ||||  :: |  | | :|     :::     || || | ||
Db        258 QLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRVLRL 315

Qy        219 VLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSV 278
                        :|:  |   | ::       ::|:::             |
Db        316 -------------SHNAIASLRPRTFKDL------HFLEEL------------QLGHN 342

Qy        279 TIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDLPSLE 336
              | :: : |:  |   ||::     |   :|  :   || :  |  ||     :||
Db        343 RIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NLPEQV 399

Qy        337 FLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLEHLDF 389
              |  | : : |  :| |       :  | : |: | |  ||:: :    | || :|  ||
Db        400 FRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELLELDL 459

Qy        390 QHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLP 449
              : |                      ||     : :| ||  || | :: |   |  ||
Db        460 TSNQL---------------------THLP---HRLFQGLGKLEYLLLSRNRLAE--LP 492

Qy        450 -DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQV 508
               |    |:   :||:|  :|| |  :    |  |: |:: :|   || ||  :
Db        493 ADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ------- 542

Qy        509 LDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD---------QRQ 559
                                |  |  | |  | : | |      |: ::|           |
Db        543 ------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSAVPRF 579

Qy        560 LLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 598
              :    |  :|  |:          ||||     ::|: :
Db        580 VQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 612


RESULT 13
US-08-190-802A-50
; Sequence 50, Application US/08190802A
; Patent No. 5519003
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  P.O. Box 60850
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306-0850
;    COMPUTER READABLE FORM:
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;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/190,802A
;      FILING DATE:  01-FEB-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  8600-0139
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  603 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor bind.
;      INDIVIDUAL ISOLATE:  pro. complex-rat, Fig. 33
US-08-190-802A-50

  Query Match          7.0%;  Score 290;  DB 1;  Length 603;
  Best Local Similarity   24.1%;  Pred. No. 7.8e-18;
  Matches  154;  Conservative   84;  Mismatches  240;  Indels  162;  Gaps   24;

Qy          4 NFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH 63
              |   :||::| ||: | | | | : | :| :   |  |:|    ::::| |   | | :
Db         64 NLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALLGLQN 123

Qy         64 LSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVA----- 118
              |  | |  | :::||:| |:   ||  |       |  ||      |  | :||:
Db        124 LYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGWNSLV 183

Qy        119 -------------HNLI-----QSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQ 160
                          | |:      ::  |  |  |  |  ||||  | ::|:      |
Db        184 VLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSV---KANVFVH 240

Qy        161 MPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLV 219
              :| |   | |  | :  : ||||  :: |  | | :|     :|:    || || | ||
Db        241 LPRLQ-KLYLDRNLITAVAPGAFLGMKALRWLDLSHN-RVAGLMEDTFPGLLGLHVLRLA 298

Qy        220 -----------------LGEFR-NEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI- 260
                              | | :     : :  :   |||  | :    |    |  : ::
Db        299 HNAIASLRPRTFKDLHFLEELQLGHNRIRQLGERTFEGLGQLEV----LTLNDNQITEVR 354

Qy        261 IDLFNCLTNVSSPSLVSVTI----ERV---KDFSYNFGWQHLELVNCKFGQPFPTLKLKSL 313
              :  |: | ||:  :|    :    |||    |  ::   :|  | : :    |     |  |
Db        355 VGAFSGLFNVAVMNLSGNCLRSLPERVFQGLDKLHSLHLEHSCLGHVRLHTF--AGLSGL 412

Qy        314 KRLTFTSNKGGNAFSEVD------LPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLS 367
              :||        |: | ::      |  |  |||: | |:      |   |   |:|| ||
Db        413 RRLFLRD----NSISSIEEQSLAGLSELLELDLTTNRLTH--LPRQLFQGLGHLEYLLLS 466

Qy        368 FNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIF 427
              :| : |:|:  ||                        |:   :|||| |       |:|
Db        467 YNQLTTLSAEVLG----------------------PLQRAFWLDISHNHLETLAEGLF 502

Qy        428 NGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNM 487
              : |  :  | :  || |  | |                 |  ||:|
Db        503 SSLGRVRYLSLRNNSLQ-TFSP--------------QPGLERL---------------- 530

Qy        488 SHNNFFSLDTFPYKCLNSLQVL-DYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCE 546
                  ||  |: |   |: | |::| :           |  :     |            ||
Db        531 ------WLDANPWDCSCPLKALRDFALQN-----------PGVVPRFVQT------VCE 566

Qy        547 HQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNIT 586
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                  |  | :     : || |::  |: :  :: |
Db        567 --------GDDCQPVYTYNNITCAGPANVSGLDLRDVSET 598

RESULT 14
US-08-477-346-50
; Sequence 50, Application US/08477346
; Patent No. 6262023
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,346
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/487,072
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  603 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor bind.
;      INDIVIDUAL ISOLATE:  pro. complex-rat, Fig. 33
US-08-477-346-50

  Query Match          7.0%;  Score 290;  DB 3;  Length 603;
  Best Local Similarity   24.1%;  Pred. No. 7.8e-18;
  Matches  154;  Conservative   84;  Mismatches  240;  Indels  162;  Gaps   24;

Qy          4 NFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH 63
              |   :||::| ||: | | | | : | :| :   |  |:|    ::::| |   | | :
Db         64 NLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALLGLQN 123

Qy         64 LSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVA----- 118
              |  | |  | :::||:| |:   ||  |       |  ||      |  | :||:
Db        124 LYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGWNSLV 183

Qy        119 -------------HNLI-----QSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQ 160
                          | |:      ::  |  |  |  |  ||||  | ::|:      |
Db        184 VLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSV---KANVFVH 240

Qy        161 MPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLV 219
              :| |   | |  | :  : ||||  :: |  | | :|     :|:    || || | ||
Db        241 LPRLQ-KLYLDRNLITAVAPGAFLGMKALRWLDLSHN-RVAGLMEDTFPGLLGLHVLRLA 298
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Qy        220 -----------------LGEFR-NEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI- 260
Db        299 HNAIASLRPRTFKDLHFLEELQLGHNRIRQLGERTFEGLGQLEV----LTLNDNQITEVR 354

Qy        261 IDLFNCLTNVSSFSLVSVTI----ERV---KDFSYNFGWQHLELVNCKFGQFPTLKLKSL 313
Db        355 VGAFSGLFNVAVMNLSGNCLRSLPERVFQGLDKLHSLHLEHSCLGHVRLHTF--AGLSGL 412

Qy        314 KRLTFTSNKGGNAFSEVD------LPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLS 367
Db        413 RRLFLRD----NSISSIEEQSLAGLSELLELDLTTNRLTH--LPRQLFQGLGHLEYLLLS 466

Qy        368 FNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIF 427
Db        467 YNQLTTLSAEVLG-----------------------PLQRAFWLDISHNHLETLAEGLF 502

Qy        428 NGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNM 487
Db        503 SSLGRVRYLSLRNNSLQ-TFSP--------------QPGLERL---------------- 530

Qy        488 SHNNFFSLDTFPYKCLNSLQVL-DYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCE 546
Db        531 ------WLDANPWDCSCPLKALRDFALQN------------PGVVPRFVQT------VCE 566

Qy        547 HQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNIT 586
Db        567 --------GDDCQPVYTYNNITCAGPANVSGLDLRDVSET 598
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RESULT 15
US-08-473-089-50
; Sequence 50, Application US/08473089
; Patent No. 6342368
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/473,089
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  603 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor bind.
;      INDIVIDUAL ISOLATE:  pro. complex-rat, Fig. 33
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US-08-473-089-50

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  Query Match             7.0%;  Score 290;  DB 3;  Length 603;
  Best Local Similarity   24.1%;  Pred. No. 7.8e-18;
  Matches  154;  Conservative   84;  Mismatches  240;  Indels  162;  Gaps   24;

Qy          4 NFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH 63
Db         64 NLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALLGLQN 123

Qy         64 LSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVA----- 118
Db        124 LYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGWNSLV 183

Qy        119 -------------HNLI-----QSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQ 160
Db        184 VLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSV---KANVFVH 240

Qy        161 MPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLV 219
Db        241 LPRLQ-KLYLDRNLITAVAPGAFLGMKALRWLDLSHN-RVAGLMEDTFPGLLGLHVLRLA 298

Qy        220 -----------------LGEFR-NEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI- 260
Db        299 HNAIASLRPRTFKDLHFLEELQLGHNRIRQLGERTFEGLGQLEV----LTLNDNQITEVR 354

Qy        261 IDLFNCLTNVSSFSLVSVTI----ERV---KDFSYNFGWQHLELVNCKFGQFPTLKLKSL 313
Db        355 VGAFSGLFNVAVMNLSGNCLRSLPERVFQGLDKLHSLHLEHSCLGHVRLHTF--AGLSGL 412

Qy        314 KRLTFTSNKGGNAFSEVD------LPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLS 367
Db        413 RRLFLRD----NSISSIEEQSLAGLSELLELDLTTNRLTH--LPRQLFQGLGHLEYLLLS 466

Qy        368 FNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIF 427
Db        467 YNQLTTLSAEVLG-----------------------PLQRAFWLDISHNHLETLAEGLF 502

Qy        428 NGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNM 487
Db        503 SSLGRVRYLSLRNNSLQ-TFSP--------------QPGLERL---------------- 530

Qy        488 SHNNFFSLDTFPYKCLNSLQVL-DYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCE 546
Db        531 ------WLDANPWDCSCPLKALRDFALQN------------PGVVPRFVQT------VCE 566

Qy        547 HQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNIT 586
Db        567 --------GDDCQPVYTYNNITCAGPANVSGLDLRDVSET 598
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Search completed: March 12, 2005, 19:58:59
Job time : 32.9643 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:55:29 ; Search time 70.7097 Seconds
(without alignments)
3727.157 Million cell updates/sec

Title: US-09-396-985B-4
Perfect score: 4141
Sequence: 1 MELNFYKIPDNLPFSTKNLD.....SWNPEGTVGTGCNWQEATSI 799

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4141	100.0	799	10	US-09-950-041-8	Sequence 8, Appli
2	4141	100.0	799	14	US-10-128-166-7	Sequence 7, Appli
3	4141	100.0	799	16	US-10-732-563-8	Sequence 8, Appli
4	4141	100.0	799	16	US-10-732-796A-8	Sequence 8, Appli
5	4141	100.0	837	10	US-09-950-041-26	Sequence 26, Appl
6	625.5	15.1	661	15	US-10-038-854-135	Sequence 135, App
7	625.5	15.1	661	15	US-10-037-417-107	Sequence 107, App
8	603.5	14.6	784	10	US-09-950-041-4	Sequence 4, Appli
9	603.5	14.6	784	15	US-10-456-947-46	Sequence 46, Appl
10	602.5	14.5	784	14	US-10-095-627-12	Sequence 12, Appl
11	602.5	14.5	784	16	US-10-732-563-4	Sequence 4, Appli
12	602.5	14.5	784	16	US-10-732-796A-4	Sequence 4, Appli
13	602.5	14.5	784	17	US-10-741-600-1390	Sequence 1390, Ap
14	602.5	14.5	784	17	US-10-741-600-1391	Sequence 1391, Ap
15	599.5	14.5	784	13	US-10-145-014-23	Sequence 23, Appl
16	590	14.2	661	13	US-10-114-893-10	Sequence 10, Appl
17	590	14.2	661	15	US-10-038-854-134	Sequence 134, App
18	573	13.8	1032	10	US-09-954-987B-192	Sequence 192, App
19	573	13.8	1032	14	US-10-272-502A-31	Sequence 31, Appl
20	573	13.8	1032	15	US-10-407-952-32	Sequence 32, Appl
21	567	13.7	1050	10	US-09-954-987B-175	Sequence 175, App
22	567	13.7	1050	14	US-10-272-502A-22	Sequence 22, Appl
23	567	13.7	1050	15	US-10-407-952-26	Sequence 26, Appl
24	531.5	12.8	1032	10	US-09-950-041-37	Sequence 37, Appl
25	531.5	12.8	1040	9	US-09-864-761-38325	Sequence 38325, A
26	531.5	12.8	1041	10	US-09-954-987B-184	Sequence 184, App
27	531.5	12.8	1041	10	US-09-954-987B-186	Sequence 186, App
28	531.5	12.8	1041	14	US-10-272-502A-26	Sequence 26, Appl
29	531.5	12.8	1041	15	US-10-407-952-28	Sequence 28, Appl
30	531.5	12.8	1041	16	US-10-732-563-16	Sequence 16, Appl
31	531.5	12.8	1041	16	US-10-732-796A-16	Sequence 16, Appl
32	530.5	12.8	1041	9	US-09-168-978-3	Sequence 3, Appli
33	530.5	12.8	1041	9	US-09-978-295A-498	Sequence 498, App
34	530.5	12.8	1041	9	US-09-978-697-498	Sequence 498, App
35	530.5	12.8	1041	9	US-09-978-192A-498	Sequence 498, App
36	530.5	12.8	1041	9	US-09-999-832A-498	Sequence 498, App
37	530.5	12.8	1041	10	US-09-978-189-498	Sequence 498, App
38	530.5	12.8	1041	10	US-09-978-608A-498	Sequence 498, App
39	530.5	12.8	1041	10	US-09-978-585A-498	Sequence 498, App
40	530.5	12.8	1041	10	US-09-978-191A-498	Sequence 498, App
41	530.5	12.8	1041	10	US-09-978-403A-498	Sequence 498, App
42	530.5	12.8	1041	10	US-09-978-564A-498	Sequence 498, App
43	530.5	12.8	1041	10	US-09-999-833A-498	Sequence 498, App
44	530.5	12.8	1041	10	US-09-981-915A-498	Sequence 498, App
45	530.5	12.8	1041	10	US-09-978-824-498	Sequence 498, App

ALIGNMENTS

RESULT 1
US-09-950-041-8
; Sequence 8, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XK1
; CURRENT APPLICATION NUMBER: US/09/950,041
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-8

Query Match 100.0%; Score 4141; DB 10; Length 799;

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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  799;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180
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Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240
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Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300
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Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360
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Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480
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Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600
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Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600

Qy        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

Qy        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720
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Db        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720

Qy        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Qy        781 WNPEGTVGTGCNWQEATSI 799
              |||||||||||||||||||
Db        781 WNPEGTVGTGCNWQEATSI 799


RESULT 2
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US20030077279A1
; GENERAL INFORMATION:
;  APPLICANT: ARDITI, MOSHE
;  APPLICANT:  RAJAVASHISTH, TRIPATHI
;  APPLICANT:  SHAH, PREDIMAN K.
;  TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
;  TITLE OF INVENTION:  TOLL-LIKE RECEPTOR-4
;  FILE REFERENCE: 81476-0255398
;  CURRENT APPLICATION NUMBER: US/10/128,166
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-128-166-7

  Query Match           100.0%;  Score 4141;  DB 14;  Length 799;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  799;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60
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Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300
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Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420
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Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540
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Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600
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Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600

Qy        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660
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Db        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

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Db        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Qy        781 WNPEGTVGTGCNWQEATSI 799
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Db        781 WNPEGTVGTGCNWQEATSI 799


RESULT 3
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
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; GENERAL INFORMATION:
;  APPLICANT: Gupta, Shalley K.
;  APPLICANT:  Ghosh, Tarun K.
;  APPLICANT:  Fink, Jason R.
;  TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
;  FILE REFERENCE: 58183WO003
;  CURRENT APPLICATION NUMBER: US/10/732,563
;  CURRENT FILING DATE:  2003-12-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-732-563-8

  Query Match           100.0%;  Score 4141;  DB 16;  Length 799;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  799;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60
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Qy         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120
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Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180
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Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240
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Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360
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Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420
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Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600
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Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600

Qy        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660
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Db        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

Qy        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720
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Db        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720

Qy        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780
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Db        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Qy        781 WNPEGTVGTGCNWQEATSI 799
              ||||||||||||||||||||
Db        781 WNPEGTVGTGCNWQEATSI 799


RESULT 4
US-10-732-796A-8
; Sequence 8, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
;  APPLICANT: Gupta, Shalley K.
;  APPLICANT:  Ghosh, Tarun K.
;  APPLICANT:  Fink, Jason R.
;  TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
;  FILE REFERENCE: 58182US004
;  CURRENT APPLICATION NUMBER: US/10/732,796A
;  CURRENT FILING DATE:  2003-12-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-732-796A-8

  Query Match           100.0%;  Score 4141;  DB 16;  Length 799;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  799;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60
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Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120
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Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180
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Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240
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Qy        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360
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Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420
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Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480
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Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540
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Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600
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Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600

Qy        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

Qy        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720

Qy        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Qy        781 WNPEGTVGTGCNWQEATSI 799
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Db        781 WNPEGTVGTGCNWQEATSI 799


RESULT 5
US-09-950-041-26
; Sequence 26, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
;  APPLICANT: Hardiman, Gerard T.
;  APPLICANT:  Rock, Fernando L.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  APPLICANT:  Ho, Stephen W.K.
;  APPLICANT:  Liu, Yong-Jun
;  TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
;  FILE REFERENCE: DX0724XK1
;  CURRENT APPLICATION NUMBER: US/09/950,041
;  CURRENT FILING DATE:  2002-05-06
;  PRIOR APPLICATION NUMBER: 09/728,540
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 60/207,558
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 09/073,363
;  PRIOR FILING DATE: 1999-06-05
;  PRIOR APPLICATION NUMBER: 60/044,293
;  PRIOR FILING DATE: 1997-05-07
;  PRIOR APPLICATION NUMBER: 60/072,212
;  PRIOR FILING DATE: 1998-01-22
;  PRIOR APPLICATION NUMBER: 60/076,947
;  PRIOR FILING DATE: 1998-03-05
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 837
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-950-041-26

  Query Match           100.0%;  Score 4141;  DB 10;  Length 837;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  799;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         39 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 98

Qy         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 158

Qy        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 218

Qy        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 278

Qy        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 338

Qy        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 398

Qy        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 458

Qy        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 518

Qy        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 578

Qy        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 638

Qy        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 698

Qy        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 758

Qy        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 818

Qy        781 WNPEGTVGTGCNWQEATSI 799
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Db        819 WNPEGTVGTGCNWQEATSI 837


RESULT 6
US-10-038-854-135
; Sequence 135, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
;  APPLICANT: Spytek, Kimberly A
;  APPLICANT:  Li, Li
;  APPLICANT:  Wolenc, Adam R
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Eisen, Andrew J
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Tchernev, Velizar
;  APPLICANT:  Spaderna, Steven K
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Gusev, Vladimir Y
;  APPLICANT:  Gangolli, Esha A
;  APPLICANT:  Guo, Xiaojia S
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  MacDougall, John R
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-230
;  CURRENT APPLICATION NUMBER: US/10/038,854
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 60/258,928
;  PRIOR FILING DATE: 2000-12-29
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;  PRIOR APPLICATION NUMBER: 60/259,415
;  PRIOR FILING DATE: 2001-01-02
;  PRIOR APPLICATION NUMBER: 60/259,785
;  PRIOR FILING DATE: 2001-01-04
;  PRIOR APPLICATION NUMBER: 60/269,814
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/279,832
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/279,833
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/279,863
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/283,889
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,447
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: 60/286,683
;  PRIOR FILING DATE: 2001-04-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 411
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
;   LENGTH: 661
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-038-854-135

  Query Match             15.1%;  Score 625.5;  DB 15;  Length 661;
  Best Local Similarity   28.5%;  Pred. No. 2.6e-41;
  Matches  186;  Conservative  113;  Mismatches  273;  Indels   81;  Gaps   15;

Qy          3 LNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLS 62
              |   :||  || ||: |: ||| |  : : :|      | |||:||:|  | :  :||
Db         42 LGLNEIPGTLPNSTECLEFSFNVLPTIQNTTFSRLINLTFLDLTRCQIYWIHEDTFQSQH 101

Qy         63 HLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLI 122
               | ||:|| ||:  :|  | ||  :|: |  ::| ::|::  |: : |||: | :  | |
Db        102 RLDTLVLTANPLIFMAETALSGPKALKHLFFIQTGISSIDFIPLHNQKTLESLYLGSNHI 161

Qy        123 QSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGA 182
               | |||: |     |: ||  :| |  :   |:  | |    ||||:|: | :  |:|||
Db        162 SSIKLPKGFPT-EKLKVLDFQNNAIHYLSKEDMSSLQQ--ATNLSLNLNGNDIAGIEPGA 218

Qy        183 FKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCN 242
               |       |    ||      :    :||     :  | || | :  : |     :  ||||
Db        219 FDSAVFQSL----NFGGTQNLLVIFKGLKNSTIQSLWLGTFEDMDD-EDISPAVFEGLCE 273

Qy        243 LTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKF 302
              :::|   |    |: :   : |:| :                          | | |:|
Db        274 MSVESINL-QKHYFFNISSNTFHCFS----------------------GLQELDLTATHL 310

Qy        303 GQFPT--LKLKSLKRLTFTSNKGGN--AFSEVDLPSLEF---------------------- 337
              : |:  : | :||:|  ::||  |    |  : |||
Db        311 SELPSGLVGLSTLKKLVLSANKFENLCQISASNFPSLTHLSIKGNTKRLELGTGCLENLE 370

Qy        338 ----LDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSN-FLGLEQLEHLDFQHS 392
                  |||| : :    ||:      : |: |:||:|  ::: :  |     ||| ||   :
Db        371 NLRELDLSHDDIETSDCCNLQLRNLSHLQSLNLSYNEPLSLKTEAFKECPQLELLDLAFT 430

Qy        393 NLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFL--PD 450
               ||     | | :|  |  |::||:   ::   :|:|| :|: | : || | :  :   :
Db        431 RLKVKDAQSPFQNLHLLKVLNLSHSLLDISSEQLFDGLPALQHLNLQGNHFPKGNIQKTN 490

Qy        451 IFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQ--V 508
                |  |  | || | |  :   || ||  :  :::|||    | :   :'|: |:
Db        491 SLQTLGRLEILVLSFCDLSSIDQHAFTSLKMMNHVDLSHNR---LTSSSIEALSHLKGIY 547

Qy        509 LDYSLNHIMTSKKQELQHFPSSLAFL------NLTQNDFACTCEHQSFLQWIKDQRQLLV 562
              |: : |||            || | |       || ||   ||| :  ||:| |:  | |
Db        548 LNLASNHISII-------LPSLLPILSQQRTINLRQNPLDCTCSNIYFLEWYKENMQKLE 600

Qy        563 EVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFY 615
              : |   | '|   :|: :  : ::| |    |   :: :|| ::: :   |::
Db        601 DTEDTLCENPPLLRGVRLSDVTLSCSMAAVGIFFLIVFLLVFAILLIFAVKYF 653


RESULT 7
US-10-037-417-107
; Sequence 107, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
;  APPLICANT: Kekuda, Ramesh
;  APPLICANT:  Alsobrook II, John P
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Li, Li
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Sciore, Paul
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Rothenberg, Mark
;  APPLICANT:  Stone, David J
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Anderson, David W
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Eisen, Andrew J
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-235
;  CURRENT APPLICATION NUMBER: US/10/037,417
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: 60/260;018
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: 60/260,360
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/272,411
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/272,817
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: 60/291,186
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: 60/303,231
;  PRIOR FILING DATE: 2001-07-05
;  PRIOR APPLICATION NUMBER: 60/305,060
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: 60/318,405
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/318,700
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
;   LENGTH: 661
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-037-417-107

  Query Match             15.1%;  Score 625.5;  DB 15;  Length 661;
  Best Local Similarity   28.5%;  Pred. No. 2.6e-41;
  Matches  186;  Conservative  113;  Mismatches  273;  Indels   81;  Gaps   15;

Qy          3 LNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLS 62
              |   :||  || ||: |: ||| |  : : :|      | |||:||:|  | :  :||
Db         42 LGLNEIPGTLPNSTECLEFSFNVLPTIQNTTFSRLINLTFLDLTRCQIYWIHEDTFQSQH 101

Qy         63 HLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLI 122
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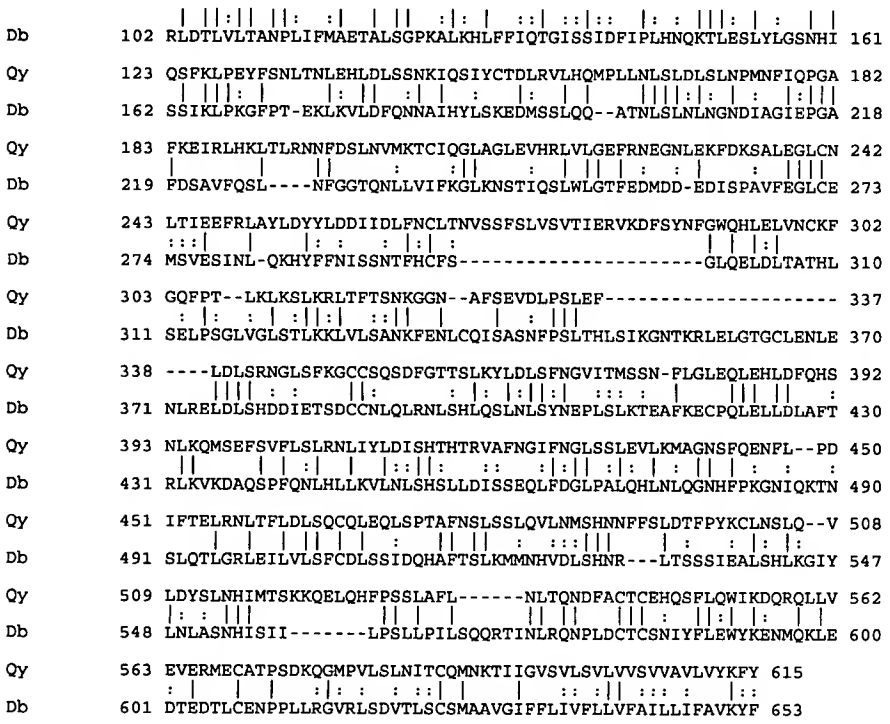
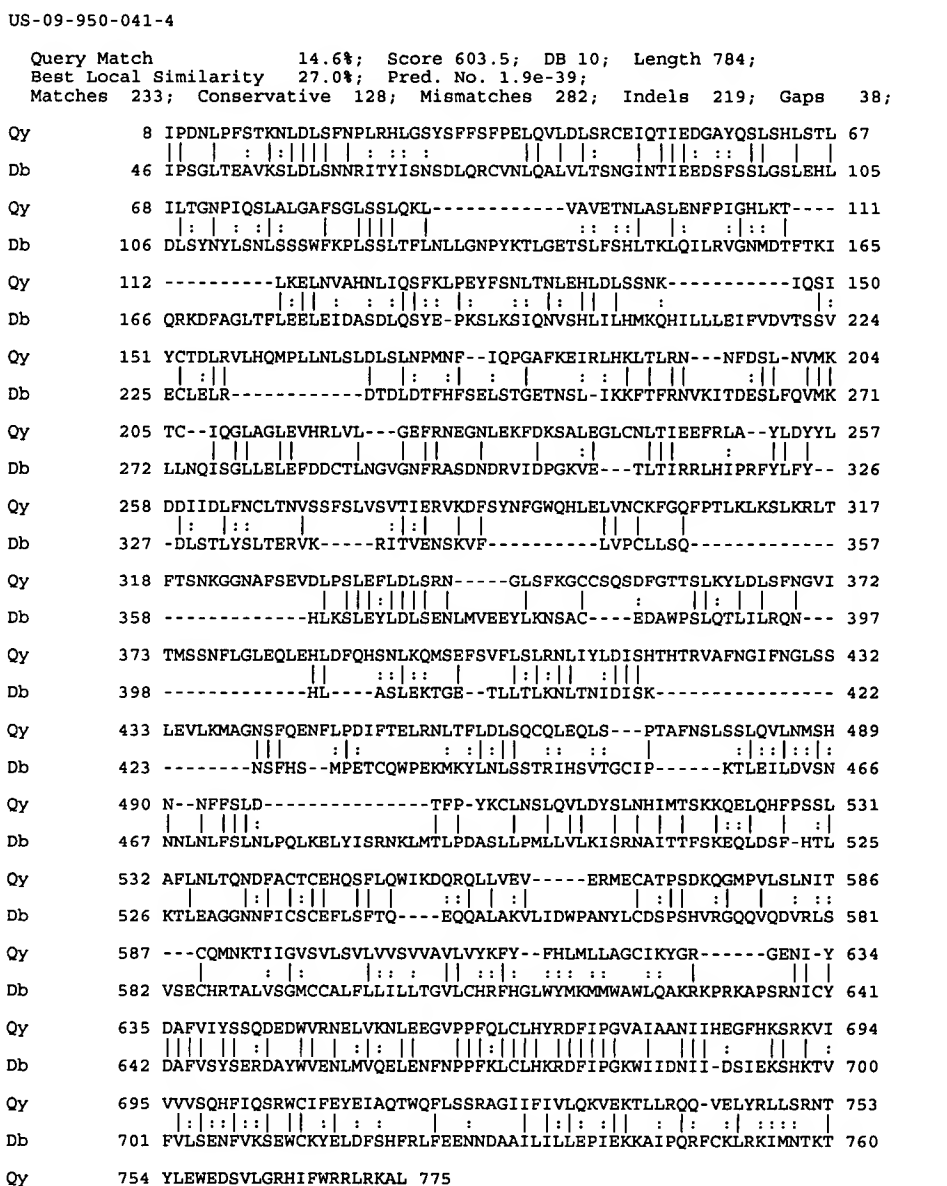


RESULT 8
US-09-950-041-4
; Sequence 4, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XK1
; CURRENT APPLICATION NUMBER: US/09/950,041
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-950-041-4

Query Match 14.6%; Score 603.5; DB 10; Length 784;
Best Local Similarity 27.0%; Pred. No. 1.9e-39;
Matches 233; Conservative 128; Mismatches 282; Indels 219; Gaps 38;



RESULT 9
US-10-456-947-46
; Sequence 46, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey

```
;  APPLICANT:  Huan Yang
;  TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
;  TITLE OF INVENTION:  HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3268.1001-007
;  CURRENT APPLICATION NUMBER: US/10/456,947
;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
;   LENGTH: 784
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-456-947-46

  Query Match             14.6%;  Score 603.5;  DB 15;  Length 784;
  Best Local Similarity   27.0%;  Pred. No. 1.9e-39;
  Matches  233;  Conservative  128;  Mismatches  282;  Indels  219;  Gaps   38;

Qy          8 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 67
              ||  |  : |:|||| | : :: :         || | |:   | |||: :: ||  |  |
Db         46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 105

Qy         68 ILTGNPIQSLALGAFSGLSSLQKL-----------VAVETNLASLENFPIGHLKT---- 111
               |: | : :|:   |  ||||  |             :: ::|  |:   :|:: |
Db        106 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 165

Qy        112 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK----------IQSI 150
                       |:|| :  : :||:: |:   :: |: || |   :             |:
Db        166 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 224

Qy        151 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 204
              | :||              |  |:  :|  :  |    : : | | ||     :||  |||
Db        225 ECLELR-----------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 271

Qy        205 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 257
              | ||  ||     |   | ||   |     |   :|    |||    :   || |
Db        272 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 326

Qy        258 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 317
               |:  |::    |       :|:|  | |          || |   |
Db        327 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------- 357

Qy        318 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 372
                        | |||:|||| |      |    |    :    ||: | |  |
Db        358 -------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 397

Qy        373 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 432
                      ||    ::|::  |    |:|:||  :|||
Db        398 -------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 422

Qy        433 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 489
                  |||    :|:       : :|:||  ::  ::   |       :|::|::|:
Db        423 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 466

Qy        490 N--NFFSLD---------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 531
              |  | |||:               | |    |  | ||  | | | |  |::|  |  :|
Db        467 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 525

Qy        532 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 586
                |    |:| |:||  || |    ::| | :|         | :||  :|  |  | : ::
Db        526 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 581

Qy        587 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 634
                  |     : |:     |:: :  || ::|:  ::: ::   ::  |       || |
Db        582 VSECHRTALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 641

Qy        635 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 694
              |||| || :|  || | :|: ||   |||:|||| ||||||  |  ||| :   || | :

Db        642 DAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 700

Qy        695 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQ-VELYRLLSRNT 753
                  |:|::|::| || :| : :    |  :    | |:|: :||  : |:  :| ::::  |
Db        701 FVLSENFVKSEWCKYELDFSHFRLFEENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKT 760

Qy        754 YLEWEDSVLGRHIFWRRLRKAL 775
              ||||      |  ||  || |:
Db        761 YLEWPMDEAQREGFWVNLRAAI 782


RESULT 10
US-10-095-627-12
; Sequence 12, Application US/10095627
; Publication No. US20030027260A1
;  GENERAL INFORMATION:
;       APPLICANT: Goddard, Audrey
;                  Godowski, Paul J.
;                  Gurney, Austin
;                  Mark, Melanie
;                  Yang, Ruey-Bing
;       TITLE OF INVENTION: Human Toll Homologues
;       NUMBER OF SEQUENCES: 32
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 1 DNA Way
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/095,627
;            FILING DATE: 11-Mar-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/105,413A
;            FILING DATE: 26-Jun-1998
;            APPLICATION NUMBER: 60/083322
;            FILING DATE: 28-APR-1998
;            APPLICATION NUMBER: 60/065311
;            FILING DATE: 13-NOV-1997
;            APPLICATION NUMBER: 60/062250
;            FILING DATE: 17-OCT-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Marschang, Diane L.
;            REGISTRATION NUMBER: 35,600
;            REFERENCE/DOCKET NUMBER: P1154-2
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650/225-5416
;            TELEFAX: 650/952-9881
;  INFORMATION FOR SEQ ID NO: 12:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 784 amino acids
;            TYPE: Amino Acid
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-095-627-12

  Query Match             14.5%;  Score 602.5;  DB 14;  Length 784;
  Best Local Similarity   27.0%;  Pred. No. 2.3e-39;
  Matches  233;  Conservative  128;  Mismatches  282;  Indels  219;  Gaps   38;

Qy          8 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 67
              ||  |  : |:|||| | : :: :         || | |:   | |||: :: ||  |  |
Db         46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 105

Qy         68 ILTGNPIQSLALGAFSGLSSLQKL-----------VAVETNLASLENFPIGHLKT---- 111
               |: | : :|:   |  ||||  |             :: ::|  |:   :|:: |
Db        106 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 165
```

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Db        106 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 165

Qy        112 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK----------IQSI 150
                       |:|| :  : :||:: |:   :: |: || |   :             |:
Db        166 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 224

Qy        151 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 204
               | :||           |  |:  :|  :  |    : : | | ||     :|| |||
Db        225 ECLELR-----------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 271

Qy        205 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 257
                 | ||  ||      |   | ||   |     |   :|    |||    :   || |
Db        272 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 326

Qy        258 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 317
               |:  |::     |       :|:|  | |          || |   |
Db        327 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------- 357

Qy        318 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 372
                     | |||:|||| |      |    |    :    ||: | |  |
Db        358 ------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 397

Qy        373 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 432
                       ||    ::|::  |    |:|:||  :|||
Db        398 ------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 422

Qy        433 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 489
                    |||    :|:       : :|:|| :: ::   |       :|::|::|:
Db        423 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 466

Qy        490 N--NFFSLD---------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 531
              |  | |||:                | |    |  | ||  | | | |  |::|  | :|
Db        467 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 525

Qy        532 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 586
                |    |:| |:||  || |    ::| | :|         | :||  :|  |  : ::
Db        526 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 581

Qy        587 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 634
                   |     : |:     |:: :  || ::|:  ::: ::   ::  |        || |
Db        582 VSECHRTALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 641

Qy        635 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 694
              |||| || :|  || | :|: ||   |||:|||| ||||||  |  ||| :   || | :
Db        642 DAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 700

Qy        695 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQ-VELYRLLSRNT 753
               |:|::|::| || :| : :    |  :    | |:|: :||  : |:  :| :::: |
Db        701 FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKT 760

Qy        754 YLEWEDSVLGRHIFWRRLRKAL 775
              ||||       |  ||  || |:
Db        761 YLEWPMDEAQREGFWVNLRAAI 782


RESULT 11
US-10-732-563-4
; Sequence 4, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
;  APPLICANT: Gupta, Shalley K.
;  APPLICANT:  Ghosh, Tarun K.
;  APPLICANT:  Fink, Jason R.
;  TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
;  FILE REFERENCE: 58183WO003
;  CURRENT APPLICATION NUMBER: US/10/732,563
;  CURRENT FILING DATE:  2003-12-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 784
;   TYPE: PRT
;   ORGANISM: Homo sapiens

US-10-732-563-4

  Query Match           14.5%;  Score 602.5;  DB 16;  Length 784;
  Best Local Similarity   27.0%;  Pred. No. 2.3e-39;
  Matches  233;  Conservative  128;  Mismatches  282;  Indels  219;  Gaps   38;

Qy          8 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 67
              ||  |  : |:|||| | : :: :        || | |:   | |||: :: ||  |  |
Db         46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 105

Qy         68 ILTGNPIQSLALGAFSGLSSLQKL------------VAVETNLASLENFPIGHLKT---- 111
               |: | : :|:   |  ||||  |             :: ::|  |:   :|:: |
Db        106 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 165

Qy        112 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK----------IQSI 150
                       |:|| :  : :||:: |:   :: |: || |   :             |:
Db        166 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 224

Qy        151 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 204
               | :||           |  |:  :|  :  |    : : | | ||     :|| |||
Db        225 ECLELR-----------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 271

Qy        205 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 257
                 | ||  ||      |   | ||   |     |   :|    |||    :   || |
Db        272 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 326

Qy        258 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 317
               |:  |::     |       :|:|  | |          || |   |
Db        327 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------- 357

Qy        318 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 372
                     | |||:|||| |      |    |    :    ||: | |  |
Db        358 ------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 397

Qy        373 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 432
                       ||    ::|::  |    |:|:||  :|||
Db        398 ------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 422

Qy        433 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 489
                    |||    :|:       : :|:|| :: ::   |       :|::|::|:
Db        423 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 466

Qy        490 N--NFFSLD---------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 531
              |  | |||:                | |    |  | ||  | | | |  |::|  | :|
Db        467 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 525

Qy        532 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 586
                |    |:| |:||  || |    ::| | :|         | :||  :|  |  : ::
Db        526 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 581

Qy        587 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 634
                   |     : |:     |:: :  || ::|:  ::: ::   ::  |        || |
Db        582 VSECHRTALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 641

Qy        635 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 694
              |||| || :|  || | :|: ||   |||:|||| ||||||  |  ||| :   || | :
Db        642 DAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 700

Qy        695 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQ-VELYRLLSRNT 753
               |:|::|::| || :| : :    |  :    | |:|: :||  : |:  :| :::: |
Db        701 FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKT 760

Qy        754 YLEWEDSVLGRHIFWRRLRKAL 775
              ||||       |  ||  || |:
Db        761 YLEWPMDEAQREGFWVNLRAAI 782


RESULT 12
US-10-732-796A-4
; Sequence 4, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
;  APPLICANT: Gupta, Shalley K.
```

```
;  APPLICANT:  Ghosh, Tarun K.
;  APPLICANT:  Fink, Jason R.
;  TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
;  FILE REFERENCE: 58182US004
;  CURRENT APPLICATION NUMBER: US/10/732,796A
;  CURRENT FILING DATE:  2003-12-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 784
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-732-796A-4

  Query Match             14.5%;  Score 602.5;  DB 16;  Length 784;
  Best Local Similarity   27.0%;  Pred. No. 2.3e-39;
  Matches  233;  Conservative  128;  Mismatches  282;  Indels  219;  Gaps   38;

Qy          8 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 67
              ||  |  : |:|||| | : :: :        || | |:   | |||: :: ||  |  |
Db         46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 105

Qy         68 ILTGNPIQSLALGAFSGLSSLQKL------------VAVETNLASLENFPIGHLKT---- 111
                |: | : :|:   |  ||||  |              :: ::|  |:   :|:: |
Db        106 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 165

Qy        112 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK-----------IQSI 150
                       |:|| :  : :||:: |:   :: |: || |   :                |:
Db        166 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 224

Qy        151 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 204
              | :||             |  |:  :|  :  |    : : | | ||     :||  |||
Db        225 ECLELR------------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 271

Qy        205 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 257
                | ||  ||      |   | ||   |     |   :|    |||    :   || |
Db        272 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 326

Qy        258 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 317
              |:  |::   |      :|:|  | |          || |   |
Db        327 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------- 357

Qy        318 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 372
                      | |||:|||| |      |    :    ||: | | |
Db        358 ------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 397

Qy        373 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 432
                        ||    ::|::  |     |:|:||  :|||
Db        398 ------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 422

Qy        433 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 489
                  |||    :|:       : :|:||  ::  ::    |       :|::|::|:
Db        423 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 466

Qy        490 N--NFFSLD--------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 531
              |  | |||:              | |    |  | || | | | |  |::|  |  :|
Db        467 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 525

Qy        532 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 586
                |    |:| |:||  || |    ::| | :|          | :||  :|  |  : ::
Db        526 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 581

Qy        587 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 634
                  |    : |:      |::  :  || ::|:  ::: ::    ::  |         || |
Db        582 VSECHRTALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 641

Qy        635 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 694
              |||| || :|  || | :|: ||   |||:|||| ||||||  |  ||| :  || | :
Db        642 DAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 700

Qy        695 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQ-VELYRLLSRNT 753
              |:|::|::| || :| : :    |  :    | |:|: :||  : |:  :| ::::  |
Db        701 FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKT 760

Qy        754 YLEWEDSVLGRHIFWRRLRKAL 775
                ||||      |  ||  || |:
Db        761 YLEWPMDEAQREGFWVNLRAAI 782


RESULT 13
US-10-741-600-1390
; Sequence 1390, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1390
;   LENGTH: 784
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-600-1390

  Query Match             14.5%;  Score 602.5;  DB 17;  Length 784;
  Best Local Similarity   27.0%;  Pred. No. 2.3e-39;
  Matches  233;  Conservative  128;  Mismatches  282;  Indels  219;  Gaps   38;

Qy          8 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 67
              ||  |  : |:|||| | : :: :        || | |:   | |||: :: ||  |  |
Db         46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 105

Qy         68 ILTGNPIQSLALGAFSGLSSLQKL------------VAVETNLASLENFPIGHLKT---- 111
                |: | : :|:   |  ||||  |              :: ::|  |:   :|:: |
Db        106 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 165

Qy        112 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK-----------IQSI 150
                       |:|| :  : :||:: |:   :: |: || |   :                |:
Db        166 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 224

Qy        151 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 204
              | :||             |  |:  :|  :  |    : : | | ||     :||  |||
Db        225 ECLELR------------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 271

Qy        205 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 257
                | ||  ||      |   | ||   |     |   :|    |||    :   || |
Db        272 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 326

Qy        258 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 317
              |:  |::   |      :|:|  | |          || |   |
Db        327 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------- 357

Qy        318 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 372
                      | |||:|||| |      |    :    ||: | | |
Db        358 ------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 397

Qy        373 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 432
                        ||    ::|::  |     |:|:||  :|||
Db        398 ------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 422

Qy        433 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 489
                  |||    :|:       : :|:||  ::  ::    |       :|::|::|:
Db        423 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 466

Qy        490 N--NFFSLD--------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 531
              |  | |||:              | |    |  | || | | | |  |::|  |  :|
Db        467 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 525

Qy        532 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 586
                |    |:| |:||  || |    ::| | :|          | :||  :|  |  : ::
Db        526 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 581
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Qy        587 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 634
Db        582 VSECHRTALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 641

Qy        635 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 694
Db        642 DAFVSYSERDAYWVENLMVQELENFNPPPKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 700

Qy        695 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQ-VELYRLLSRNT 753
Db        701 FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKT 760

Qy        754 YLEWEDSVLGRHIFWRRLRKAL 775
Db        761 YLEWPMDEAQREGFWVNLRAAI 782


RESULT 14
US-10-741-600-1391
; Sequence 1391, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1391
;   LENGTH: 784
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-600-1391

  Query Match             14.5%;  Score 602.5;  DB 17;  Length 784;
  Best Local Similarity   27.0%;  Pred. No. 2.3e-39;
  Matches  233;  Conservative  128;  Mismatches  282;  Indels  219;  Gaps   38;

Qy          8 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 67
Db         46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 105

Qy         68 ILTGNPIQSLALGAFSGLSSLQKL------------VAVETNLASLENFPIGHLKT---- 111
Db        106 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 165

Qy        112 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK-----------IQSI 150
Db        166 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 224

Qy        151 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 204
Db        225 ECLELR------------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 271

Qy        205 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 257
Db        272 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 326

Qy        258 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 317
Db        327 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------- 357

Qy        318 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 372
Db        358 -------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 397

Qy        373 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 432
Db        398 -------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 422

Qy        433 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 489
Db        423 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 466

Qy        490 N--NFFSLD---------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 531
Db        467 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 525

Qy        532 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 586
Db        526 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 581

Qy        587 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 634
Db        582 VSECHRTALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 641

Qy        635 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 694
Db        642 DAFVSYSERDAYWVENLMVQELENFNPPPKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 700

Qy        695 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQ-VELYRLLSRNT 753
Db        701 FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKT 760

Qy        754 YLEWEDSVLGRHIFWRRLRKAL 775
Db        761 YLEWPMDEAQREGFWVNLRAAI 782


RESULT 15
US-10-145-014-23
; Sequence 23, Application US/10145014
; Publication No. US20020168755A1
; GENERAL INFORMATION:
;  APPLICANT: Dalie, Barbara
;  APPLICANT:  Fan, Xuedong
;  APPLICANT:  Lundell, Daniel
;  APPLICANT:  Lunn, Charles A.
;  APPLICANT:  Tan, Jimmy C.
;  APPLICANT:  Zavodny, Paul J.
;  TITLE OF INVENTION: Mammalian TNF-alpha Convertases
;  FILE REFERENCE: JB0601QD
;  CURRENT APPLICATION NUMBER: US/10/145,014
;  CURRENT FILING DATE:  2002-05-14
;  PRIOR APPLICATION NUMBER: 09/982,308
;  PRIOR FILING DATE: 2001-10-17
;  PRIOR APPLICATION NUMBER: 09/156,163
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 08/889,909
;  PRIOR FILING DATE: 1997-07-10
;  PRIOR APPLICATION NUMBER: 60/021,710
;  PRIOR FILING DATE: 1996-07-12
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;   LENGTH: 784
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-145-014-23

  Query Match             14.5%;  Score 599.5;  DB 13;  Length 784;
  Best Local Similarity   27.0%;  Pred. No. 4e-39;
  Matches  233;  Conservative  128;  Mismatches  282;  Indels  219;  Gaps   38;

Qy          8 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 67
Db         46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 105

Qy         68 ILTGNPIQSLALGAFSGLSSLQKL------------VAVETNLASLENFPIGHLKT---- 111
Db        106 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 165

Qy        112 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK-----------IQSI 150
                       |:|| :  : :||:: |:   :: |: || |   :             |:
Db        166 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 224
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Db        166 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 224

Qy        151 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 204

Db        225 ECLELR-----------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 271

Qy        205 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 257

Db        272 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 326

Qy        258 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 317

Db        327 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------ 357

Qy        318 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 372

Db        358 ------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 397

Qy        373 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 432

Db        398 ------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 422

Qy        433 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 489

Db        423 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 466

Qy        490 N--NFFSLD---------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 531

Db        467 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 525

Qy        532 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 586

Db        526 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 581

Qy        587 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 634

Db        582 VSECHRIALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 641

Qy        635 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 694

Db        642 DAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 700

Qy        695 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQ-VELYRLLSRNT 753

Db        701 FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKT 760

Qy        754 YLEWEDSVLGRHIFWRRLRKAL 775

Db        761 YLEWPMDEAQREGFWVNLRAAI 782
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Search completed: March 12, 2005, 20:27:52
Job time : 74.7097 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:01 ; Search time 20.6156 Seconds
(without alignments)
3729.074 Million cell updates/sec

Title: US-09-396-985B-4
Perfect score: 4141
Sequence: 1 MELNFYKIPDNLPFSTKNLD.....SWNPEGTVGTGCNWQEATSI 799

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	625.5	15.1	661	2	I56258	RP105 - mouse
2	474	11.4	786	2	T08664	Toll protein-like
3	452	10.9	1097	2	A29943	Toll protein precu
4	433	10.5	1389	2	T13852	gene wheeler prote
5	421	10.2	1385	2	T13887	tlr protein - frui
6	392	9.5	1066	2	T15864	hypothetical prote
7	333.5	8.1	1134	1	A29944	chaoptin precursor
8	309	7.5	605	2	JC5239	insulin-like growt
9	302	7.3	853	2	T17461	disease resistance
10	297	7.2	605	2	A41915	insulin-like growt
11	296	7.1	1531	2	T42218	slit-1 protein hom
12	292	7.1	994	2	H96510	probable disease r
13	291	7.0	845	2	T07039	Hcr9-0 protein - t
14	290	7.0	603	2	JC1282	insulin-like growt
15	290	7.0	855	2	T07015	Cf-4A protein - to
16	289.5	7.0	603	2	T24315	hypothetical prote
17	289.5	7.0	1112	2	T10504	disease resistance
18	289	7.0	855	2	T17460	disease resistance
19	287.5	6.9	662	2	S42799	garp precursor - h
20	284.5	6.9	907	2	JE0176	orphan G protein-c
21	284	6.9	603	2	JC6128	insulin-like growt
22	284	6.9	907	2	JG0193	G protein-coupled
23	281.5	6.8	622	2	JC7973	synleurin - human
24	281	6.8	1134	2	T04587	hypothetical prote
25	280	6.8	890	2	T00800	disease resistance
26	278.5	6.7	1019	2	C96519	probable disease r
27	276.5	6.7	768	2	T17462	disease resistance
28	276	6.7	983	2	G84524	probable disease r
29	276	6.7	1027	2	B85089	receptor protein k
30	270.5	6.5	1523	2	T13953	MEGF5 protein - ra
31	270	6.5	1143	2	T10636	hypothetical prote
32	266.5	6.4	1091	2	A58532	glial cell membran
33	266.5	6.4	1784	2	C96615	hypothetical prote
34	265.5	6.4	863	2	A55173	cf-9 protein precu
35	265	6.4	910	2	G84648	probable disease r
36	264.5	6.4	766	2	T01817	hypothetical prote
37	264	6.4	1469	2	B36665	slit protein 2 pre
38	264	6.4	1480	2	A36665	slit protein 1 pre
39	262.5	6.3	967	2	T48210	hypothetical prote
40	261.5	6.3	1051	2	T13174	gp150 protein - fr
41	260.5	6.3	1109	2	T18536	receptor-like prot
42	259	6.3	1029	2	T00712	protein kinase hom
43	257	6.2	738	2	T19938	hypothetical prote
44	254	6.1	771	2	T02565	disease resistance
45	253.5	6.1	991	2	T52400	receptor-like prot

ALIGNMENTS

RESULT 1
I56258
RP105 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56258
R;Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995
A;Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a m
A;Reference number: I56258; MUID:95204928; PMID:7897216
A;Accession: I56258
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-661 <RES>
A;Cross-references: UNIPROT:Q62192; GB:D37797; NID:g761711; PIDN:BAA07043.1; PID:g761717

Query Match 15.1%; Score 625.5; DB 2; Length 661;
Best Local Similarity 28.5%; Pred. No. 9.6e-32;
Matches 186; Conservative 113; Mismatches 273; Indels 81; Gaps 15;

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Qy          3 LNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLS 62
              |   :||  || ||: |: ||| |  : : :|      | |||:||:|  | :  :||
Db         42 LGLNEIPGTLPNSTECLEFSFNVLPTIQNTTFSRLINLTFLDLTRCQIYWIHEDTFQSQH 101

Qy         63 HLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLI 122
              | ||:|| ||:  :|  | ||  :|: |  ::| ::|::  |: : |||: | :  | |
Db        102 RLDTLVLTANPLIFMAETALSGPKALKHLFFIQTGISSIDFIPLHNQKTLESLYLGSNHI 161

Qy        123 QSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGA 182
              | |||: |      |: ||  :| |  :   |:  | |    ||||:|: | :  |:|||
Db        162 SSIKLPKGFPT-EKLKVLDFQNNAIHYLSKEDMSSLQQ--ATNLSLNLNGNDIAGIEPGA 218

Qy        183 FKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCN 242
              |      |   ||    :    :||   :  | || | :  : |    :  ||||
Db        219 FDSAVFQSL----NFGGTQNLLVIFKGLKNSTIQSLWLGTFEDMDD-EDISPAVFEGLCE 273

Qy        243 LTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKF 302
              :::|   |    |: :   : |:| :                      | | |:|
Db        274 MSVESINL-QKHYFFNISSNTFHCFS--------------------GLQELDLTATHL 310

Qy        303 GQFPT--LKLKSLKRLTFTSNKGGN--AFSEVDLPSLEF---------------------- 337
              : |:  : | :||:|  ::||  |    |  : |||
Db        311 SELPSGLVGLSTLKKLVLSANKFENLCQISASNFPSLTHLSIKGNTKRLELGTGCLENLE 370

Qy        338 ----LDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSN-FLGLEQLEHLDFQHS 392
                  |||| : :   ||:      : |: |:||:|  ::: :  |    ||| ||   :
Db        371 NLRELDLSHDDIETSDCCNLQLRNLSHLQSLNLSYNEPLSLKTEAFKECPQLELLDLAFT 430

Qy        393 NLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFL--PD 450
              ||     | | :|  |  |::||:   ::   :|:|| :|: | : || | :  :   :
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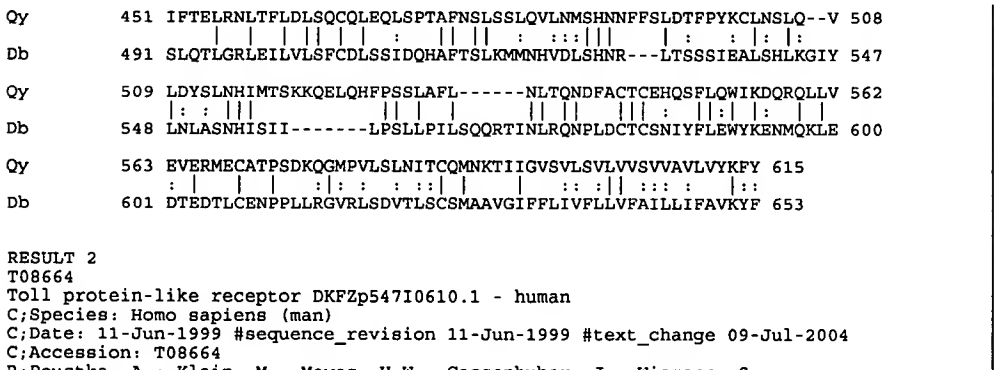
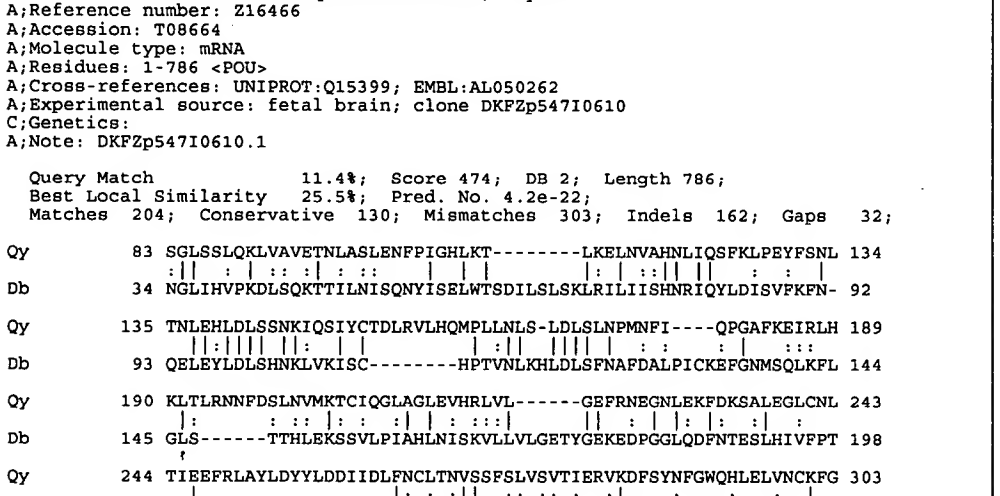
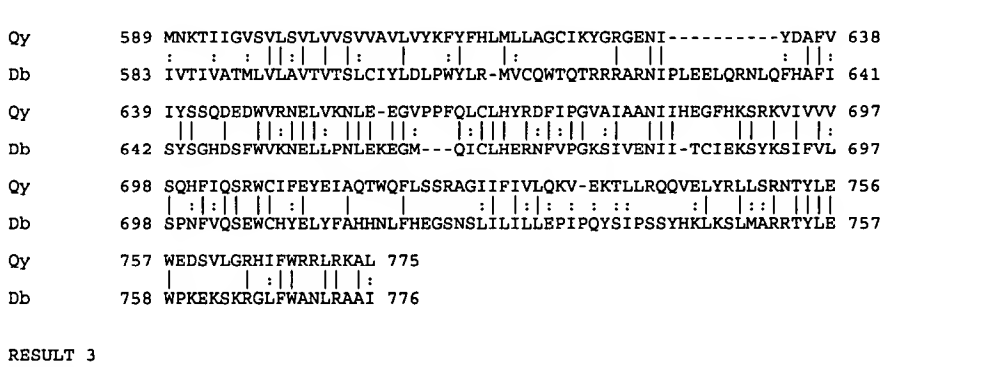


RESULT 2
T08664
Toll protein-like receptor DKFZp547I0610.1 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08664
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16466
A;Accession: T08664
A;Molecule type: mRNA
A;Residues: 1-786 <POU>
A;Cross-references: UNIPROT:Q15399; EMBL:AL050262
A;Experimental source: fetal brain; clone DKFZp547I0610
C;Genetics:
A;Note: DKFZp547I0610.1

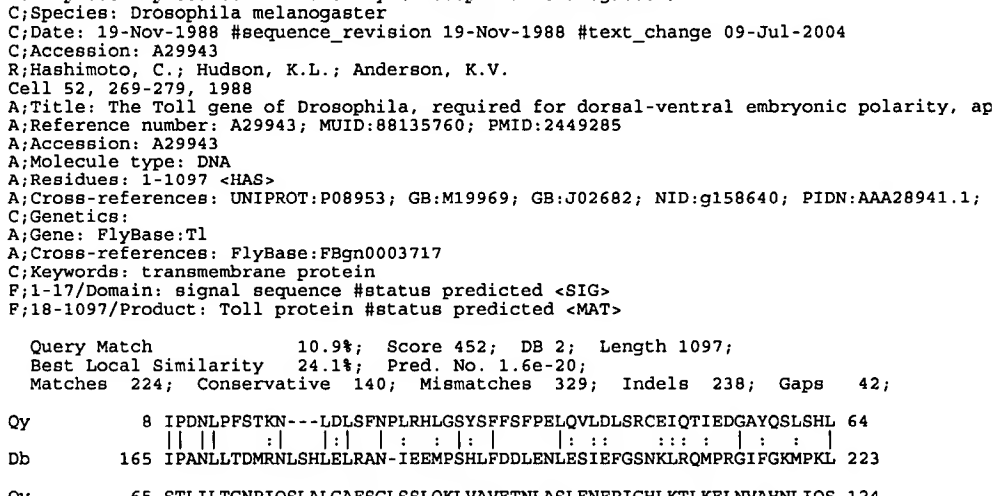
Query Match 11.4%; Score 474; DB 2; Length 786;
Best Local Similarity 25.5%; Pred. No. 4.2e-22;
Matches 204; Conservative 130; Mismatches 303; Indels 162; Gaps 32;





RESULT 3
A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A29943
R;Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A;Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, ap
A;Reference number: A29943; MUID:88135760; PMID:2449285
A;Accession: A29943
A;Molecule type: DNA
A;Residues: 1-1097 <HAS>
A;Cross-references: UNIPROT:P08953; GB:M19969; GB:J02682; NID:g158640; PIDN:AAA28941.1;
C;Genetics:
A;Gene: FlyBase:Tl
A;Cross-references: FlyBase:FBgn0003717
C;Keywords: transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-1097/Product: Toll protein #status predicted <MAT>

Query Match 10.9%; Score 452; DB 2; Length 1097;
Best Local Similarity 24.1%; Pred. No. 1.6e-20;
Matches 224; Conservative 140; Mismatches 329; Indels 238; Gaps 42;



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Db        529 MTHNKIRRIALPEDVHLGEGYNNNLVHVDLNDNPLVCDCTILWFIQLVRGVHKPQYSRQF 588

Qy        431 ------------------------------------------------------SSLEV 435
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Db        589 KLRTDRLVCSQPNVLEGTPVRQIEPQTLICPLDFSDDPRERKCPRGCNCHVRTYDKALVI 648

Qy        436 LKMAGNSFQENFLPDIFTELRNLTFLDL-----SQCQLEQLSPTAFNSLSSLQVLNMSHN 490
                :||      ||::    :|:  ::|     :  :|   :   : |::|   |::: |
Db        649 NCHSGNLTHVPRLPNLH---KNMQLMELHLENNTLLRLPSANTPGYESVTS---LHLAGN 702

Qy        491 NFFSLDT--FPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLN---------LTQN 539
              |  |:|    |     :|  || | ||:     | |    : | |||          |: |
Db        703 NLTSIDVDQLP----TNLTHLDISWNHL-----QMLN--ATVLGFLNRTMKWRSVKLSGN 751

Qy        540 DFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTI-IGVSV 598
              : | |   :  | : :|  : : :   | |         |  || | |   | : | ::|
Db        752 PWMCDCTAKPLLLFTQDNFERIGDRNEMMCVNAEMPTRMVELSTNDICPAEKGVFIALAV 811

Qy        599 ---LSVLVVSVVAVLVYKP--------YFHLMLLAGCIKYGRGENI-----YDAFVIYSS 642
                 |: |:    | | |||         | | :||     :   |::     :|||: ||
Db        812 VIALTGLLAGFTAALYYKFQTEIKIWLYAHNLLL----WFVTEEDLDKDKKFDAFISYSH 867

Qy        643 QDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFI 702
              :|: :: : ||  || |   ||||:| ||:: |  |  ||:       ||: |:|:||:||
Db        868 KDQSFIEDYLVPQLEHGPQKFQLCVHERDWLVGGHIPENIM-RSVADSRRTIIVLSQNFI 926

Qy        703 QSRWCIFEYEIAQTWQFLSSRAGIIFIV---LQKVEKTLLRQQVELYRLLSRNTYLEWED 759
              :| |   |:  |       |: || |:   :  |||  | :::: |  |  ||||:| |
Db        927 KSEWARLEFRAAHRSALNEGRSRIIVIIYSDIGDVEK--LDEELKAY--LKMNTYLKWGD 982

Qy        760 SVLGRHIFWRRLRKALLDGKSWNPEGTVGTG 790
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Db        983 P-----WFWDKLRFALPHRR---PVGNIGNG 1005


RESULT 4
T13852
gene wheeler protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13852
R;Eldon, E.; Kooyer, S.; D'evelyn, D.; Duman, M.; Lawinger, P.; Botas, J.; Bellen, H.
Development 120, 885-899, 1994
A;Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simila
A;Reference number: Z17796; MUID:95324375; PMID:7600965
A;Accession: T13852
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1389 <ELD>
A;Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:g415682; PID:g1019104; PIDN:AAA7920
C;Genetics:
A;Gene: wheeler
A;Cross-references: FlyBase:FBgn0004364

  Query Match           10.5%;  Score 433;  DB 2;  Length 1389;
  Best Local Similarity   24.4%;  Pred. No. 3.4e-19;
  Matches  217;  Conservative  138;  Mismatches  356;  Indels  178;  Gaps   34;

Qy         19 LDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLA 78
              |:|| | |  :|| :|     ||:||:    |  ||:||:  | :| || |  | : :|
Db        338 LNLSNNALTRIGSKTFKELYFLQILDMRNNSIGHIEEGAFLPLYNLHTLNLAENRLHTLD 397

Qy         79 LGAFSGLSSLQKLVAVETNLASL-ENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNL 137
                |:||  | ||  :  || |: |:     :   ||||::: |  |  ::||   :|: |
Db        398 NRIFNGLYVLTKL-TLNNNLVSIVESQAFRNCSDLKELDLSSN--QLTEVPEAVQDLSML 454

Qy        138 EHLDLSSNKIQSIYCTDLRVLHQMPLLNL--------------------SLDLSLNPMNF 177
              : |||  |:|         | |:|:  | |                    |:|: | :
Db        455 KTLDLGENQISEFKNNTFRNLNQLTGLRLIDNRIGNITVGMFQDLPRLSVLNLAKNRIQS 514

Qy        178 IQPGAF-KEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNE---------- 226
              |: ||| |   :  : |  ||       | | |:       | |    |
Db        515 IERGAFDKNTEIEAIRLDKNF------LTDINGIFATLASLLWLNLSENHLVWFDYAFIP 568

Qy        227 GNLEKFD--KSALEGLCNL--TIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIER 282
              ||:  |   : :| | |      || |:  ||   : | ::   ::  :|  |: :
Db        569 SNLKWLDIHGNYIEALGNYYKLQEEIRVTTLDASHNRITEI-GAMSVPNSIELLFINNNI 627

Qy        283 VKDFSYN--FGWQHLELVNCKFGQFPTLKLKSLKRLTFTSNK-------GGNAFS----- 328
              :     |       | |:       : | :|:    :: |       ||| |
Db        628 IGQIQANTFVDKTRLARVDLYANVLSKISLNALRVAPVSAEKPVPEFYLGGNPFECDCSM 687

Qy        329 ----------------EVDLPSLEFL-------------DLSRNGLSFK---------GC 350
                             ||| ::| |                || :    |         |
Db        688 EWLQRINNLTTRQHPHVVDLGNIECLMPHSRSAPLRPLASLSASDFVCKYESHCPPTCHC 747

Qy        351 CSQSDFGTTSLKYLDLSFNGVITMSSNFL--GLEQLEHLDFQHSNLKQMSEFSVFLSLRN 408
              |         :   : |      | ::| :  | : |  |      |         ::|   |
Db        748 CEYEQCECEVICPGNCSCFHDATWATNIVDCGRQDLAAL----PNRIPQDVSDLYLDGNN 803

Qy        409 LIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQL 468
              :  |:: |   |     ::   |:|  |:                   :| ||  | |   :|
Db        804 MPELEVGHLTGRRNLRALYLNASNLMTLQNGS-----------LAQLVNLRVLHLENNKL 852

Qy        469 EQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFP 528
               |  | | ||  |: | : :|    :    :: | ||:||    | : :    : :|
Db        853 TALEGTEFRSLGLLRELYLHNNMLTHISNATFEPLVSLEVLRLDNNRLSSLPHLQYRH-- 910

Qy        529 SSLAFLNLTQNDFACTCEH-QSFLQWIKDQRQLLVEVERMECATPSDKQGMPVL------ 581
              || | | :| ::| |:  :   |:: |   :: :   : |      |: : ::
Db        911 -SLQGLTLGRNAWSCRCQQLRELAQFVSDNAMVVRDAHDIYCLDAGIKRELELIGNLANG 969

Qy        582 ----------SLNITCQMNKT-IIG------VSVLSVLVVSVVAVLVYKFYFHLMLLAGC 624
                         : ||:   :    ||       | ||  ||| :: | |::    : | |
Db        970 PDCSDLLDASASNISSSQDLAGAIGCPCWPAVLVLIFLVVVLIIVFVFRESVRMWLFA-- 1027

Qy        625 IKYG------RGEN---IYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPG 675
               ||      | |:   :|||:::| :| ::|   :    || | |||:||:  || :|
Db       1028 -HYGVRVCEPRFEDAGKLYDAIILHSEKDYEFVCRNIAAELEHGRPPFRLCIQQRD-LPP 1085

Qy        676 VAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQK-- 733
              |    :: ||   |||:|:|:::: : : |   |:  |    |  |  |:     ||
Db       1086 QASHLQLV-EGARASRKIILVLTRNLLATEWNRIEFRNA----FHESLRGL----AQKLV 1136

Qy        734 -VEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHI------FWRRLRKAL 775
              :|:| :  : |    ||   ||:   ||    :       || :|| |:
Db       1137 IIEETSVSAEAEDVAELS--PYLK---SVPSNRLLTCDRYFWEKLRYAI 1180


RESULT 5
T13887
tlr protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13887
R;Chiang, C.; Beachy, P.A.
Mech. Dev. 47, 225-239, 1994
A;Title: Expression of a novel Toll-like gene spans the parasegment boundary and contrib
A;Reference number: Z17805; MUID:95151581; PMID:7848870
A;Accession: T13887
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1385 <CHI>
A;Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PIDN:AAB33383
C;Genetics:
A;Cross-references: FlyBase:FBgn0004364
A;Note: tlr

  Query Match           10.2%;  Score 421;  DB 2;  Length 1385;
  Best Local Similarity   24.0%;  Pred. No. 1.9e-18;
  Matches  213;  Conservative  139;  Mismatches  359;  Indels  178;  Gaps   33;

Qy         19 LDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLA 78
              |:|| | |  :|| :|     ||:||:    |  ||:||:  | :| || |  | : :|
Db        338 LNLSNNALTRIGSKTFKELYFLQILDMRNNSIGHIEEGAFLPLYNLHTLNLAENRLHTLD 397
```

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Qy          79 LGAFSGLSSLQKLVAVETNLASL-ENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNL 137
               |:||  | ||  :  || |: |:   :    ||||::: |  |  ::||  :|: |
Db         398 NRIFNGLYVLTKL-TLNNNLVSIVESQAFRNCSDLKELDLSSN--QLTEVPEAAQDLSML 454

Qy         138 EHLDLSSNKIQSIYCTDLRVLHQMPLLNL--------------------SLDLSLNPMNF 177
               : |||  |:|         | |:|:  | |                    |:|: | :
Db         455 KTLDLGENQISEFKNNTFRNLNQLTGLRLIDNRIGNITVGMFQDLPRLSVLNLAKNRIQS 514

Qy         178 IQPGAF-KEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNE---------- 226
               |: ||| |   :  : |   |       | | |:       | |    |
Db         515 IERGAFDKNTEIEAIRLDKKF------LTDINGIFATLASLLWLNLSENHLVWFDYAFIP 568

Qy         227 GNLEKFD--KSALEGLCNL--TIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIER 282
               ||:  |   : :| | |     || |:  ||  : | ::   ::  :|  |: :
Db         569 SNLKWLDIHGNYIEALGNYYKLQEEIRVTTLDASHNRITEI-GAMSVPNSIELLFINNNI 627

Qy         283 VKDFSYN--FGWQHLELVNCKFGQFPTLKLKSLKRLTFTSNK-------GGNAFS----- 328
               :     |      |  |:        : | :|:    :: |       ||| |
Db         628 IGQIQANTFVDKTRLARVDLYANVLSKISLNALRVAPVSAEKPVPEFYLGGNPFECDCSM 687

Qy         329 ----------------EVDLPSLEFL-------------DLSRNGLSFK---------GC 350
                             ||| ::| |               || :    |          |
Db         688 EWLQRINNLTTRQHPHVVDLGNIECLMPHSRSAPLRPLASLSASDFVCKYESHCPPTCHC 747

Qy         351 CSQSDFGTTSLKYLDLSFNGVITMSSNFL--GLEQLEHLDFQHSNLKQMSEFSVFLSLRN 408
               |      :   : |     | ::| :  | : |  |      |        ::|  |
Db         748 CEYEQCECEVICPGNCSCFHDATWATNIVDCGRQDLAAL----PNRIPQDVSDLYLDGNN 803

Qy         409 LIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQL 468
               :  |:: |   |     ::   |:|  |:                 :| ||  | |   :|
Db         804 MPELEVGHLTGRRNLRALYLNASNLMTLQNGS-----------LAQLVNLRVLHLENNKL 852

Qy         469 EQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFP 528
               |  | | ||  |: | : :|    :    :: | ||:||     | : :    : :|
Db         853 TALEGTEFRSLGLLRELYLHNNMLTHISNATFEPLVSLEVLRLDNNRLSSLPHLQYRH-- 910

Qy         529 SSLAFLNLTQNDFACTCEH-QSFLQWIKDQRQLLVEVERMECATPSDKQGMPVL------ 581
               ||  | | :| ::| |:  :   |:: |   :: :   : |     |: : ::
Db         911 -SLQGLTLGRNAWSCRCQQLRELAQFVSDNAMVVRDAHDIYCLDAGIKRELELIGNLANG 969

Qy         582 ----------SLNITCQMN-------KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGC 624
                         : ||:   :          :  | ||  | | :: | |::    : | |
Db         970 PDCSDLLDASASNISSSQDLAGGYRLPLLAAVLVLIFLDVVLIIVFVFRESVRMWLFA-- 1027

Qy         625 IKYG------RGEN---IYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPG 675
               ||       | |:   :|||  :::| :| ::|   :    || | |||:||:  || :|
Db        1028 -HYGVRVCEPRFEDAGKLYDAIILHSEKDYEFVCRNIAAELEHGRPPFRLCIQQRD-LPP 1085

Qy         676 VAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQK-- 733
               |    :: ||   |||:|:|:::: : : |   |:  |    |  |  |:          ||
Db        1086 QASHLQLV-EGARASRKIILVLTRNLLATEWNRIEFRNA----FHESLRGL----AQKLV 1136

Qy         734 -VEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHI------FWRRLRKAL 775
              :|:| :  : |    ||   ||:  ||    :      || :|| |:
Db        1137 IIEETSVSAEAEDVAELS--PYLK---SVPSNRLLTCDRYFWEKLRYAI 1180
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RESULT 6
T15864
hypothetical protein C56E6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15864
R;Fulton, L.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C56E6.
A;Reference number: S69019
A;Accession: T15864
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1066 <FUL>
A;Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:g1055114; PID:g1055120; PIDN:AAA810
C;Genetics:
A;Gene: CESP:C56E6.6
A;Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3; 9

  Query Match   9.5%; Score 392; DB 2; Length 1066;
  Best Local Similarity   27.2%; Pred. No. 9e-17;
  Matches 150; Conservative   96; Mismatches 214; Indels   92; Gaps   22;

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Qy          24 NPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFS 83
               | :| |  :|| || ::: ||:|  :|||:|| ::::: |: :| |: | |  |  |
Db         154 NKVRRLDKHSFRSFRKIRELDISYNQIQTVEDSSFETVGHMQSLDLSYNRIAYLPRG--- 210

Qy          84 GLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLS 143
                                  |:||     |||| | :| |:|  :   ||   :| || ||:|:
Db         211 ----------------MLKNF----AKTLKTLKLAENMIHA--TPEALRDLRNLTHLNLN 248

Qy         144 SNKIQSI------YCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNF 197
               ||:  |      |||  |          | :: | :  |  |    ::
Db         249 GNKLNRIDGDVLKGCTDTLV---------ELFIANNYLEHIPHGVLSGMK--------QL 291

Qy         198 DSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYL 257
               : |:: |  |  |              :   :|    |      :  | :   |:  :  ||
Db         292 EHLDISKNKIMSL------------KKPTSLLSITKEETSTVRRLNLAGNRINNMSDYL 338

Qy         258 DDIIDLFNCLTNVS-SFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTL-KLKSLKR 315
               | :    || |  ||: :     || :   |  : | | | :    ||:| :|  |:
Db         339 --IFEHMPLLTYVDVSFNRIRFISPRVFEKLKNL--ESLFLQNNQLAHFPSLFRLDKLRH 394

Qy         316 LTFTSN---KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS---LKYLDLSFN 369
               |   :|   |  | ||  ||| |: | |: | |      ::: ||::|   || |:|: |
Db         395 LMLDNNQIQKIDN-FSLADLPKLQHLSLAGNQLDI---ITENMFGSSSSSELKSLNLAHN 450

Qy         370 GVITMSS-NFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFN 428
               : ::|| :|  |: |: |  |:|:: ::  : | :|||| |||:||
Db         451 KIHSISSRSFSDLDNLQQLRLSHNNIRTITSMT-FSNLRNLRYLDLSHNRIIKILPSALY 509

Qy         429 GLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMS 488
               | :|:|| :  |:  |  | |    :|  | ||     : |     |:| :  |:|
Db         510 QLPALDVLHLDHNNLNE-IDRDAFRSFSDLQSLKLSHNAFRRFSCEFLGSISQVHQLDLS 568

Qy         489 HNNFFSLDTFPYKCL-NSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQN-------D 540
               |    :| |   |:   :: |  : | :    :: ||  : |  :::: |          |
Db         569 SNQINEIDIF---CIARGIRKLSLASNSVEKINRKLLQD-ATELTSIDISHNGIIDVDSD 624

Qy         541 FACTCEHQSFLQ 552
               | |   | ::
Db         625 AFCECRKLSHIK 636
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RESULT 7
A29944
chaoptin precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: photoreceptor cell-specific membrane protein
C;Species: Drosophila melanogaster
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29944; A21123
R;Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
Cell 52, 291-301, 1988
A;Title: Chaoptin, a cell surface glycoprotein required for Drosophila photoreceptor cel
A;Reference number: A29944; MUID:88135762; PMID:3124963
A;Accession: A29944
A;Molecule type: DNA
A;Residues: 1-1134 <REI>
A;Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M1901
R;Zipursky, S.L.; Venkatesh, T.R.; Teplow, D.B.; Benzer, S.
Cell 36, 15-26, 1984
A;Title: Neuronal development in the Drosophila retina: monoclonal antibodies as molecul
A;Reference number: A21123; MUID:84106810; PMID:6420071
A;Accession: A21123
A;Molecule type: protein
A;Residues: 31-43,'HX',46-49,'H' <ZIP>
C;Genetics:
A;Gene: FlyBase:chp
A;Cross-references: FlyBase:FBgn0000313

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A;Introns: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
C;Superfamily: chaoptin; leucine-rich alpha-2-glycoprotein repeat homology
C;Keywords: cell adhesion; glycoprotein; membrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-1134/Product: chaoptin #status predicted <MAT>
F;80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR
F;103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;303-325/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F;551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
F;577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
F;601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>
F;625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR23>
F;649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>
F;673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR25>
F;708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>
F;733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR27>
F;757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR28>
F;781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>
F;805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR30>
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F;854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
F;879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
F;903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
F;928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F;949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
F;973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
F;996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
F;1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
F;1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

  Query Match             8.1%;  Score 333.5;  DB 1;  Length 1134;
  Best Local Similarity   23.0%;  Pred. No. 4.7e-13;
  Matches  177;  Conservative  114;  Mismatches  249;  Indels  231;  Gaps   30;

Qy         10 DNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQV-------------------------L 43
              |:|  | : ||||  | |   |    | :|  |:|                         |
Db        346 DSLVNSLQILDLSGNNLTKLHHKLFNNFDVLRVISMRDNKIKIQKPTETFNAVHYTLLKL 405

Qy         44 DLS-----RCEIQTIEDGA----YQSLS------------------HLSTLILTGNPIQ 75
              |||        :||: :       :|||                  | | :|  :
Db        406 DLSGDRNDPTNLQTLRNMTRMRNMRSLSISRLGSSSVGPEDFKDFGVELEDLQITRASLS 465

Qy         76 SLALGAFSGLSSLQKLVAVETNLASLEN---FPIGHLKTLKELNVAHNLIQSFKLPEYFS 132
                :   ||  :  |::|    |  ::|:||     |||  :|  | ::|     |    |
Db        466 GIQSHAFKHVRGLKRLDFSENGISSIENDAFHEIGH--SLISLKMSHGYSGSALPAEPLR 523

Qy        133 NLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFK---EIRLH 189
              :||:|: || |:| | |:  |    | : |    |:|  | :  : | |:     :|
Db        524 HLTSLQELDFSNNHISSMSDTSFHFLKNLRL----LELHDNRIEQVLKGTFQGDIHSKLE 579

Qy        190 KLTLRNN---------FDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEG- 239
              :::|| |           |  |  ::        |: :::   | |   ||:: :  :| |
Db        580 EISLRFNHLTSISQHTFFDLEALRK-----LHLDDNKIDKIERRAFMNLDELEYLSLRGN 634

Qy        240 -LCNLTIEEF----RLAYLDYYLDDI----IDLFNCLTNVSSFSLVSVTIERVKDFSYNF 290
               : ||  | |    :|  ||   : :      | |: :  :|: : |:|:  :::   ||
Db        635 KINNLADESFQNLPKLEILDMAFNQLPNFNFDYFDQVGTLSNLN-VNVSHNQIRQLMYNS 693

Qy        291 GWQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSF--K 348
              |                                 | |    :   ::: |||| | :|
Db        694 SW----------------------------SGRNEHGGMYHSNIKILDLSHNNISIIHP 724

Qy        349 GCCSQSDFGTT--------------------SLKYLDLSFNGVITMSSN-FLGLEQLEH 386
              |    ::   |                    |::||||:| :  :  : |   :||:
Db        725 GYFRPAEISLTHLHLGYNSLMNTTRDVFGNMPHLQWLDLSYNWIHELDFDAFKNTKQLQL 784

Qy        387 LDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR-VAFNGIFNG---------------- 429
              : | |: |  : :  :|  :: |  :| || | | :  |  :||
Db        785 VFFGHNYLSDIPQ-DIFKPVQGLRIVDFSHNHLRGLPDNLFYNGGMEKLDVSHNMMLKIP 843

Qy        430 ---LSSLEVLKMAGNSFQENFLP-----DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSS 481
                 ||||  | :       ||:       |:  : |:| :||:|   | ::    | ::
Db        844 SSSLSSLAALTLCELHLSNNFISTIHSMDLSNKFRSLRYLDISYNYLLRIDDAVFATMPK 903

Qy        482 LQVLNMSHN--------NFF--------------SLDTFPYKCLNSLQVLDYSLNHIMTS 519
              | ||::|||        :|                || | |   |  |:       | : |
Db        904 LAVLDLSHNRDLKVMDKSFMGLENSLIKLGLENVSLSTVPEIRLKYLREFRLGYNE-LPS 962

Qy        520 KKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQ--- 576
              |||  |  |:|  |:|: ||                    |  |  |   |  ::
Db        963 IPQELAHNMSNLRMLDLSNND-------------------LTNVPLMTQALPHLRRLML 1002

Qy        577 -GMPVLSLNITCQMNKTIIGVSV-LSVLVVSVVAVLVYKFYFHLMLLAGCI 625
               | |: |||     | :  ||:  | :| :|   :  :::        ||:
Db       1003 SGNPITSLN-----NNSFDGVNEDLEMLDISNFRLHYFEY--------GCL 1040


RESULT 8
JC5239
insulin-like growth factor acid-labile chain - baboon
C;Species: Papio sp. (baboon)
C;Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C;Accession: JC5239
R;Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-lik
A;Reference number: JC5239; MUID:97040714; PMID:8886027
A;Contents: liver
A;Accession: JC5239
A;Molecule type: mRNA
A;Residues: 1-605 <DEL>
C;Comment: This factor is structurally related to proinsulin and have insuline-like meta

  Query Match             7.5%;  Score 309;  DB 2;  Length 605;
  Best Local Similarity   24.5%;  Pred. No. 7.2e-12;
  Matches  155;  Conservative   92;  Mismatches  235;  Indels  150;  Gaps   23;

Qy          4 NFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH 63
              |  ::|| :|  |: | | | |  :  :| :  |  |:|   :: ::|  |   | :
Db         64 NLTRLPDGIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGSLEPQALLGLEN 123

Qy         64 LSTLILTGNPIQSLALGAFS-----------------------GLSSLQKLVAVETNLA 99
              |  | |  | ::|||:| |:                     || :|  |     :||
Db        124 LCHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLEDGLFEGLGNLWDLNLGWNSLA 183

Qy        100 SLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLH 159
              | :    |  |:|| :| | : ::  |  || |  |  ||| | :::|     |
Db        184 VLPDAAFRGLGGLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KANVFA 239

Qy        160 QMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEVHRL 218
              |:| |   | |  | :  : ||||  :: |  | | :|     :::     || || | ||
Db        240 QLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRVLRL 297

Qy        219 VLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSV 278
                          :|:  |  | |:       ::|:::                 |
Db        298 -------------SHNAIASLRPRTFEDL------HFLEEL-------------QLGHN 324

Qy        279 TIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDLPSLE 336
              | :: : |:  |   ||::     |   :|: :   ||  :  | ||     :||
Db        325 RIRQLAERSFE-GLGQLEVLTLDHNQLQEVKVGAFLGLTNVAVMNLSGNCLR--NLPEQV 381
```

```
Qy        337 FLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLEHLDF 389
Db        382 FRGLGKLHSLHLEGSCLGRIRPHTFAGLSGLRRLFLKDNGLVGIEEQSLWGLAELLELDL 441

Qy        390 QHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLP 449
Db        442 TSNQL----------------------THLP---HQLFQGLGKLEYLLLSHNRLAE--LP 474

Qy        450 -DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQV 508
Db        475 ADALGPLQRAFWLDVSHNRLEALPGSLLASLGRLRYLNLRNN---SLRTFTPQ------- 524

Qy        509 LDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQS--------------FLQWI 554
Db        525 -------------------PPGLERLWLEGNPWDCSCPLKALRDFALQNPSAVPRFVQAI 565

Qy        555 ---KDQRQLLVEVERMECATPSDKQGMPVLSL 583
Db        566 CEGDDCQPPVYTYNNITCASPPEVAGLDLRDL 597


RESULT 9
T17461
disease resistance protein D - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17461
R;Parniske, M.; Jones, J.D.
Proc. Natl. Acad. Sci. U.S.A. 96, 5850-5855, 1999
A;Title: Recombination between diverged clusters of the tomato Cf-9 plant disease resist
A;Reference number: Z18801; MUID:99254130; PMID:10318973
A;Accession: T17461
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-853 <PAR>
A;Cross-references: UNIPROT:Q9ZS82; EMBL:AF119040; NID:g4235640; PID:g4235641; PIDN:AAD1
C;Genetics:
A;Gene: NL0D

  Query Match             7.3%;  Score 302;  DB 2;  Length 853;
  Best Local Similarity   24.6%;  Pred. No. 3.1e-11;
  Matches  185;  Conservative  102;  Mismatches  280;  Indels  184;  Gaps   33;

Qy         17 KNLDLSFN-----PLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTG 71
Db        111 KRLDLSYNDFTGSPI----SPKFGEFSNLTHLDLFDSNFTGIIPSEISHLSKLYVLRTST 166

Qy         72 NPIQSLALG------AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSF 125
Db        167 DYPYGLSLGPHNFELLLKNLTQLRELNLYDVNLSS--TIPSNFSSHLTNLRLAYTELRGI 224

Qy        126 KLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKE 185
Db        225 -LPERFFHLSNLESLDLSFNPQLTVRFPTTKWNSSASLVNLYL-AGVNIADRI-PESFSH 281

Qy        186 IRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLT- 244
Db        282 L-------------------------TALHKLHMGYTNLSGPIPK-------PLWNLTH 308

Qy        245 IEEFRLAYLDY-YLDDIIDLFNCLTNVSSFSLVSVTIE-RVKDFSYNFGWQHLELV---- 298
Db        309 IESL---FLDYNHLEGPISHFTIFEKLKSLSLGNNNFDGRLEFLSFNRSWMKLERLDFSS 365

Qy        299 NCKFGQFPT--LKLKSLKRLTFTSNK-GGNAFSEV-DLPSLEFLDLSRNGLSFK------ 348
Db        366 NFLTGPIPSNVSGLQNLQQLILSSNHLNGTIPSWIFSLPSLTVLNLSDNTLSGKIQEFKS 425

Qy        349 --------------GCCSQSDFGTTSLKYLDLSFNGVI-TMSSNFLGLEQLEHLDFQHSN 393
Db        426 KTLYFVSLEQNKLEGPIPRSLLNQQFLQALLLSHNNISGHISSAICNLKTFILLNLKSNN 485

Qy        394 LK--------QMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQE 445
Db        486 LEGTIPQCLGEMSELQV---------LDLSNNSLSGTMNTTFSIGNPLHIIKLDWNKLQG 536

Qy        446 NFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHN---------------- 490
Db        537 KVPPSLI-NCKKLELLDLSNNELNDTFPKWLGDLPNLQVLNFRSNKLYGPIRTNNLFAKI 595

Qy        491 -------NFFSLDTFPYKCLNSLQVL------------------DYSLNHIMTSKK---Q 522
Db        596 RVVDLSSNGFSGD-LPVSFFENFEAMKINGENNGTRKYVADLYSDYYKNYLIVTTKGLDQ 654

Qy        523 ELQHFPSSLAFLNLTQNDFACTCEH-QSFLQWIKDQRQLLVEVERMECATPSDKQGMPVL 581
Db        655 ELSRVLTTQIIIDLSKNKFE---GHIPNIIGDLIGLRTLNLSHNVLEGHIPASFQNLSVL 711

Qy        582 ------SLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYD 635
Db        712 ESLDLSSNKISGAIPQQLASLTFLEVLNLS---------HNHLV---GCIPKGKQ---FD 756

Qy        636 AFVIYSSQDEDWVRNELVKNLEEGVPPFQLC 666
Db        757 SFENSSYLGNDGLR---------GLPPSRDC 778


RESULT 10
A41915
insulin-like growth factor-binding complex acid-labile chain precursor - human
N;Alternate names: Acid-Labile Subunit (ALS)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A41915
R;Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
Mol. Endocrinol. 6, 870-876, 1992
A;Title: Structure and functional expression of the acid-labile subunit of the insulin-l
A;Reference number: A41915; MUID:92357025; PMID:1379671
A;Accession: A41915
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-605 <LEO>
A;Cross-references: UNIPROT:P35858; GB:M86826; NID:g184807; PIDN:AAA36047.1; PID:g184808
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:110171)
F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

  Query Match             7.2%;  Score 297;  DB 2;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 4.1e-11;
  Matches  156;  Conservative   91;  Mismatches  240;  Indels  152;  Gaps   24;

Qy          4 NFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH 63
Db         64 NLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALLGLEN 123

Qy         64 LSTLILTGNPIQSLALGAFS----------------------GLSSLQKLVAVETNLA 99
Db        124 LCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGWNSLA 183
```

```
Qy        100 SLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLH 159
Db        184 VLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KANVFV 239

Qy        160 QMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEVHRL 218
Db        240 QLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRVLRL 297

Qy        219 VLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSV 278
Db        298 --------------SHNAIASLRPRTFKDL------HFLEEL-------------QLGHN 324

Qy        279 TIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDLPSLE 336
Db        325 RIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NLPEQV 381

Qy        337 FLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLEHLDF 389
Db        382 FRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELLELDL 441

Qy        390 QHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLP 449
Db        442 TSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE--LP 474

Qy        450 -DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQV 508
Db        475 ADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ------- 524

Qy        509 LDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD---------QRQ 559
Db        525 ------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSAVPRF 561

Qy        560 LLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 598
Db        562 VQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594
```

RESULT 11
T42218
slit-1 protein homolog - rat
N;Alternate names: MEGF4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42218
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T42218
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1531 <NAK>
A;Cross-references: UNIPROT:O88279; EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF4
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r

  Query Match   7.1%; Score 296; DB 2; Length 1531;
  Best Local Similarity   22.2%; Pred. No. 1.6e-10;
  Matches 158; Conservative   94; Mismatches 241; Indels 218; Gaps   25;

```
Qy          8 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 67
Db        303 IPANLPETMTEIRLELNGIKSIPPGAFSPYRKLRRIDLSNNQIAEIAPDAFQGLRSLNSL 362

Qy         68 ILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKL 127
Db        363 VLYGNKITDLPRGVFGGLYTLQLLL---------------------LNA--NKINCIR- 397

Qy        128 PEYFSNLTNLEHLDLSSNKIQSI---YCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFK 184
```

```
Db        398 PDAFQDLQNLSLLSLYDNKIQSLAKGTFTSLRAIQ-------TLHLAQNP--FICDCNLK 448

Qy        185 EIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLV---LGEFRNEGNLEKFDKSALEGLC 241
Db        449 WLA--------DFLRTNPIET--TGARCASPRRLANKRIGQIKS----KKFRCSAKE--- 491

Qy        242 NLTIEEFRLAYLDYYLD-----DIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLE 296
Db        492 ----QYFIPGTEDYHLNSECTSDVACPHKCRCEASVVECSGLKLSKIPE-RIPQSTTELR 546

Qy        297 LVNCKF------GQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGC 350
Db        547 LNNNEISILEATGLFK--KLSHLKKINLSNNK----VSEIEDGTFE-------------- 586

Qy        351 CSQSDFGTTSLKYLDLSFNGVITMSSN-FLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNL 409
Db        587 ------GATSVSELHLTANQLESVRSGMFRGLDGLRTLMLRNNRISCIHNDS-FTGLRNV 639

Qy        410 IYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENF---------------------- 447
Db        640 RLLSLYDNHITTISPGAFDTLQALSTLNLLANPFNCNCQLAWLGDWLRKRKIVTGNPRCQ 699

Qy        448 ------------------------------------------------------------L 448
Db        700 NPDFLRQIPLQDVAFPDFRCEEGQEEVGCLPRPQCPQECACLDTVVRCSNKHLQALPKGI 759

Qy        449 PDIFTEL-----------------RNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNN 491
Db        760 PKNVTELYLDGNQFTLVPGQLSTFKYLQLVDLSNNKISSLSNSSFTNMSQLTTLILSYNA 819

Qy        492 FFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFL 551
Db        820 LQCIPPLAFQGLRSLRLLSLHGNDVSTLQEGIFADV-TSLSHLAIGANPLYCDCHLRWLS 878

Qy        552 QWIKDQRQLLVEVERMECA------------TPSDK---QGMPVLSLNITC 587
Db        879 SWVKTGYK---EPGIARCAGPPEMEGKLLLTTPAKKFECQGPPSLAVQAKC 926
```

RESULT 12
H96510
probable disease resistance protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H96510
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96510
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-994 <STO>
A;Cross-references: UNIPROT:Q9C637; GB:AE005173; NID:g11321768; PIDN:AAG34245.1; GSPDB:G
C;Genetics:
A;Gene: F2G19.6
A;Map position: 1

  Query Match   7.1%; Score 292; DB 2; Length 994;
  Best Local Similarity   23.6%; Pred. No. 1.6e-10;
  Matches 152; Conservative   92; Mismatches 241; Indels 158; Gaps   30;

```
Qy          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60
Db        281 LKLSIY----NTSFS-GTIPNSISNLKHLTS----------LKLQQSAFSGRIPSSLRS 324
```

```
Qy          61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFP--IGHLKTLKELNVA 118
               ||||| |:|: |       : | |  |       : ||    |||  : :|  |: :::
Db         325 LSHLSNLVLSENNFVGEIPSSVSNLKQLTLFDVSDNNLNG--NFPSSLLNLNQLRYIDIC 382

Qy         119 HNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMP--LLNLS----LDLSL 172
                 |    | ||   | |:|||      |                :|  | |:|    | ||
Db         383 SNHFTGF-LPPTISQLSNLEFFSACDNSFTG----------SIPSSLFNISSLTTLGLSY 431

Qy         173 NPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKF 232
               | :|                  |: |:                  :|   |
Db         432 NQLN--------------------DTTNI--------------------KNISLLHNL 449

Qy         233 DKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSV---TIERVKDFSYN 289
                 :  |:          |: : :|       :|:|  |  : | :|  :   |     |  ::
Db         450 QRLLLDN------NNFKASQVD------LDVFLSLKRLVSLALSGIPLSTTNITSDSEFS 497

Qy         290 FGWQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVD-----LPSLEFLDLSRNG 344
                 ::|||  |   :||   ::: : |:        |   :|      || |  :||| |
Db         498 SHLEYLELSGCNIIEFPEF-IRNQRNLSSIDLSNNNIKGQVPNWLWRLPELSTVDLSNNS 556

Qy         345 L-SFKGCCSQSDFGTTSLKYLDLSFNGVITMSSN------FLGLEQLEHLDFQHSNLKQM 397
               |  | |           ||| |  |   :: :|||       |:   :::    ::|
Db         557 LIGFNG----------SLKALSGSKIVMLDLSSNAFQGPLFMPPRGIQYFLGSYNNFTGY 606

Qy         398 SEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGL---------SSLEVLKMAGNSFQENFL 448
                 |:   | | : ||:|       |  :||          ||| || :  ||  :  |
Db         607 IPPSI-CGLANPLILDLS--------NNNLHGLIPRCLEAQMSSLSVLNLRNNSL-DGSL 656

Qy         449 PDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY--KCLNSL 506
               |:||   : |: ||:|    ||    | :    |:|::||:  ||    ||||:    | |
Db         657 PNIFMNAKVLSSLDVSHNTLEGKLPASLAGCSALEILNVESNNI--NDTFPFWLNSLPKL 714

Qy         507 QVLDYSLNHIMTSKKQELQH-------FPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQ 559
               |||    |:     :  | :        ||  |   ::: |||  |       |: |    :
Db         715 QVLVLRSNNF----RGTLHNVDGVWFGFP-LLRITDVSHNDFVGTLPSDYFMNWTAISKS 769

Qy         560 LLVEVERMECATPSD---KQGMPVLSLNITCQMNKTIIGVSVL 599
                  | |      | |      : :::  :: :| : :   :|:
Db         770 ---ETELQYIGDPEDYGYYTSLVLMNKGVSMEMQRILTKYTVI 809
```

RESULT 13
T07039
Hcr9-0 protein - tomato
N;Alternate names: cf-9 protein homolog
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T07039
R;Parniske, M.; Hammond-Kosack, K.E.; Golstein, C.; Thomas, C.M.; Jones, D.A.; Harrison,
Cell 91, 821-832, 1997
A;Title: Novel disease resistance specificities result from sequence exchange between ta
A;Reference number: Z15879; MUID:98074802; PMID:9413991
A;Accession: T07039
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-845 <PAR>
A;Cross-references: UNIPROT:O49879; EMBL:AJ002237; NID:g2826843; PIDN:CAA05279.1; PID:g2
A;Experimental source: cultivar Moneymaker (Cf0)
C;Genetics:
A;Gene: Hcr9-0
A;Map position: 1
C;Keywords: membrane bound

  Query Match   7.0%; Score 291; DB 2; Length 845;
  Best Local Similarity   25.0%; Pred. No. 1.5e-10;
  Matches 188; Conservative   96; Mismatches 285; Indels 182; Gaps   34;

```
Qy          17 KNLDLSFNPLR-HLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL-ILTGNPI 74
               | ||||||     | |  |  | :|  ||||      :       :|||| | :|  : :
Db          98 KRLDLSFNDFTGSLISPKFGEFSDLTHLDLSDSNFTGV---IPSEISHLSKLHVLRIHDL 154

Qy          75 QSLALGAFSGLSSLQKLVAVETNLASLENFP--IGHLKTLKELNVAHNLIQSFKLPEYFS 132
                    |:||                    ||   : :|  |:|||:    | |     : |
```

```
Db         155 NELSLGP--------------------HNFELLLKNLTQLRELNLDSVNISSTIPSNFSS 194

Qy         133 NLTNLEHLDLSSNKIQSI------YCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFK-- 184
               :||||    |   ::: :      : :||  ||           || ||   ::    |
Db         195 HLTNLW---LPYTELRGVLPERVFHLSDLEFLH----------LSYNPQLTVRFPTTKWN 241

Qy         185 -EIRLHKLTLRNNFDSLNVMKTCIQGLAGL-EVHRLVLGEFRNEGNLEKFDKSALEGLCN 242
                  | || :     |:|:     :  : |  :| | :|     |:: |         | |
Db         242 SSASLMKLYVH----SVNIADRIPESFSHLTSLHALYMGRCNLSGHIPK-------PLWN 290

Qy         243 LT-IEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDF-SYNFGWQHLELV-- 298
               || ||   |   | :|:  |         :   || :  :    :| |:|  |  ||::
Db         291 LTNIESLFLG--DNHLEGPIPQLTRFEKLKRLSLGNNNLHGGLEFLSFNRSWTQLEILYF 348

Qy         299 --NCKFGQFPT--LKLKSLKRLTFTSNK-GGNAFSEV-DLPSLEFLDLSRNGLSFK---- 348
                 |   |  |:     |::|  |  :||   |:  | :  ||||  |||| |  | |
Db         349 SSNYLTGPIPSNVSGLQNLGWLFLSSNHLNGSIPSWIFSLPSLVVLDLSNNTFSGKIQEF 408

Qy         349 ----------------GCCSQSDFGTTSLKYLDLSFNGVI-TMSSNFLGLEQLEHLDFQH 391
                             |    |    ||::| || | :   :||:    |: |  ||
Db         409 KSKTLSTVTLKQNQLEGPIPNSLLNQESLQFLLLSHNNISGYISSSICNLKTLMVLDLGS 468

Qy         392 SNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDI 451
               :||:       |       |: ||:|:       |  |:  :| : : : ||      :|
Db         469 NNLEGTIPQCVGERNEYLLDLDLSNNRLSGTINTTFSIGNSFKAISLHGNKLTGK-VPRS 527

Qy         452 FTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNS------ 505
                  :  |  |||     ||      |      || |::|::  |       | |   |
Db         528 LINCKYLKLLDLGNNQLNDTFPNWLGYLSQLKILSLRSNKLHG----PIKSSGSTNLFMR 583

Qy         506 LQVLDYS------------LNHIMTSKK-QELQHFPSSLA-------------------- 532
               ||:|| |             | :: | ||   |   ||  ::
Db         584 LQILDLSSNGFSGNLPERILGNLQTMKKIDENTRFPEYISDQYEIYYVYLTTITTKGQDY 643

Qy         533 ----------FLNLTQNDFACTCEH-QSFLQWIKDQRQLLVEVERMECATPSDKQGMPVL 581
                         :||::| |      |  | :  :    | | :    :|    |:  | : ||
Db         644 DSVRILDSNMIINLSKNRFE---GHIPSIIGDLVGLRTLNLSRNALEGHIPASFQNLSVL 700

Qy         582 ------SLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYD 635
                     |  |: :: : :  :: | || :|          : ||:   |||  |:    :|
Db         701 ESLDLSSNRISGEIPQQLASLTFLEVLNLS---------HNHLV---GCIPKGKQ---FD 745

Qy         636 AFVIYSSQDEDWVRNELVKNLEEGVPPFQLC 666
               :|   | |  | :|        | |  :||
Db         746 SFGNTSYQGNDGLR---------GFPLSKLC 767

RESULT 14
JC1282
insulin-like growth factor-binding protein acid labile chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1282
R;Dai, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A;Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A;Reference number: JC1282; MUID:93038676; PMID:1384485
A;Accession: JC1282
A;Molecule type: mRNA
A;Residues: 1-603 <DAI>
A;Cross-references: UNIPROT:P35859; GB:S46785; NID:g258002; PIDN:AAB23770.2; PID:g570593
A;Experimental source: liver
A;Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

  Query Match             7.0%;  Score 290;  DB 2;  Length 603;
  Best Local Similarity   24.1%;  Pred. No. 1.1e-10;
  Matches  154;  Conservative   84;  Mismatches  240;  Indels  162;  Gaps   24;

```
Qy   4 NFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH 63
                 | :||::| ||: | | | | : | :| : | |:| ::::| | | :
```
```

```
Db         64 NLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALLGLQN 123

Qy         64 LSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVA----- 118

Db        124 LYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGWNSLV 183

Qy        119 ------------HNLI-----QSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQ 160

Db        184 VLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSV---KANVFVH 240

Qy        161 MPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLV 219

Db        241 LPRLQ-KLYLDRNLITAVAPGAFLGMKALRWLDLSHN-RVAGLMEDTFPGLLGLHVLRLA 298

Qy        220 -----------------LGEFR-NEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI- 260

Db        299 HNAIASLRPRTFKDLHFLEELQLGHNRIRQLGERTFEGLGQLEV----LTLNDNQITEVR 354

Qy        261 IDLFNCLTNVSSFSLVSVTI----ERV---KDFSYNFGWQHLELVNCKFGQFPTLKLKSL 313

Db        355 VGAFSGLFNVAVMNLSGNCLRSLPERVFQGLDKLHSLHLEHSCLGHVRLHTF--AGLSGL 412

Qy        314 KRLTFTSNKGGNAFSEVD------LPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLS 367

Db        413 RRLFLRD----NSISSIEEQSLAGLSELLELDLTTNRLTH--LPRQLFQGLGHLEYLLLS 466

Qy        368 FNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIF 427

Db        467 YNQLTTLSAEVLG----------------------PLQRAFWLDISHNHLETLAEGLF 502

Qy        428 NGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNM 487

Db        503 SSLGRVRYLSLRNNSLQ-TFSP--------------QPGLERL---------------- 530

Qy        488 SHNNFFSLDTFPYKCLNSLQVL-DYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCE 546

Db        531 ------WLDANPWDCSCPLKALRDFALQN-----------PGVVPRFVQT------VCE 566

Qy        547 HQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNIT 586

Db        567 --------GDDCQPVYTYNNITCAGPANVSGLDLRDVSET 598
```

RESULT 15
T07015
Cf-4A protein - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T07015
R;Takken, F.L.; Schipper, D.; Nijkamp, H.J.; Hill, J.
Plant J. 14, 401-411, 1998
A;Title: Identification and Ds-tagged isolation of a new gene at the Cf-4 locus of tomat
A;Reference number: Z15863; MUID:98335213; PMID:9670557
A;Accession: T07015
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-855 <TAK>
A;Cross-references: UNIPROT:O50024; EMBL:Y12640; NID:e1289424; PIDN:CAA73187.1; PID:e128
A;Experimental source: strain Cf-4; isolate MM-Cf-4
C;Genetics:
A;Gene: Cf-4A
A;Map position: 1

  Query Match   7.0%; Score 290; DB 2; Length 855;
  Best Local Similarity   24.8%; Pred. No. 1.8e-10;
  Matches 187; Conservative   95; Mismatches 281; Indels 190; Gaps   36;

```
Qy         19 LDLSFNPLR---HLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQ 75

Db         85 LDLGCSQLQGKFHSNS-SLFQLSNLKRLDLSSND-----------------FTGSPI- 123

Qy         76 SLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKL---PEYF- 131
```

```
Db        124 SPKFGEFSDLTHLD---LSDSNFTGVIPSEISHLSKLHVLRIS----DQYKLSLGPHNFE 176

Qy        132 ---SNLTNLEHLDLSSNKIQ-------SIYCTDLRVLHQ-----MP-----LLNLS-LDL 170

Db        177 LLLKNLTQLRELHLESVNISSTIPSNFSFHLTNLRLSYTELRGVLPERVFHLSNLELLDL 236

Qy        171 SLNPMNFIQ--------PGAFKEIRLHKLTLRNNF-DSLNVMKTCIQGLAGLEVHRLVLG 221

Db        237 SYNPQLTVRFPTTIWNSSASLVKLYLSRVNIAGNIPDSFSYLTA---------LHELDMV 287

Qy        222 EFRNEGNLEKFDKSALEGLCNLT-IEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTI 280

Db        288 YTNLSGPIPK-------PLWNLTNIESLDLDY--NHLEGPIPQLPIFEKLKSLTLGNNNL 338

Qy        281 ERVKDF-SYNFGWQHLELV----NCKFGQFPT--LKLKSLKRLTFTSNK-GGNAFSEV-D 331

Db        339 DGGLEFLSFNRSWTQLEELDFSSNSLTGPIPSNVSGLRNLQSLYLSSNNLNGSIPSWIFD 398

Qy        332 LPSLEFLDLSRNGLS-------------------FKGCCSQSDFGTTSLKYLDLSFNGV 371

Db        399 LPSLRSLDLSNNTFSGKIQEFKSKTLSIVTLKQNQLKGPIPNSLLNQESLQFLLLSHNNI 458

Qy        372 I-TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGL 430

Db        459 SGHISSSICNLKILMVLDLGSNNLEGTIPQCVVERNEYLSHLDLSNNRLSGTINTTFSIG 518

Qy        431 SSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHN 490

Db        519 NSFRAISLHGNKLTGK-VPRSLINCKYLTLLDLGNNQLNDTFPNWLGYLSQLKILSLRSN 577

Qy        491 NFFSLDTFPYKCLNS------LQVLDYS------------LNHIMTSKK-QELQHFPSSL 531

Db        578 KLHG----PIKSSGNTNLFMRLQILDLSSNGFSGNLPERILGNLQTMKKFDENTRFPEYI 633

Qy        532 A----------------------------FLNLTQNDFACTCEHQSFLQWIKDQRQLLV 562

Db        634 SDRYIYYDYLTTITTKGQDYDSVRIFTFNMIINLSKNRFEGRI--PSIIGDLVGLRTLNL 691

Qy        563 EVERMECATPSDKQGMPVL------SLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYF 616

Db        692 SHNVLEGHIPVSLQNLSVLESLDLSSNKISGAIPQQLASLTFLEVLNLS---------HN 742

Qy        617 HLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVR 649

Db        743 HLV---GCIPKGKQ---FDSFGNTSYQGNDGLR 769
```

Search completed: March 12, 2005, 19:57:00
Job time : 28.6156 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:15:31 ; Search time 86.9834 Seconds
(without alignments)
3712.721 Million cell updates/sec

Title: US-09-396-985B-6
Perfect score: 4335
Sequence: 1 MMPLLHLAGTLIMALFLSCL.....GKALNPDETSEEEQEATTLT 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2860.5	66.0	839	6	ABU04773	Abu04773 Human exp
2	2860.5	66.0	839	6	ABU04774	Abu04774 Human exp
3	2860.5	66.0	839	6	ABU04775	Abu04775 Human exp
4	2860.5	66.0	839	7	ADC78785	Adc78785 Human PRO
5	2860.5	66.0	839	7	ADD48826	Add48826 Human Pro
6	2844	65.6	837	2	AAW86361	Aaw86361 Human DNA
7	2844	65.6	837	5	AAE16102	Aae16102 Human DNA
8	2844	65.6	837	6	ABU04776	Abu04776 Human exp
9	2837	65.4	837	5	AAE16116	Aae16116 Human DNA
10	2796.5	64.5	801	8	ADO57797	Ado57797 Squirrel
11	2782.5	64.2	795	8	ADO57791	Ado57791 Rhesus mo
12	2781.5	64.2	795	8	ADO57800	Ado57800 Hamadryas
13	2777	64.1	808	8	ADO57803	Ado57803 Chimpanze
14	2773	64.0	808	8	ADO57782	Ado57782 Chimpanze
15	2761	63.7	808	8	ADO57785	Ado57785 Gorilla t
16	2751.5	63.5	801	8	ADO57788	Ado57788 Gibbon to
17	2726	62.9	799	2	AAW86352	Aaw86352 Human DNA
18	2726	62.9	799	5	AAE16093	Aae16093 Human DNA
19	2726	62.9	799	5	ABB83162	Abb83162 Human Tol
20	2726	62.9	799	6	ABR42963	Abr42963 Human Tol
21	2726	62.9	799	7	ADB39121	Adb39121 Human tol
22	2726	62.9	799	8	ADP56656	Adp56656 Human Tol
23	2726	62.9	799	8	ADP48597	Adp48597 Human Tol
24	2558.5	59.0	745	8	ADO57794	Ado57794 White-fac
25	2440	56.3	738	8	ADP29455	Adp29455 Human sec
26	898.5	20.7	208	3	AAY88059	Aay88059 Human Tol
27	883	20.4	179	7	ADC42707	Adc42707 Murine To
28	761.5	17.6	178	8	ADN12270	Adn12270 IL-1R/TLR
29	602.5	13.9	661	2	AAW28510	Aaw28510 Product o
30	602.5	13.9	661	2	AAW87556	Aaw87556 B cell su
31	602.5	13.9	661	7	ADC38652	Adc38652 Human sec
32	602.5	13.9	661	7	ADF69098	Adf69098 Human MP5
33	595	13.7	650	3	AAY82527	Aay82527 Human RP1
34	588.5	13.6	661	2	AAW47274	Aaw47274 Human B-c
35	575	13.3	1032	5	AAO21588	Aao21588 Murine To
36	575	13.3	1032	7	ADE85953	Ade85953 Mouse Tol
37	575	13.3	1032	7	ABW01559	Abw01559 Murine To
38	559	12.9	1050	5	AAO21579	Aao21579 Murine To
39	559	12.9	1050	7	ADE85947	Ade85947 Mouse Tol
40	559	12.9	1050	7	ABW01556	Abw01556 Murine To
41	546	12.6	1059	5	AAO21587	Aao21587 Murine To
42	546	12.6	1059	7	ADE85951	Ade85951 Human Tol
43	546	12.6	1059	8	ADQ88188	Adq88188 Human 122
44	541.5	12.5	859	6	AAE33341	Aae33341 Mouse tol
45	541	12.5	1041	2	AAY41768	Aay41768 Human PRO

ALIGNMENTS

RESULT 1
ABU04773
ID ABU04773 standard; protein; 839 AA.
XX
AC ABU04773;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1439.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1439; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a

```
CC   mammal an immunogenic response directed against any of the purified
CC   polypeptide. The purified polypeptide, or the antibody that binds to this
CC   polypeptide, is useful for treating cancer. The polypeptide is also
CC   useful for identifying compounds that binds to a naturally processed
CC   class I or class II MHC-binding polypeptide. The polypeptides and
CC   polynucleotides are particularly useful for treating or preventing
CC   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC   lymphoma or leukaemia. These are also useful for screening agents for
CC   treating the above mentioned diseases. This sequence represents an
CC   expressed protein tag (EPT) isolated from human tissue for translational
CC   profiling. Note: This sequence does not appear in the printed
CC   specification but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 839 AA;

  Query Match             66.0%;  Score 2860.5;  DB 6;  Length 839;
  Best Local Similarity   66.5%;  Pred. No. 4.1e-244;
  Matches  559;  Conservative  115;  Mismatches  159;  Indels    7;  Gaps    5;

Qy          1 MMPLLHLAGTLIMAL-FLSCLRPGSLNPCIEVLPNITYQCMDQNLSKIPHDIPYSTKNLD 59
              ||    |||||| |: ||||:|| |  ||:||:||||||||: |  ||| ::|:||||||
Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         60 LSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPG 119
              ||||||: | |||| :| :|| |||||||||:|||| |:  |: ||||:||||||:| : |
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        120 SFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHV 179
              :||||::|: ||||||  : ||| | || | :||:|||||||| ||||||||||||||||:
Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        180 DLSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRSNFNSS 239
              ||| | ||:|   ||: | : | :|||||||||:: ||  ||: ||||:||||:||:|
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        240 NVLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDI 299
              ||:| |:| : || ||||:||||:|| ||| ||:| :|||||::|:|||| |:::: |||
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        300 YNL-NCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTT 358
               :| ||| |:|: |   | |: : |   :| || | :: |    || | |  ||  | |:
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        359 NREDISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSANFMG 418
              |:   :| :: |||| :|||||| :||:|||| ||||| :|||||||||||| ||:||:|
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        419 LEELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAG 478
              ||:||:|||||| ||:::|||||||  |:|||||:|:|:: |:||| || ||  |||||
Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        479 NSFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHY 538
              |||::| | ::||   ||||||||:|||||:|   |::|  ||:|||||||   ||   |
Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        539 KQLYSLRTLDCSFNRIETS-KGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMF 597
              | | ||: || | | | || |  ||||| |||  ||| |  || ||:|:||||:|||:
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        598 LVNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVVSVLVVATVAFLIYHFYFHLI 657
              || ||:|:||:| | :   ||   | || : |||| |||:|||||: || |:| |||||:
Db        601 LVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLM 659

Qy        658 LIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFQLCLHYRDFIPGVAIA 717
              |:||| || |||:||||||||||:|||||||||||||||| ||||||||||||||||
Db        660 LLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIA 719

Qy        718 ANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLL 777
              |||| ||||||||||||:|||||||||||||||||||||:|||||||:||||:||
Db        720 ANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLL 779

Qy        778 RQQVELYRLLSRNTYLEWEDNALGRHIFWRRLKKALLDGKALNPD---ETSEEEQEATTL 834
              |||||||||||||||||||: ||||||||||:|||||: ||:    |    ||||::
Db        780 RQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839


RESULT 2
ABU04774
ID   ABU04774 standard; protein; 839 AA.
XX
AC   ABU04774;
XX
DT   29-JAN-2003  (first entry)
XX
DE   Human expressed protein tag (EPT) #1440.
XX
KW   Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW   protease; protease inhibitor; transporter; cytoskeletal protein;
KW   receptor; transcription factor; cancer; MHC;
KW   major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW   adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200278524-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US009671.
XX
PR   28-MAR-2001; 2001US-0279495P.
PR   21-MAY-2001; 2001US-0292544P.
PR   08-AUG-2001; 2001US-0310801P.
PR   01-OCT-2001; 2001US-0326370P.
PR   04-DEC-2001; 2001US-0336780P.
PR   20-FEB-2002; 2002US-0358985P.
XX
PA   (ZYCO-) ZYCOS INC.
XX
PI   Chicz RM,  Tomlinson AJ,  Urban RG;
XX
DR   WPI; 2003-040607/03.
XX
PT   New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT   cytoskeletal proteins, receptors or transcription factors), useful for
PT   treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT   leukemia.
XX
PS   Example 2; SEQ ID NO 1440; 134pp; English.
XX
CC   The invention describes a purified polypeptide, which comprises a
CC   fragment of a kinase, phosphatase, protease, protease inhibitor,
CC   transporter, cytoskeletal protein, receptor or transcription factor. The
CC   polypeptide is useful as an immunogenic composition for eliciting in a
CC   mammal an immunogenic response directed against any of the purified
CC   polypeptide. The purified polypeptide, or the antibody that binds to this
CC   polypeptide, is useful for treating cancer. The polypeptide is also
CC   useful for identifying compounds that binds to a naturally processed
CC   class I or class II MHC-binding polypeptide. The polypeptides and
CC   polynucleotides are particularly useful for treating or preventing
CC   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC   lymphoma or leukaemia. These are also useful for screening agents for
CC   treating the above mentioned diseases. This sequence represents an
CC   expressed protein tag (EPT) isolated from human tissue for translational
CC   profiling. Note: This sequence does not appear in the printed
CC   specification but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 839 AA;

  Query Match             66.0%;  Score 2860.5;  DB 6;  Length 839;
  Best Local Similarity   66.5%;  Pred. No. 4.1e-244;
  Matches  559;  Conservative  115;  Mismatches  159;  Indels    7;  Gaps    5;

Qy          1 MMPLLHLAGTLIMAL-FLSCLRPGSLNPCIEVLPNITYQCMDQNLSKIPHDIPYSTKNLD 59
```

```
Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         60 LSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPG 119

Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        120 SFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHV 179

Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        180 DLSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRSNFNSS 239

Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        240 NVLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDI 299

Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        300 YNL-NCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTT 358

Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        359 NREDISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSANFMG 418

Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        419 LEELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAG 478

Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        479 NSFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHY 538

Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        539 KQLYSLRTLDCSFNRIETS-KGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMF 597

Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        598 LVNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVVSVLVVATVAFLIYHFYFHLI 657

Db        601 LVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLM 659

Qy        658 LIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFQLCLHYRDFIPGVAIA 717

Db        660 LLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIA 719

Qy        718 ANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLL 777

Db        720 ANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLL 779

Qy        778 RQQVELYRLLSRNTYLEWEDNALGRHIFWRRLKKALLDGKALNPD---ETSEEEQEATTL 834

Db        780 RQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
```

```
RESULT 3
ABU04775
ID   ABU04775 standard; protein; 839 AA.
XX
AC   ABU04775;
XX
DT   29-JAN-2003  (first entry)
XX
DE   Human expressed protein tag (EPT) #1441.
XX
KW   Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW   protease; protease inhibitor; transporter; cytoskeletal protein;
KW   receptor; transcription factor; cancer; MHC;
KW   major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW   adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200278524-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US009671.
XX
PR   28-MAR-2001; 2001US-0279495P.
PR   21-MAY-2001; 2001US-0292544P.
PR   08-AUG-2001; 2001US-0310801P.
PR   01-OCT-2001; 2001US-0326370P.
PR   04-DEC-2001; 2001US-0336780P.
PR   20-FEB-2002; 2002US-0358985P.
XX
PA   (ZYCO-) ZYCOS INC.
XX
PI   Chicz RM,  Tomlinson AJ,  Urban RG;
XX
DR   WPI; 2003-040607/03.
XX
PT   New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT   cytoskeletal proteins, receptors or transcription factors), useful for
PT   treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT   leukemia.
XX
PS   Example 2; SEQ ID NO 1441; 134pp; English.
XX
CC   The invention describes a purified polypeptide, which comprises a
CC   fragment of a kinase, phosphatase, protease, protease inhibitor,
CC   transporter, cytoskeletal protein, receptor or transcription factor. The
CC   polypeptide is useful as an immunogenic composition for eliciting in a
CC   mammal an immunogenic response directed against any of the purified
CC   polypeptide. The purified polypeptide, or the antibody that binds to this
CC   polypeptide, is useful for treating cancer. The polypeptide is also
CC   useful for identifying compounds that binds to a naturally processed
CC   class I or class II MHC-binding polypeptide. The polypeptides and
CC   polynucleotides are particularly useful for treating or preventing
CC   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC   lymphoma or leukaemia. These are also useful for screening agents for
CC   treating the above mentioned diseases. This sequence represents an
CC   expressed protein tag (EPT) isolated from human tissue for translational
CC   profiling. Note: This sequence does not appear in the printed
CC   specification but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 839 AA;
```

```
  Query Match           66.0%;  Score 2860.5;  DB 6;  Length 839;
  Best Local Similarity  66.5%;  Pred. No. 4.1e-244;
  Matches  559;  Conservative  115;  Mismatches  159;  Indels    7;  Gaps    5;

Qy          1 MMPLLHLAGTLIMAL-FLSCLRPGSLNPCIEVLPNITYQCMDQNLSKIPHDIPYSTKNLD 59

Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         60 LSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPG 119

Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        120 SFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHV 179

Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        180 DLSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRSNFNSS 239

Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        240 NVLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDI 299

Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        300 YNL-NCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTT 358
```

```
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        359 NREDISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSANFMG 418
              |:   :| :: |||| :|||||| :||:|||| ||||| :|||||||||||| ||:||:|
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        419 LEELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAG 478
              ||:||:|||||| ||:::|||||||  |:|||||:|:|:: |:||| || ||  ||||
Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        479 NSFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHY 538
              |||::| | ::||   |||||||:|||||:|   |::|  ||:|||||||   ||   |
Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        539 KQLYSLRTLDCSFNRIETS-KGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMF 597
              | | ||: || | | || |  ||||| |||  ||| |  || ||:|:||||:|||:
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        598 LVNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVVSVLVVATVAFLIYHFYFHLI 657
              || ||:|:||:| | :   ||   | || : |||| |||:|||||: || |:| |||||:
Db        601 LVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLM 659

Qy        658 LIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFQLCLHYRDFIPGVAIA 717
              |:||| || |||:|||||||||||:|||||||||||||||| ||||||||||||||||
Db        660 LLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIA 719

Qy        718 ANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLL 777
              |||| |||||||||||||:|||||||||||||||||||||||:||||:|||:||||||||
Db        720 ANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLL 779

Qy        778 RQQVELYRLLSRNTYLEWEDNALGRHIFWRRLKKALLDGKALNPD---ETSEEEQEATTL 834
              |||||||||||||||||||: ||||||||||:|||||||: ||:    |    ||||::
Db        780 RQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
```

RESULT 4
ADC78785
ID ADC78785 standard; protein; 839 AA.
XX
AC ADC78785;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human PRO protein #7.
XX
KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease.
XX
OS Homo sapiens.
XX
PN WO2003034984-A2.
XX
PD 01-MAY-2003.
XX
PF 15-OCT-2002; 2002WO-US033070.
XX
PR 19-OCT-2001; 2001US-0340083P.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Gurney AL;
XX
DR WPI; 2003-481990/45.
DR N-PSDB; ADC78784.
XX
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
PT medicament for diagnosing or treating cancer or inflammatory bowel
PT disorder e.g., ulcerative colitis or Crohn's disease.
XX
PS Claim 12; SEQ ID NO 14; 327pp; English.
XX
CC The invention comprises the amino acid and coding sequences of human PRO
CC proteins. The DNA and protein sequences of the invention are useful for
CC the diagnosis and treatment of cancer and inflammatory bowel disease
CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
CC sequence represents a human PRO protein of the invention.
XX
SQ Sequence 839 AA;

Query Match 66.0%; Score 2860.5; DB 7; Length 839;
Best Local Similarity 66.5%; Pred. No. 4.1e-244;
Matches 559; Conservative 115; Mismatches 159; Indels 7; Gaps 5;

```
Qy          1 MMPLLHLAGTLIMAL-FLSCLRPGSLNPCIEVLPNITYQCMDQNLSKIPHDIPYSTKNLD 59
              ||    |||||| |: ||||:|| |  ||:||:||||||||: |  ||| ::|:||||||
Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         60 LSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPG 119
              ||||||: | |||| :| :|| |||||||||:|||| |:  |: ||||:||||||:| : |
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        120 SFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHV 179
              :||||::|: |||||| : ||| | || | :||:|||||||| ||||||||||||||||:
Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        180 DLSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRSNFNSS 239
              ||| | ||:|  ||: | : | :|||||||||:: ||  ||: ||||:||||:||:|
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        240 NVLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDI 299
              ||:| |:| : || |||||:|| ||| ||:| :|||||::|:|||| |:::: |||
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        300 YNL-NCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTT 358
               :| ||| |:|: |   | |: : |   :| || | :: |    || | |  ||  | |:
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        359 NREDISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSANFMG 418
              |:   :| :: |||| :|||||| :||:|||| ||||| :|||||||||||| ||:||:|
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        419 LEELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAG 478
              ||:||:|||||| ||:::|||||||  |:|||||:|:|:: |:||| || ||  ||||
Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        479 NSFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHY 538
              |||::| | ::||   |||||||:|||||:|   |::|  ||:|||||||   ||   |
Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        539 KQLYSLRTLDCSFNRIETS-KGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMF 597
              | | ||: || | | || |  ||||| |||  ||| |  || ||:|:||||:|||:
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        598 LVNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVVSVLVVATVAFLIYHFYFHLI 657
              || ||:|:||:| | :   ||   | || : |||| |||:|||||: || |:| |||||:
Db        601 LVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLM 659

Qy        658 LIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFQLCLHYRDFIPGVAIA 717
              |:||| || |||:|||||||||||:|||||||||||||||| ||||||||||||||||
Db        660 LLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIA 719

Qy        718 ANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLL 777
              |||| |||||||||||||:|||||||||||||||||||||||:||||:|||:||||||||
Db        720 ANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLL 779

Qy        778 RQQVELYRLLSRNTYLEWEDNALGRHIFWRRLKKALLDGKALNPD---ETSEEEQEATTL 834
              |||||||||||||||||||: ||||||||||:|||||||: ||:    |    ||||::
Db        780 RQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
```

RESULT 5
ADD48826
ID ADD48826 standard; protein; 839 AA.
XX
AC ADD48826;
XX

```
DT   02-DEC-2004  (revised)
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein AAF05316, SEQ ID NO 14536.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; AAF05316.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Example 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (described in Table 3
CC   of the specification) which is differentially expressed during pain.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 839 AA;

  Query Match             66.0%;  Score 2860.5;  DB 7;  Length 839;
  Best Local Similarity   66.5%;  Pred. No. 4.1e-244;
  Matches  559;  Conservative  115;  Mismatches  159;  Indels    7;  Gaps    5;

Qy          1 MMPLLHLAGTLIMAL-FLSCLRPGSLNPCIEVLPNITYQCMDQNLSKIPHDIPYSTKNLD 59
              ||    |||||| |: ||||:|| |  ||:||:||||||||: |  ||| ::|:||||||
Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         60 LSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPG 119
              ||||||: | |||| :| :|| ||||||||:|||| |:  |: ||||:||||||:| : |
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        120 SFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHV 179
              :||||::|: |||||| : ||| | || | :||:|||||||| ||||||||||||||||:
Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        180 DLSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRSNFNSS 239
              ||| | ||:|   ||: | : | :|||||||||:: ||  ||: ||||:||||:||:|
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        240 NVLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDI 299
              ||:| |:| : || ||||:||||:|| ||| ||:| :|||||::|:|||| |::::: |||
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        300 YNL-NCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTT 358
               :| ||| |:|: |   | |: : |   :| || | :: |    || | |  ||  | |:
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        359 NREDISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSANFMG 418
              |:   :| :: |||| :|||||| :||:|||| ||||| :|||||||||| ||:||:|
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        419 LEELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAG 478
              ||:||:|||||| ||:::|||||||   |:|||||:|:|:: |:||| || ||  |||||
Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        479 NSFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHY 538
              |||::| | ::||   |||||||:|||||:|   |::|  ||:|||||||   ||   |
Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        539 KQLYSLRTLDCSFNRIETS-KGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMF 597
              | | ||: || | | | || |  |||| |||  ||| |  || ||:|:||||:|||:
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        598 LVNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVVSVLVVATVAFLIYHFYFHLI 657
              || ||:|:||:| | :   ||   | || : |||| |||:|||||: || |:| |||||:
Db        601 LVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLM 659

Qy        658 LIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFQLCLHYRDFIPGVAIA 717
              |:||| || |||:||||||||||:|||||||||||||||||| ||||||||||||||||
Db        660 LLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIA 719

Qy        718 ANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLL 777
              |||| ||||||||||||:|||||||||||||||||||||||:|||||||:||||:||
Db        720 ANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLL 779

Qy        778 RQQVELYRLLSRNTYLEWEDNALGRHIFWRRLKKALLDGKALNPD---ETSEEEQEATTL 834
              |||||||||||||||||: ||||||||||:|||||||: ||:    |    ||||::
Db        780 RQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
```

```
RESULT 6
AAW86361
ID   AAW86361 standard; protein; 837 AA.
XX
AC   AAW86361;
XX
DT   15-MAR-1999  (first entry)
XX
DE   Human DNAX toll-like receptor DTLR4.
XX
KW   DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KW   interleukin 1 receptor; phosphate metabolism; innate immunity response;
KW   modulate inflammatory function; morphological effect;
KW   immunological disorder.
XX
OS   Homo sapiens.
XX
PN   WO9850547-A2.
XX
PD   12-NOV-1998.
```

```
XX
PF   07-MAY-1998;   98WO-US008979.
XX
PR   07-MAY-1997;   97US-0044293P.
PR   22-JAN-1998;   98US-0072212P.
PR   05-MAR-1998;   98US-0076947P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Hardiman GT,  Rock FL,  Bazan JF,  Kastelein RA;
XX
DR   WPI; 1999-059670/05.
DR   N-PSDB; AAV80675.
XX
PT   Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
PT   metabolism, modulate inflammatory function or innate immunity responses.
XX
PS   Claim 3; Page 147-149; 171pp; English.
XX
CC   The present invention specifically describes human DNAX toll-like
CC   receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
CC   in the present invention. Also described are: (1) a fusion protein
CC   comprising a DTLR protein or peptide; (2) a binding compound, preferably
CC   an antibody or antibody fragment which specifically binds to a DTLR
CC   protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
CC   ; (4) an expression vector comprising the nucleic acid of (3); and (5) a
CC   host cell comprising the vector of (4). The host cell of (5) can be used
CC   to produce the DTLR proteins. The DTLR proteins can be used to alter
CC   phosphate metabolism, to modulate inflammatory function, innate immunity
CC   responses or morphological effects. The DTLR proteins can be used in the
CC   treatment of conditions exhibiting abnormal expression of the receptors
CC   of their ligands. These abnormalities are typically manifested by
CC   immunological disorders
XX
SQ   Sequence 837 AA;

  Query Match             65.6%;  Score 2844;  DB 2;  Length 837;
  Best Local Similarity   66.5%;  Pred. No. 1.2e-242;
  Matches  558;  Conservative  114;  Mismatches  159;  Indels    8;  Gaps    6;

Qy          2 MPLLHLAGTLIMAL-FLSCLRPGSLNPCIEVLPNITYQCMDQNLSKIPHDIPYSTKNLDL 60
              |    |||||| |: ||||:|| |  ||:|| ||||||||: |  ||| ::|:|||||||
Db          1 MSASRLAGTLIPAMAFLSCVRPESWEPCVEV-PNITYQCMELNFYKIPDNLPFSTKNLDL 59

Qy         61 SFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGS 120
              |||||: | |||| :| :|| |||||||||:|||| |:  |: ||||:||||||:| : |:
Db         60 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 119

Qy        121 FSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVD 180
              ||||::|: |||||| : ||| | || | :||:|||||||| ||||||||||||||||:|
Db        120 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 179

Qy        181 LSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRSNFNSSN 240
              || | ||:|   ||: | : | :|||||||||:: ||  ||: ||||:||||:||:| |
Db        180 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 239

Qy        241 VLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDIY 300
              |:| |:| : || ||||:||||:|| ||| ||:| :|||||::|:|||| |:::: |||
Db        240 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 299

Qy        301 NL-NCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTTN 359
              :| ||| |:|: |   | |: : |   :| || | :: |    || | |  ||  | |:|
Db        300 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 359

Qy        360 REDISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSANFMGL 419
              :   :| :: |||| :|||||| :||:|||| ||||| :||||||||||| ||:||:||
Db        360 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 419

Qy        420 EELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAGN 479
              |:||:|||||| ||:::|||||||   |:|||||:|:|:: |:||| || ||  ||||||
Db        420 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 479

Qy        480 SFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHYK 539
              ||::| | ::||   ||||||||:|||||:|   |::|  ||:|||||||   ||   ||
Db        480 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 539

Qy        540 QLYSLRTLDCSFNRIETS-KGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMFL 598
              | ||: || | | | || |  ||||| |||  ||| |  || ||:|:||||:|||:  |
Db        540 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 599

Qy        599 VNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVVSVLVVATVAFLIYHFYFHLIL 658
              | ||:|:||:| | :   ||   | || : |||| |||:|||||: || |:| |||||:|
Db        600 VEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 658

Qy        659 IAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFQLCLHYRDFIPGVAIAA 718
              :||| || |||:|||||||||||:|||||||||||||||| |||||||||||||||||||
Db        659 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 718

Qy        719 NIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLLR 778
              ||| |||||||||||||:|||||||||||||||||||||||:|||||||:||||:|||
Db        719 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 778

Qy        779 QQVELYRLLSRNTYLEWEDNALGRHIFWRRLKKALLDGKALNPD---ETSEEEQEATTL 834
              |||||||||||||||||: |||||||||:|||||||: ||:    |    ||||::
Db        779 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 837


RESULT 7
AAE16102
ID   AAE16102 standard; protein; 837 AA.
XX
AC   AAE16102;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human DNAX Toll like receptor (DTLR) 4 #2.
XX
KW   Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW   interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS   Homo sapiens.
XX
PN   WO200190151-A2.
XX
PD   29-NOV-2001.
XX
PF   23-MAY-2001; 2001WO-US016766.
XX
PR   25-MAY-2000; 2000US-0207558P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Hardiman GT,  Rock FL,  Bazan JF,  Kastelein RA,  Ho SWK,  Liu Y;
XX
DR   WPI; 2002-083085/11.
DR   N-PSDB; AAD26292.
XX
PT   New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT   conditions exhibiting abnormal expression of the receptors of their
PT   ligands, particularly abnormalities manifested by immunological
PT   disorders.
XX
PS   Claim 3; Page 41; 297pp; English.
XX
CC   The invention relates to mammalian receptor proteins, e.g., primate,
CC   human DNAX Toll like receptor (DTLR) protein and their corresponding
CC   nucleic acids. The DTLR is useful for treating conditions exhibiting
CC   abnormal expression of the receptors of their ligands. Such abnormality
CC   is manifested by immunological disorders. In particular, the DTLR is
CC   useful for treating various disease or disorders associated with abnormal
CC   expression or abnormal triggering of response to a ligand. The DTLR is
CC   also useful as an immunogen for the production of antisera or antibodies
CC   specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC   receptor family members, for the DTLR or its various fragments. The
CC   purified DTLR can be used to screen monoclonal antibodies or antigen-
CC   binding fragments. The antibodies are useful for screening expression
```

CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTLR or cells that express it. The present sequence is
CC human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33.
CC Note: The present sequence SEQ ID NO 26 is stated to be similar to the
CC sequence shown in page 240-243 (AAE16116). However these sequences differ
CC at several locations
XX
SQ Sequence 837 AA;

Query Match 65.6%; Score 2844; DB 5; Length 837;
Best Local Similarity 66.5%; Pred. No. 1.2e-242;
Matches 558; Conservative 114; Mismatches 159; Indels 8; Gaps 6;

```
Qy          2 MPLLHLAGTLIMAL-FLSCLRPGSLNPCIEVLPNITYQCMDQNLSKIPHDIPYSTKNLDL 60
              |    |||||| |: ||||:|| |  ||:|| ||||||||: |  ||| ::|:|||||||
Db          1 MSASRLAGTLIPAMAFLSCVRPESWEPCVEV-PNITYQCMELNFYKIPDNLPFSTKNLDL 59

Qy         61 SFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGS 120
              |||||: | |||| :| :|| |||||||||:|||| |:  |: ||||:||||||:| : |:
Db         60 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 119

Qy        121 FSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVD 180
              ||||::|: |||||| : ||| | || | :||:|||||||| ||||||||||||||:|
Db        120 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 179

Qy        181 LSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRSNFNSSN 240
              || | ||:|   ||: | : | :|||||||||:: ||  ||: ||||:||||:||:| |
Db        180 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 239

Qy        241 VLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDIY 300
              |:| |:| : || ||||:||||:|| ||| ||:| :|||||::|:|||| |:::: |||
Db        240 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 299

Qy        301 NL-NCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTTN 359
              :| ||| |:|: |   | |: : |   :| || | :: |    || | |  ||  | |:|
Db        300 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 359

Qy        360 REDISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSANFMGL 419
              :   :| :: |||| :|||||| :||:|||| ||||| :||||||||||| ||:||:||
Db        360 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 419

Qy        420 EELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAGN 479
              |:||:|||||| ||:::|||||||  |:|||||:|:|:: |:||| || ||  ||||||
Db        420 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 479

Qy        480 SFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHYK 539
              ||::| | ::||   |||||||:|||||:|   |::|  ||:|||||||   ||   ||
Db        480 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 539

Qy        540 QLYSLRTLDCSFNRIETS-KGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMFL 598
              | ||: || | | || |  ||||| |||  ||| |  || ||:|:||||:|||:  |
Db        540 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 599

Qy        599 VNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVVSVLVVATVAFLIYHFYFHLIL 658
              | ||:|:||:| | :   ||   | || : |||| |||:||||: || |:| |||||:|
Db        600 VEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 658

Qy        659 IAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFQLCLHYRDFIPGVAIAA 718
              :||| || |||:||||||||||:|||||||||||||||| ||||||||||||||||||
Db        659 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 718

Qy        719 NIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLLR 778
              ||| ||||||||||||||:|||||||||||||||||||||:|||||||:||||:|||
Db        719 NIIHEGPHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 778

Qy        779 QQVELYRLLSRNTYLEWEDNALGRHIFWRRLKKALLDGKALNPD---ETSEEEQEATTL 834
              |||||||||||||||||: |||||||||:|||||||: ||:    |    ||||::
Db        779 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 837
```

RESULT 8
ABU04776

ID ABU04776 standard; protein; 837 AA.
XX
AC ABU04776;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1442.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1442; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 837 AA;

Query Match 65.6%; Score 2844; DB 6; Length 837;
Best Local Similarity 66.5%; Pred. No. 1.2e-242;
Matches 558; Conservative 114; Mismatches 159; Indels 8; Gaps 6;

```
Qy          2 MPLLHLAGTLIMAL-FLSCLRPGSLNPCIEVLPNITYQCMDQNLSKIPHDIPYSTKNLDL 60
              |    |||||| |: ||||:|| |  ||:|| ||||||||: |  ||| ::|:|||||||
Db          1 MSASRLAGTLIPAMAFLSCVRPESWEPCVEV-PNITYQCMELNFYKIPDNLPFSTKNLDL 59

Qy         61 SFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGS 120
              |||||: | |||| :| :|| |||||||||:|||| |:  |: ||||:||||||:| : |:
Db         60 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 119
```

```
Qy        121 FSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVD 180
Db        120 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 179

Qy        181 LSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRSNFNSSN 240
Db        180 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 239

Qy        241 VLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDIY 300
Db        240 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 299

Qy        301 NL-NCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTTN 359
Db        300 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 359

Qy        360 REDISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSANFMGL 419
Db        360 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 419

Qy        420 EELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAGN 479
Db        420 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 479

Qy        480 SFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHYK 539
Db        480 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 539

Qy        540 QLYSLRTLDCSFNRIETS-KGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMFL 598
Db        540 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 599

Qy        599 VNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVVSVLVVATVAFLIYHFYFHLIL 658
Db        600 VEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 658

Qy        659 IAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFQLCLHYRDFIPGVAIAA 718
Db        659 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 718

Qy        719 NIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLLR 778
Db        719 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 778

Qy        779 QQVELYRLLSRNTYLEWEDNALGRHIFWRRLKKALLDGKALNPD---ETSEEEQEATTL 834
Db        779 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 837
```

RESULT 9
AAE16116
ID AAE16116 standard; protein; 837 AA.
XX
AC AAE16116;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX Toll like receptor (DTLR) 4 #2, alternative version.
XX
KW Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Misc-difference 211
FT   /label= Unknown
FT   /note= "Encoded by AAY"
XX
PN WO200190151-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US016766.
XX
PR 25-MAY-2000; 2000US-0207558P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX
DR WPI; 2002-083085/11.
DR N-PSDB; AAD26306.
XX
PT New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
XX
PS Claim 3; Page 240-243; 297pp; English.
XX
CC The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTLR or its various fragments. The
CC purified DTLR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTLR or cells that express it. The present sequence is
CC human DTLR4 protein, alternative version. The DTLR4 gene is located on
CC chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
CC be similar to the sequence shown in page 41 (AAE16102). However these
CC sequences differ at several locations
XX
SQ Sequence 837 AA;

Query Match 65.4%; Score 2837; DB 5; Length 837;
Best Local Similarity 66.4%; Pred. No. 5e-242;
Matches 557; Conservative 114; Mismatches 160; Indels 8; Gaps 6;

```
Qy          2 MPLLHLAGTLIMAL-FLSCLRPGSLNPCIEVLPNITYQCMDQNLSKIPHDIPYSTKNLDL 60
Db          1 MSASRLAGTLIPAMAFLSCVRPESWEPCVEV-PNITYQCMELNFYKIPDNLPFSTKNLDL 59

Qy         61 SFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGS 120
Db         60 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 119

Qy        121 FSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVD 180
Db        120 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 179

Qy        181 LSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRSNFNSSN 240
Db        180 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLXPMNFIQPGAFKEIRLHKLTLRNNFDSLN 239

Qy        241 VLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDIY 300
Db        240 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 299

Qy        301 NL-NCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTTN 359
Db        300 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 359

Qy        360 REDISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSANFMGL 419
Db        360 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 419
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```
Qy        420 EELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAGN 479
              |:||:|||||| ||:::|||||||  |:|||||:|:|:: |:||| || ||  ||||||
Db        420 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 479

Qy        480 SFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHYK 539
              ||::| | ::||   ||||||||:|||||:|   |::|  ||:|||||||   ||   ||
Db        480 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 539

Qy        540 QLYSLRTLDCSFNRIETS-KGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMFL 598
              | ||: || | | | || |  ||||| |||  ||| |  || ||:|:||||:|||:  |
Db        540 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 599

Qy        599 VNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVVSVLVVATVAFLIYHFYFHLIL 658
              | ||:|:||:| | :   ||   | || : |||| |||:|||||: || |:| |||||:|
Db        600 VEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 658

Qy        659 IAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFQLCLHYRDFIPGVAIAA 718
              :||| || |||:|||||||||||:|||||||||||||||| ||||||||||||||||||
Db        659 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 718

Qy        719 NIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLLR 778
              ||| |||||||||||||:|||||||||||||||||||||||:|||||||:||||:|||
Db        719 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 778

Qy        779 QQVELYRLLSRNTYLEWEDNALGRHIFWRRLKKALLDGKALNPD---ETSEEEQEATTL 834
              ||||||||||||||||||: |||||||||:|||||||: ||:    |    ||||::
Db        779 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 837


RESULT 10
ADO57797
ID   ADO57797 standard; protein; 801 AA.
XX
AC   ADO57797;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Squirrel monkey toll-like receptor 4 SEQ ID NO:18.
XX
KW   toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW   immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW   sepsis; severe sepsis; septic shock; asthma; squirrel monkey.
XX
OS   Saimiri sciureus.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 14
FT                   /label= Leu, Phe
XX
PN   WO2004042365-A2.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-US036247.
XX
PR   01-NOV-2002; 2002US-0423113P.
XX
PA   (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI   Messier W;
XX
DR   WPI; 2004-400726/37.
DR   N-PSDB; ADO57795, ADO57796.
XX
PT   Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT   in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT   sequence of the Old World monkey with that of a human.
XX
PS   Disclosure; SEQ ID NO 18; 111pp; English.
XX
CC   The invention relates to a novel method for identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an old world monkey
CC   comprising comparing the TLR4 polynucleotide sequence of the Old World
CC   monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC   method of the invention has antibacterial, immunosuppressive, and
CC   antiasthmatic activity. The method is useful in identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC   change may be associated with reduced sensitivity to Gram-negative
CC   bacterial infection. The methods, agents and composition are useful in
CC   treating sepsis, severe sepsis or septic shock and asthma. The present
CC   sequence represents squirrel monkey TLR4.
XX
SQ   Sequence 801 AA;

  Query Match           64.5%;  Score 2796.5;  DB 8;  Length 801;
  Best Local Similarity   67.7%;  Pred. No. 1.8e-238;
  Matches  539;  Conservative  105;  Mismatches  149;  Indels    3;  Gaps    3;

Qy         31 VLPNITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIE 90
              |:||:|||||: |  ||| :||:|||||||||||: | |:|| || :|| ||||||:|:
Db          1 VVPNVTYQCMELNXYKIPDNIPFSTKNLDLSFNPLRHLGSHSFFNFPELQVLDLSRCDIQ 60

Qy         91 TIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLIS 150
              |||| |:  |: |||:|||||:: : |:||||::|: |||||| : ||| | || | :
Db         61 TIEDGAYQSLSHLSTLILTGNPIQNLALGAFSGLSSLQKLVAVETHLLSLENFPIGHLKT 120

Qy        151 LKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSLDLS 210
              || |||||||| |||||||||||||||:||| | || |  |||| | : | :|||||||
Db        121 LKDLNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNNIQNIYCKDLQVLHQMPLLNLSLDLS 180

Qy        211 LNPIDSIQAQAFQGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLES 270
              ||||: ||  ||: ||||:||||:||:| | :| |:| : || ||||:||||:||||:|
Db        181 LNPINFIQPGAFKEIRLHKLTLRNNFDSLNAMKTCIQGLAGLEVHRLVLGEFRNERNIED 240

Qy        271 FDRSVMEGLCNVSIDEFRLTYINHFSDDIYNL-NCLANISAMSFTGVHIKHIADVPRHFK 329
              ||:| :|||||::|:|||| |:: | ||| :| |||||:|: |   |||| : |   :|:
Db        241 FDKSALEGLCNLTINEFRLAYLDDFLDDIIDLFNCLANVSSFSLVNVHIKRVEDFSYNFR 300

Qy        330 WQSLSIIRCHLKPFPKLSLPFLKSWTLTTNREDISFGQLALPSLRYLDLSRNAMSFRGCC 389
              || | :: |  : || | |  ||  | | |:    | :: |||| :|||||| :||:|||
Db        301 WQHLELVNCVFQQFPPLKLKSLKRLTFTANKGRNHFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        390 SYSDFGTNNLKYLDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKLLY 449
              | ||||| :||||||||| || | :||:|||:||:|||||| ||:::|||||||  |:|
Db        361 SQSDFGTTSLKYLDLSFNDVITMGSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 420

Qy        450 LDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQLEQI 509
              ||||:|:|:: |:||| || ||  |||||||: | | ::||:  || |||||:|||||:
Db        421 LDISHTHTRVAFNGIFNGLFSLKVLKMAGNSFQQNFLEDIFTDLNNLIFLDLSECQLEQL 480

Qy        510 SRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSLRTLDCSFNRIETSKG-ILQHFPKSL 568
              |   ||:| ||::|||||||   ||   || |||| || | | | |||  |||| ||
Db        481 SPTAFDSLPRLRILNMSHNNFFALDTFPYKHLYSLQVLDYSLNHIGTSKNQELQHFPSSL 540

Qy        569 AVFNLTNNSVACICEYQNFLQWVKDQKMFLVNVEQMKCASPIDMKASLVLDFTNSTCYIY 628
              |  ||| |  || ||:|:||||:|||:  || ||||:||:|:: |   ||   | || :
Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRRLLVEVEQMECATPLNRKGIPVLSL-NITCQMS 599

Qy        629 KTIISVSVVSVLVVATVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRN 688
              |||| |||:|||||: || |:| |||||:|:||| || |||: ||||||||||:||||||
Db        600 KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENTYDAFVIYSSQDEDWVRN 659

Qy        689 ELVKNLEEGVPRFQLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFE 748
              |||||||||| |||||||||||||||||||| ||||||||||||:|||||||||||
Db        660 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 719

Qy        749 YEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNALGRHIFWRR 808
              |||||||||||||:|||||||:|||||||||||||||||||||||||||: |||||||||
Db        720 YEIAQTWQFLSSRAGIIFIVLQKVEKSLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRR 779

Qy        809 LKKALLDGKALNPDET 824
              |:||||||:  ||: |
Db        780 LRKALLDGRPWNPEGT 795


RESULT 11
```

```
ADO57791
ID   ADO57791 standard; protein; 795 AA.
XX
AC   ADO57791;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Rhesus monkey toll-like receptor 4 SEQ ID NO:12.
XX
KW   toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW   immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW   sepsis; severe sepsis; septic shock; asthma; rhesus monkey.
XX
OS   Macaca mulatta.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 635
FT                   /label= Lys, Asn
XX
PN   WO2004042365-A2.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-US036247.
XX
PR   01-NOV-2002; 2002US-0423113P.
XX
PA   (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI   Messier W;
XX
DR   WPI; 2004-400726/37.
DR   N-PSDB; ADO57789, ADO57790.
XX
PT   Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT   in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT   sequence of the Old World monkey with that of a human.
XX
PS   Disclosure; SEQ ID NO 12; 111pp; English.
XX
CC   The invention relates to a novel method for identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an old world monkey
CC   comprising comparing the TLR4 polynucleotide sequence of the Old World
CC   monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC   method of the invention has antibacterial, immunosuppressive, and
CC   antiasthmatic activity. The method is useful in identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC   change may be associated with reduced sensitivity to Gram-negative
CC   bacterial infection. The methods, agents and composition are useful in
CC   treating sepsis, severe sepsis or septic shock and asthma. The present
CC   sequence represents rhesus monkey TLR4.
XX
SQ   Sequence 795 AA;

  Query Match             64.2%;  Score 2782.5;  DB 8;  Length 795;
  Best Local Similarity   67.5%;  Pred. No. 3.1e-237;
  Matches  537;  Conservative  109;  Mismatches  146;  Indels    3;  Gaps    3;

Qy         31 VLPNITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIE 90
              |:||||||||: |  ||| ::|:|||||||||||||: | |||| :| :|| ||||||||:
Db          1 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 60

Qy         91 TIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLIS 150
              |||| |:  |: ||||:||||||:| : |:||||::|: |||||| : ||| | || | :
Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        151 LKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSLDLS 210
              ||:|||||||| ||||||||||||||||:||| | || |  |||| | : |  |||||||
Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQNIYCKDLQVLHQMPLSNLSLDLS 180

Qy        211 LNPIDSIQAQAFQGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLES 270
              ||||: ||  ||: ||||:|||||||:  ||:| |:| : || ||||:||||:||||||
Db        181 LNPINFIQPGAFKEIRLHKLTLRSNFDDLNVMKTCIQGLAGLEVHRLVLGEFRNERNLEE 240

Qy        271 FDRSVMEGLCNVSIDEFRLTYINHFSDDIYNL-NCLANISAMSFTGVHIKHIADVPRHFK 329
              ||:| :|||||::|:||||||:::: |:| :| |||||:|: |   | || : |   :|:
Db        241 FDKSSLEGLCNLTIEEFRLTYLDYYLDNIIDLFNCLANVSSFSLVSVSIKRVEDFSYNFR 300

Qy        330 WQSLSIIRCHLKPFPKLSLPFLKSWTLTTNREDISFGQLALPSLRYLDLSRNAMSFRGCC 389
              || | :: |  : || | |  ||  | | |:   :| :: |||| :|||||| :||:|||
Db        301 WQHLELVNCKFEQFPTLELESLKRLTFTANKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        390 SYSDFGTNNLKYLDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKLLY 449
              | ||||| :||||||||| || ||:||:|||:||:|||||| ||::::|||||||  |:|
Db        361 SQSDFGTTSLKYLDLSFNDVITMSSNFLGLEKLEHLDFQHSNLKQMSQFSVFLSLRNLIY 420

Qy        450 LDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQLEQI 509
              ||||:|:|:: |:||| ||:||  ||||||||::| | ::||:  |||||||:|||||:
Db        421 LDISHTHTRVAFNGIFDGLLSLKVLKMAGNSFQENFLPDIFTDLKNLTFLDLSQCQLEQL 480

Qy        510 SRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSLRTLDCSFNRIETSKG-ILQHFPKSL 568
              |   |||| :||:|||||||   ||   || | ||: || | | | ||    ||||| ||
Db        481 SPTAFDTLNKLQVLNMSHNNFFSLDTFPYKCLPSLQVLDYSLNHIMTSNNQELQHFPSSL 540

Qy        569 AVFNLTNNSVACICEYQNFLQWVKDQKMFLVNVEQMKCASPIDMKASLVLDFTNSTCYIY 628
              |  ||| |  || ||:|:||||:|||:  ||  |:|:||:| | :   ||   | || :
Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEAERMECATPSDKQGMPVLSL-NITCQMN 599

Qy        629 KTIISVSVVSVLVVATVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRN 688
              |||| ||| |||||: || |:| |||||:|:|||  | |||:||||||||||:||||||
Db        600 KTIIGVSVFSVLVVSVVAVLVYKFYFHLMLLAGCIXYGRGENIYDAFVIYSSQDEDWVRN 659

Qy        689 ELVKNLEEGVPRFQLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFE 748
              |||||||||| |||||||||||||||||||| ||||||||||||||:||||||||||
Db        660 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 719

Qy        749 YEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNALGRHIFWRR 808
              |||||||||||:|||||||:||||:|||||||||||||||||||: ||:||||||
Db        720 YEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGQHIFWRR 779

Qy        809 LKKALLDGKALNPDE 823
              |:||||||:: ||:|
Db        780 LRKALLDGRSWNPEE 794


RESULT 12
ADO57800
ID   ADO57800 standard; protein; 795 AA.
XX
AC   ADO57800;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Hamadryas baboon toll-like receptor 4 SEQ ID NO:21.
XX
KW   toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW   immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW   sepsis; severe sepsis; septic shock; asthma; hamadryas baboon.
XX
OS   Papio hamadryas.
XX
PN   WO2004042365-A2.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-US036247.
XX
PR   01-NOV-2002; 2002US-0423113P.
XX
PA   (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI   Messier W;
XX
DR   WPI; 2004-400726/37.
DR   N-PSDB; ADO57798, ADO57799.
XX
```

PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Disclosure; SEQ ID NO 21; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents hamadryas baboon TLR4.
XX
SQ Sequence 795 AA;

Query Match 64.2%; Score 2781.5; DB 8; Length 795;
Best Local Similarity 67.7%; Pred. No. 3.9e-237;
Matches 538; Conservative 106; Mismatches 148; Indels 3; Gaps 3;

```
Qy         31 VLPNITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIE 90
              |:||||||||: |  ||| :||:||||||||||||: | ||||  | :|| ||||||||:
Db          1 VVPNITYQCMELNFYKIPDNIPFSTKNLDLSFNPLRHLGSYSFLRFPELQVLDLSRCEIQ 60

Qy         91 TIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLIS 150
              |||| |:  |: ||||:||||||:| : |:||||::|: |||||| : ||| | || | :
Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        151 LKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSLDLS 210
              ||:|||||||| |||||||||||||||:||| | || |  |||| | : |  |||||||
Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQNIYCKDLQVLHQMPLPNLSLDLS 180

Qy        211 LNPIDSIQAQAFQGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLES 270
              ||||: ||  ||: ||||:|||||||:  ||:| |:| : || ||||:||||:||||||
Db        181 LNPINFIQPGAFKEIRLHKLTLRSNFDDLNVMKTCIQGLAGLEVHRLVLGEFRNERNLEE 240

Qy        271 FDRSVMEGLCNVSIDEFRLTYINHFSDDIYNL-NCLANISAMSFTGVHIKHIADVPRHFK 329
              ||:| :|||||::|:||||||:::: |:| :| ||||| |: |   |:|| : |   :|:
Db        241 FDKSALEGLCNLTIEEFRLTYLDYYLDNIIDLFNCLANASSFSLVSVNIKRVEDFSYNFR 300

Qy        330 WQSLSIIRCHLKPFPKLSLPFLKSWTLTTNREDISFGQLALPSLRYLDLSRNAMSFRGCC 389
              || | :: |  : || | |  ||  | | |:   :| :: |||| :|||||| :||:|||
Db        301 WQHLELVNCKFEQFPTLELESLKRLTFTANKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        390 SYSDFGTNNLKYLDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKLLY 449
              | ||||| :||||||||| || | :||:|||:||:|||||| ||:::|||||||  |:|
Db        361 SQSDFGTTSLKYLDLSFNDVITMGSNFLGLEQLEHLDFQHSNLKQMSQFSVFLSLRNLIY 420

Qy        450 LDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQLEQI 509
              ||||:|:| : |:||| ||:||  ||||||||::| | ::||:  ||||||||:|||||:
Db        421 LDISHTHTTVAFNGIFDGLLSLKVLKMAGNSFQENFLPDIFTDLKNLTFLDLSQCQLEQL 480

Qy        510 SRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSLRTLDCSFNRIETSKG-ILQHFPKSL 568
              |  |||| :||:|||||||  ||  || | ||: || | | | |||  |||| ||
Db        481 SPTAFDTLNKLQVLNMSHNNFFSLDVFPYKCLPSLQVLDYSLNHIMTSKNQEPQHFPSSL 540

Qy        569 AVFNLTNNSVACICEYQNFLQWVKDQKMFLVNVEQMKCASPIDMKASLVLDFTNSTCYIY 628
              | ||| |  || ||:|:||||:|||:  ||  |:|:||:| | :   ||   | || :
Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEAERMECATPSDKQGMPVLS-VNITCQMN 599

Qy        629 KTIISVSVVSVLVVATVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRN 688
              |||| ||| |||||: || |:| |||||:|:||| || |||:||||||||||:||||||
Db        600 KTIIGVSVFSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRN 659

Qy        689 ELVKNLEEGVPRFQLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFE 748
              |||||||||| |||||||||||||||||||| ||||||||||||:|||||||||||||||
Db        660 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 719

Qy        749 YEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNALGRHIFWRR 808
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                ||||||||||||||:|||||||:||||:|||||||||||||||||||||||: ||:||||||
Db        720 YEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGQHIFWRR 779

Qy        809 LKKALLDGKALNPDE 823
              |:||||||:: ||:|
Db        780 LRKALLDGRSWNPEE 794
```

RESULT 13
ADO57803
ID ADO57803 standard; protein; 808 AA.
XX
AC ADO57803;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimpanzee toll-like receptor 4 SEQ ID NO:24.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS Pan troglodytes.
XX
PN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
DR WPI; 2004-400726/37.
DR N-PSDB; ADO57801, ADO57802.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Disclosure; SEQ ID NO 24; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents chimpanzee TLR4.
XX
SQ Sequence 808 AA;

Query Match 64.1%; Score 2777; DB 8; Length 808;
Best Local Similarity 66.7%; Pred. No. 9.9e-237;
Matches 540; Conservative 113; Mismatches 150; Indels 6; Gaps 4;

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Qy         31 VLPNITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIE 90
              |:||||||||: |  ||| ::|:||||||||||||: | ||||  :| :|| ||||||||:
Db          1 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 60

Qy         91 TIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLIS 150
              |||| |:  |: ||||:||||||:| : |:||||::|: |||||| : ||| | || | :
Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        151 LKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSLDLS 210
              ||:|||||||| |||||||||||||||:||| | || |  |||| | : |  |||||||
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```
Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 180

Qy        211 LNPIDSIQAQAFQGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLES 270

Db        181 LNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEENLEK 240

Qy        271 FDRSVMEGLCNVSIDEFRLTYINHFSDDIYNL-NCLANISAMSFTGVHIKHIADVPRHFK 329

Db        241 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIKSVKDFSYNFG 300

Qy        330 WQSLSIIRCHLKPFPKLSLPFLKSWTLTTNREDISFGQLALPSLRYLDLSRNAMSFRGCC 389

Db        301 WQHLELVKCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        390 SYSDFGTNNLKYLDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKLLY 449

Db        361 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 420

Qy        450 LDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQLEQI 509

Db        421 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 480

Qy        510 SRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSLRTLDCSFNRIETS-KGILQHFPKSL 568

Db        481 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 540

Qy        569 AVFNLTNNSVACICEYQNFLQWVKDQKMFLVNVEQMKCASPIDMKASLVLDFTNSTCYIY 628

Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQMN 599

Qy        629 KTIISVSVVSVLVVATVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRN 688

Db        600 KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRN 659

Qy        689 ELVKNLEEGVPRFQLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFE 748

Db        660 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 719

Qy        749 YEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNALGRHIFWRR 808

Db        720 YEIAQTWQFLSSRAGIIFIVLQKVEKTLLRRQVELYRLLSRNTYLEWEDSVLGRHIFWRR 779

Qy        809 LKKALLDGKALNPD---ETSEEEQEATTL 834

Db        780 LRKALLDGKSWNPEGTVGTGCNWQEATSI 808
```

RESULT 14
ADO57782
ID ADO57782 standard; protein; 808 AA.
XX
AC ADO57782;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimpanzee toll-like receptor 4 SEQ ID NO:3.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS Pan troglodytes.
XX
PN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
DR WPI; 2004-400726/37.
DR N-PSDB; ADO57780, ADO57781.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Example 1; SEQ ID NO 3; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents chimpanzee TLR4.
XX
SQ Sequence 808 AA;

Query Match 64.0%; Score 2773; DB 8; Length 808;
Best Local Similarity 66.7%; Pred. No. 2.2e-236;
Matches 540; Conservative 112; Mismatches 151; Indels 6; Gaps 4;

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Qy         31 VLPNITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIE 90

Db          1 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 60

Qy         91 TIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLIS 150

Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        151 LKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSLDLS 210

Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 180

Qy        211 LNPIDSIQAQAFQGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLES 270

Db        181 LNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEK 240

Qy        271 FDRSVMEGLCNVSIDEFRLTYINHFSDDIYNL-NCLANISAMSFTGVHIKHIADVPRHFK 329

Db        241 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIKSVKDFSYNFG 300

Qy        330 WQSLSIIRCHLKPFPKLSLPFLKSWTLTTNREDISFGQLALPSLRYLDLSRNAMSFRGCC 389

Db        301 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        390 SYSDFGTNNLKYLDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKLLY 449

Db        361 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 420

Qy        450 LDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQLEQI 509

Db        421 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 480

Qy        510 SRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSLRTLDCSFNRIETS-KGILQHFPKSL 568

Db        481 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 540

Qy        569 AVFNLTNNSVACICEYQNFLQWVKDQKMFLVNVEQMKCASPIDMKASLVLDFTNSTCYIY 628

Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQMN 599

Qy        629 KTIISVSVVSVLVVATVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRN 688

Db        600 KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRN 659
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Qy        689 ELVKNLEEGVPRFQLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFE 748
              |||||||||||| |||||||||||||||||||| |||||||||||||:||||||||||
Db        660 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 719

Qy        749 YEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNALGRHIFWRR 808
              |||||||||||||:|||||||:||||:|||:|||||||||||||||||: |||||||||
Db        720 YEIAQTWQFLSSRAGIIFIVLQKVEKTLLRRQVELYRLLSRNTYLEWEDSVLGRHIFWRR 779

Qy        809 LKKALLDGKALNPD---ETSEEEQEATTL 834
              |:|||||||: ||:    |    ||||::
Db        780 LRKALLDGKSWNPEGTVGTGCNWQEATSI 808


RESULT 15
ADO57785
ID   ADO57785 standard; protein; 808 AA.
XX
AC   ADO57785;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Gorilla toll-like receptor 4 SEQ ID NO:6.
XX
KW   toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW   immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW   sepsis; severe sepsis; septic shock; asthma; gorilla.
XX
OS   Gorilla gorilla.
XX
PN   WO2004042365-A2.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-US036247.
XX
PR   01-NOV-2002; 2002US-0423113P.
XX
PA   (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI   Messier W;
XX
DR   WPI; 2004-400726/37.
DR   N-PSDB; ADO57783, ADO57784.
XX
PT   Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT   in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT   sequence of the Old World monkey with that of a human.
XX
PS   Example 1; SEQ ID NO 6; 111pp; English.
XX
CC   The invention relates to a novel method for identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an old world monkey
CC   comprising comparing the TLR4 polynucleotide sequence of the Old World
CC   monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC   method of the invention has antibacterial, immunosuppressive, and
CC   antiasthmatic activity. The method is useful in identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC   change may be associated with reduced sensitivity to Gram-negative
CC   bacterial infection. The methods, agents and composition are useful in
CC   treating sepsis, severe sepsis or septic shock and asthma. The present
CC   sequence represents gorilla TLR4.
XX
SQ   Sequence 808 AA;

  Query Match             63.7%;  Score 2761;  DB 8;  Length 808;
  Best Local Similarity   66.5%;  Pred. No. 2.6e-235;
  Matches  538;  Conservative  112;  Mismatches  153;  Indels    6;  Gaps    4;

Qy         31 VLPNITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIE 90
              |:|||||||: |  ||| ::|:|||||||||||: | |||| :| :|| ||||||||:
Db          1 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 60

Qy         91 TIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLIS 150
              |||| |:  |: ||||:||||||:| : |:||||::|: |||||| : ||| | || | :
Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        151 LKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSLDLS 210
              ||:|||||||| ||||||||||||||::||| | ||:|   ||: | : | :|||||||
Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEYLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 180

Qy        211 LNPIDSIQAQAFQGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLES 270
              |||:  ||  ||: ||||:||||:||:| ||:| |:|  : || | ||:||||:|| |||
Db        181 LNPMTFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVRRLVLGEFRNEGNLEK 240

Qy        271 FDRSVMEGLCNVSIDEFRLTYINHFSDDIYNL-NCLANISAMSFTGVHIKHIADVPRHFK 329
              ||:| :|||||::|:|||| |:::: ||| :| ||| |:|: |   | |: : |   :|
Db        241 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFG 300

Qy        330 WQSLSIIRCHLKPFPKLSLPFLKSWTLTTNREDISFGQLALPSLRYLDLSRNAMSFRGCC 389
              || | :: |    || | |  ||  | |:|:   :| :: |||| :|||||| :||:|||
Db        301 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        390 SYSDFGTNNLKYLDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKLLY 449
              | ||||| :|||||||||||| ||:||:|||:||:|||||| ||:::|||||||  |:|
Db        361 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 420

Qy        450 LDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQLEQI 509
              ||||:|:|:: |:||| || ||  |||||||::| | ::||   ||||||||:|||||:
Db        421 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 480

Qy        510 SRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSLRTLDCSFNRIETS-KGILQHFPKSL 568
              |   |::|  ||:|||||||   ||   || | ||| || | | | || |  ||||| ||
Db        481 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLRVLDYSLNHIMTSKKQELQHFPSSL 540

Qy        569 AVFNLTNNSVACICEYQNFLQWVKDQKMFLVNVEQMKCASPIDMKASLVLDFTNSTCYIY 628
              |  ||| |  || ||:|:||||:|||:  || ||:|:||:| | :   ||   | || :
Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQMN 599

Qy        629 KTIISVSVVSVLVVATVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRN 688
              |||| |||:|||||: || |:| |||||:|:||| || |||::||||||||||:||||||
Db        600 KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENVYDAFVIYSSQDEDWVRN 659

Qy        689 ELVKNLEEGVPRFQLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFE 748
              |||||||||||| |||||||||||||||||||| |||||||||||||:||||||||||
Db        660 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 719

Qy        749 YEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNALGRHIFWRR 808
              |||||||||||||:|||||||:||||:|||:|||||||||||||||||: |||||||||
Db        720 YEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRR 779

Qy        809 LKKALLDGKALNPD---ETSEEEQEATTL 834
              |:|||||||: ||:    |    ||||::
Db        780 LRKALLDGKSWNPEGTVGTGCNWQEATSI 808


Search completed: March 12, 2005, 19:55:04
Job time : 90.9834 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:46 ; Search time 22.9539 Seconds
(without alignments)
2715.523 Million cell updates/sec

Title: US-09-396-985B-6
Perfect score: 4335
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2779.5	64.1	844	4	US-09-949-016-9438	Sequence 9438, Ap
2	602.5	13.9	661	1	US-08-514-014-4	Sequence 4, Appli
3	602.5	13.9	661	2	US-08-833-823-4	Sequence 4, Appli
4	502	11.6	784	4	US-09-982-308B-23	Sequence 23, Appl
5	439.5	10.1	775	4	US-09-949-016-8799	Sequence 8799, Ap
6	300.5	6.9	605	3	US-09-063-950-5	Sequence 5, Appli
7	290.5	6.7	603	1	US-08-190-802A-50	Sequence 50, Appl
8	290.5	6.7	603	3	US-08-477-346-50	Sequence 50, Appl
9	290.5	6.7	603	3	US-08-473-089-50	Sequence 50, Appl
10	290.5	6.7	603	4	US-08-487-072A-50	Sequence 50, Appl
11	288.5	6.7	1112	3	US-09-353-585-2	Sequence 2, Appli
12	288.5	6.7	1112	3	US-09-353-585-3	Sequence 3, Appli
13	281.5	6.5	605	1	US-08-190-802A-49	Sequence 49, Appl
14	281.5	6.5	605	3	US-08-477-346-49	Sequence 49, Appl
15	281.5	6.5	605	3	US-08-473-089-49	Sequence 49, Appl
16	281.5	6.5	605	4	US-08-487-072A-49	Sequence 49, Appl
17	281.5	6.5	605	4	US-09-538-092-1087	Sequence 1087, Ap
18	281.5	6.5	623	4	US-09-949-016-10995	Sequence 10995, A
19	279	6.4	1480	3	US-09-191-647-7	Sequence 7, Appli
20	279	6.4	1480	3	US-09-540-245A-7	Sequence 7, Appli
21	279	6.4	1480	3	US-09-540-153-7	Sequence 7, Appli
22	279	6.4	1480	5	PCT-US91-09055-2	Sequence 2, Appli
23	277	6.4	1480	3	US-09-182-024A-5	Sequence 5, Appli
24	274.5	6.3	1119	4	US-09-907-794A-294	Sequence 294, App
25	274.5	6.3	1119	4	US-09-905-125A-294	Sequence 294, App
26	274.5	6.3	1119	4	US-09-902-775A-294	Sequence 294, App
27	274.5	6.3	1119	4	US-09-906-700-294	Sequence 294, App
28	274.5	6.3	1119	4	US-09-903-603A-294	Sequence 294, App
29	274.5	6.3	1119	4	US-09-904-920A-294	Sequence 294, App
30	274.5	6.3	1119	4	US-09-909-064-294	Sequence 294, App
31	274.5	6.3	1119	4	US-09-905-381A-294	Sequence 294, App
32	274.5	6.3	1119	4	US-09-906-618-294	Sequence 294, App
33	272.5	6.3	958	4	US-09-706-594-5	Sequence 5, Appli
34	265.5	6.1	1016	3	US-09-180-439-8	Sequence 8, Appli
35	264.5	6.1	968	3	US-09-180-439-3	Sequence 3, Appli
36	264.5	6.1	968	3	US-09-180-439-4	Sequence 4, Appli
37	259	6.0	1525	3	US-09-191-647-2	Sequence 2, Appli
38	259	6.0	1525	3	US-09-540-245A-2	Sequence 2, Appli
39	259	6.0	1525	3	US-09-540-153-2	Sequence 2, Appli
40	259	6.0	1529	4	US-09-312-283C-396	Sequence 396, App
41	256	5.9	560	3	US-08-592-500-2	Sequence 2, Appli
42	256	5.9	560	3	US-08-195-006-2	Sequence 2, Appli
43	256	5.9	560	3	US-09-063-950-4	Sequence 4, Appli
44	256	5.9	560	5	PCT-US94-07644A-2	Sequence 2, Appli
45	255.5	5.9	1523	3	US-09-182-024A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9438

Query Match 64.1%; Score 2779.5; DB 4; Length 844;
Best Local Similarity 65.8%; Pred. No. 7e-246;
Matches 546; Conservative 112; Mismatches 161; Indels 11; Gaps 5;

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Qy          10 TLIMALFLSCLRPGSLNPCIEVLPNITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILR 69
               | |  |   | |         ||:||||||||: |  ||| ::|:||||||||||||: |
Db          21 TPIPLLLAKCCR-----FITEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLG 75

Qy          70 SYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLEN 129
               |||| :| :|| |||||||:|||| |:  |: ||||:||||||:| : |:||||::|:
Db          76 SYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQK 135

Qy         130 LVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTI 189
               |||||| : ||| | || | :||:|||||||| ||||||||||||||||:||| | ||:|
Db         136 LVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSI 195

Qy         190 SVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRSNFNSSNVLKMCLQNM 249
                 ||: | : | :|||||||||:: ||  ||: ||||:||||:||:| ||:| |:| :
Db         196 YCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGL 255

Qy         250 TGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDIYNL-NCLANI 308
               || ||||:||||:|| ||| ||:| :|||||::|:|||| |:::: ||| :| ||| |:
Db         256 AGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNV 315

Qy         309 SAMSFTGVHIKHIADVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTTNREDISFGQL 368
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Db        316 SSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQPFPTLKLKSLKRLTFTSNKGGNAFSEV 375

Qy        369 ALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSANFMGLEELEYLDFQ 428
              |||| :|||||| :||:|||| ||||| :|||||||||||| ||:||:|||:||:||||
Db        376 DLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQ 435

Qy        429 HSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTLSN 488
              || ||:::|||||||  |:|||||:|:|:: |:||| || ||  |||||||::| | :
Db        436 HSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPD 495

Qy        489 VFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSLRTLD 548
              :||   |||||||:|||||:|   |::|  ||:|||||||   ||   || | ||: ||
Db        496 IFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLD 555

Qy        549 CSFNRIETS-KGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMFLVNVEQMKCA 607
              | | | || |  ||||| ||| ||| |  || ||:|:||||:|||:  || ||:|:||
Db        556 YSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECA 615

Qy        608 SPIDMKASLVLDFTNSTCYIYKTIISVSVVSVLVVATVAFLIYHFYFHLILIAGCKKYSR 667
              :| | :   ||   | || : |||| |||:|||||: || |:| |||||:|:||| || |
Db        616 TPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGR 674

Qy        668 GESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFQLCLHYRDFIPGVAIAANIIQEGFHK 727
              ||:||||||||||:|||||||||||||| |||||||||||||||||||| |||||
Db        675 GENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHK 734

Qy        728 SRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVELYRLL 787
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Db        735 SRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLL 794

Qy        788 SRNTYLEWEDNALGRHIFWRRLKKALLDGKALNPD---ETSEEEQEATTL 834
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Db        795 SRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 844
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RESULT 2
US-08-514-014-4
; Sequence 4, Application US/08514014
; Patent No. 5707829
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/514,014
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI6000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-514-014-4

Query Match 13.9%; Score 602.5; DB 1; Length 661;
Best Local Similarity 28.2%; Pred. No. 3e-46;
Matches 185; Conservative 127; Mismatches 296; Indels 47; Gaps 18;

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Qy         28 CIEVLPNITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRC 87
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Db         28 CIEKEANKTYNCENLGLSEIPDTLPNTTEFLEFSFNFLPTIHNRTFSRLMNLTFLDLTRC 87

Qy         88 EIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQ 147
              :|  | :  :   :|||||||||||:   :  | :|  :|::|  ::| :::||   :
Db         88 QINWIHEDTFQSHHQLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEFIPVHN 147

Qy        148 LISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSL 207
              | :|: | :  | | | | |: |    ||: :|  | |  || :|:: | :   :||||
Db        148 LENLESLYLGSNHISSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--AINLSL 204

Qy        208 DLSLNPIDSIQAQAFQGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERN 267
              : : | :  |:  ||       |    ||  :  | :    :       | || |::  :
Db        205 NFNGNNVKGIELGAFDSTVFQSL----NFGGTPNLSVIFNGLQNSTTQSLWLGTFEDIDD 260

Qy        268 LESFDRSVMEGLCNVSIDEFRLTYINHFSD-DIYNLNCLANISAMSFTGVHIKHIADVPR 326
              |    ::::||| :|::   |   : |||       |   :  :  |  |:|    :|
Db        261 -EDISSAMLKGLCEMSVESLNLQE-HRFSDISSTTFQCFTQLQELDLTATHLK---GLPS 315

Qy        327 HFKWQSLSIIR-----------CHLKP--FPKLSLPFLKSWTLTTNREDISFGQL-ALP 371
              |   |::::           | :   || |:  :::       :  :  | |  |
Db        316 GMK--GLNLLKKLVLSVNHFDQLCQISAANFPSLTHLYIRG---NVKKLHLGVGCLEKLG 370

Qy        372 SLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVI-LMSANFMGLEELEYLDFQHS 430
              :|: |||| | :    |||      ::|: |:|| |  : | |  |    :|| ||   :
Db        371 NLQTLDLSHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKECPQLELLDLAFT 430

Qy        431 TLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTL--SN 488
              |       | | :|  |  |:::|          :  ||  |  | : || |:| |:  :|
Db        431 RLHINAPQSPFQNLHFLQVLNLTYCFLDTSNQHLLAGLPVLRHLNLKGNHFQDGTITKTN 490

Qy        489 VFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLL--FLDP-SHYKQLYSLR 545
              :    :|  | || | |  | :  | :| ::  :::|||:|    :|  || | :|
Db        491 LLQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHNSLTCDSIDSLSHLKGIY--- 547

Qy        546 TLDCSFNRIETSKGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMFLVNVEQMK 605
              |: : | |       |       :  ||::| : | |   :|| | |:    |   |:
Db        548 -LNLAANSINIISPRLLPILSQQSTINLSHNPLDCTCSNIHFLTWYKENLHKLEGSEETT 606

Qy        606 CASPIDMKASLVLDFTNS----TCYIYKTIISVSVVSVLVVATVAFLIYHFYFHL 656
              ||:|  ::   : |   |       |:  |: : ::::|:   | :|:   | |:
Db        607 CANPPSLRGVKLSDVKLSCGITAIGIFFLIVFLLLLAILLFFAVKYLLRWKYQHI 661
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RESULT 3
US-08-833-823-4
; Sequence 4, Application US/08833823
; Patent No. 5969093
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA

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;       ZIP:  02140
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/833,823
;       FILING DATE:  10-APR-1997
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/514,014
;       FILING DATE:  11-AUG-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Brown, Scott A.
;       REGISTRATION NUMBER:  32,724
;       REFERENCE/DOCKET NUMBER:  GI6000
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 498-8224
;       TELEFAX:  (617) 876-5851
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  661 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-833-823-4

  Query Match             13.9%;  Score 602.5;  DB 2;  Length 661;
  Best Local Similarity   28.2%;  Pred. No. 3e-46;
  Matches  185;  Conservative  127;  Mismatches  296;  Indels   47;  Gaps   18;

Qy         28 CIEVLPNITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRC 87
              |||    | || | :  ||:||  :| :|: |: ||| |  : : :|:    | :|||:||
Db         28 CIEKEANKTYNCENLGLSEIPDTLPNTTEFLEFSFNFLPTIHNRTFSRLMNLTFLDLTRC 87

Qy         88 EIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQ 147
              :|  | :  :   :||||||||||:   :  | :|  :|::|  ::| :::||   :
Db         88 QINWIHEDTFQSHHQLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEFIPVHN 147

Qy        148 LISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSL 207
              | :|: | :  | | | | |: |    ||: :|   | |  || :|:: | :   :||||
Db        148 LENLESLYLGSNHISSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--AINLSL 204

Qy        208 DLSLNPIDSIQAQAFQGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERN 267
              : : | :  |:  ||       |   ||  :  | :   :          | || |::  :
Db        205 NFNGNNVKGIELGAFDSTVFQSL----NFGGTPNLSVIFNGLQNSTTQSLWLGTFEDIDD 260

Qy        268 LESFDRSVMEGLCNVSIDEFRLTYINHFSD-DIYNLNCLANISAMSFTGVHIKHIADVPR 326
              |    ::::||| :|::   |   : |||       |   :  :  |  |:|    :|
Db        261 -EDISSAMLKGLCEMSVESLNLQE-HRFSDISSTTFQCFTQLQELDLTATHLK---GLPS 315

Qy        327 HFKWQSLSIIR------------CHLKP--FPKLSLPFLKSWTLTTNREDISFGQL-ALP 371
                |   |::::            | :    || |:  :::       :  :  | |  |
Db        316 GMK--GLNLLKKLVLSVNHFDQLCQISAANFPSLTHLYIRG---NVKKLHLGVGCLEKLG 370

Qy        372 SLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVI-LMSANFMGLEELEYLDFQHS 430
              :|: |||| | :    |||     ::|: |:|| |  : | |  |    :|| ||   :
Db        371 NLQTLDLSHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKECPQLELLDLAFT 430

Qy        431 TLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTL--SN 488
              |      | | :|  |  |:::|         :  ||  |  | : || |:| |:  :|
Db        431 RLHINAPQSPFQNLHFLQVLNLTYCFLDTSNQHLLAGLPVLRHLNLKGNHFQDGTITKTN 490

Qy        489 VFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLL--FLDP-SHYKQLYSLR 545
              :     :|  | || | |  | :  | :| ::  :::|||:|    :|  || | :|
Db        491 LLQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHNSLTCDSIDSLSHLKGIY--- 547

Qy        546 TLDCSFNRIETSKGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMFLVNVEQMK 605
              |: : | |       |       :  ||::| : | |   :|| | |:    |   |:
Db        548 -LNLAANSINIISPRLLPILSQQSTINLSHNPLDCTCSNIHFLTWYKENLHKLEGSEETT 606

Qy        606 CASPIDMKASLVLDFTNS----TCYIYKTIISVSVVSVLVVATVAFLIYHFYFHL 656
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Db        607 CANPPSLRGVKLSDVKLSCGITAIGIFFLIVFLLLLAILLFFAVKYLLRWKYQHI 661


RESULT 4
US-09-982-308B-23
; Sequence 23, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
;  APPLICANT: Dalie, Barbara
;  APPLICANT:  Fan, Xuedong
;  APPLICANT:  Lundell, Daniel
;  APPLICANT:  Lunn, Charles A.
;  APPLICANT:  Tan, Jimmy C.
;  APPLICANT:  Zavodny, Paul J.
;  TITLE OF INVENTION: Mammalian TNF-alpha Convertases
;  FILE REFERENCE: JB0601QC
;  CURRENT APPLICATION NUMBER: US/09/982,308B
;  CURRENT FILING DATE:  2001-10-17
;  PRIOR APPLICATION NUMBER: 09/156,163
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 08/889,909
;  PRIOR FILING DATE: 1997-07-10
;  PRIOR APPLICATION NUMBER: 60/021,710
;  PRIOR FILING DATE: 1996-07-12
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;   LENGTH: 784
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-982-308B-23

  Query Match             11.6%;  Score 502;  DB 4;  Length 784;
  Best Local Similarity   24.9%;  Pred. No. 6.5e-37;
  Matches  210;  Conservative  136;  Mismatches  324;  Indels  172;  Gaps   32;

Qy         43 NLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQ 102
              :|: ||  :  : |:|||| | :  : :            || ||
Db         42 SLNSIPSGLTEAVKSLDLSNNRITYISN----------SDLQRCV----------N 77

Qy        103 LSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIH 162
              |  |||| | | :    ||| | :||:|     :::|        | ||  ||:  |
Db         78 LQALVLTSNGINTIEEDSFSSLGSLEHLDLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYK 137

Qy        163 SFKLPEYFSNLTNLEHVDL----SYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQ 218
              :      ||:|| |: : :    ::  ||      | || |       |::  : : | :
Db        138 TLGETSLFSHLTKLQILRVGNMDTFTKIQRKDFAGLTFLEE-------LEIDASDLQSYE 190

Qy        219 AQAFQGIR------LH---ELTLRSNFNSSNVLKMCLQ----NMTGLHVHRLILGEFKN- 264
              :: : |:      ||    : |   |         ||:    ::   |   | ||  :
Db        191 PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSVECLELRDTDLDTFHFSELSTGETNSL 250

Qy        265 -----ERNLESFDRSVME---------GLCNVSIDEFRLTYINHF-SDDIYNLNCLANIS 309
                  ||::  | |: :          ||  :  |:  |  : :| : |   :    :
Db        251 IKKFTFRNVKITDESLFQVMKLLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE 310

Qy        310 AMSFTGVHIKHIADVPRHFKWQSLSIIRCHLKPFPKLSLP----FLKSWTLTTNREDISF 365
              ::   :||      || : :  ||  :    :   ::::     ||    |: :
Db        311 TLTIRRLHI------PRFYLFYDLSTLYSLTERVKRITVENSKVFLVPCLLSQH------ 358

Qy        366 GQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSANFMGLEELEYL 425
              | || |||||  | |                  :||  |          :  |: |
Db        359 ----LKSLEYLDLSENLMV-------------EEYLKNS-----ACEDAWPSLQTLILR 395

Qy        426 DFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNT 485
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Db        396 QNHLASLEKTGE--TLLTLKNLTNIDIS----------------------KNSF--HS 427

Qy        486 LSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNL-LF-LDPSHYKQLY- 542
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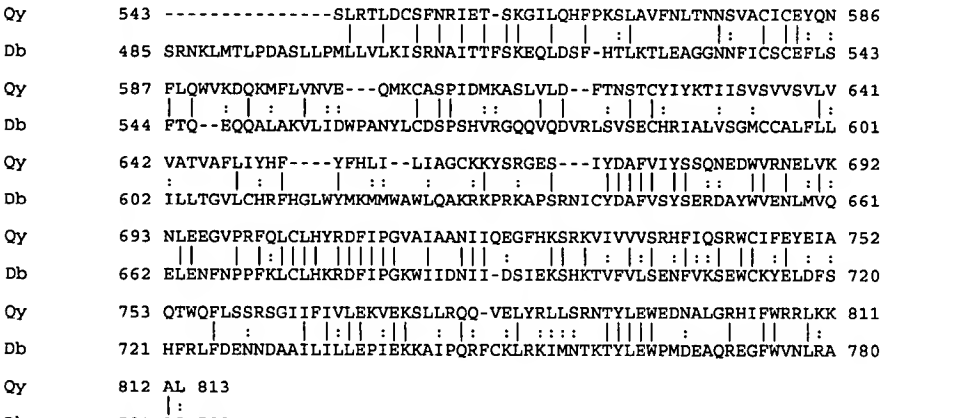
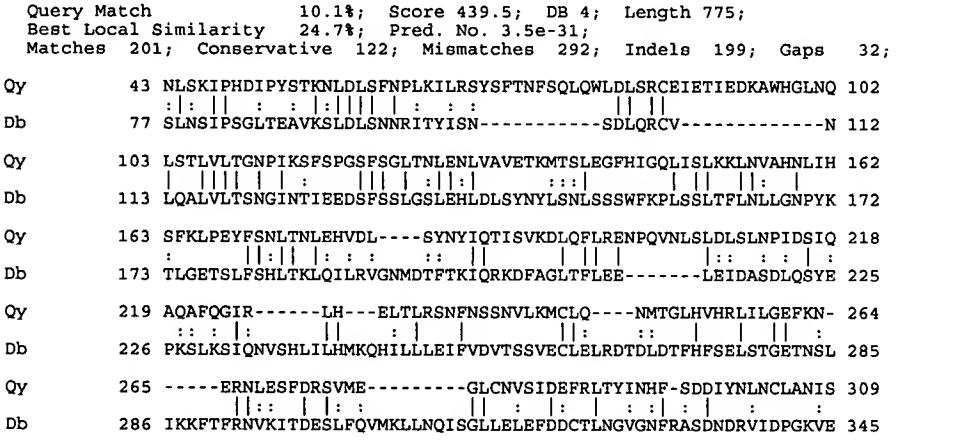
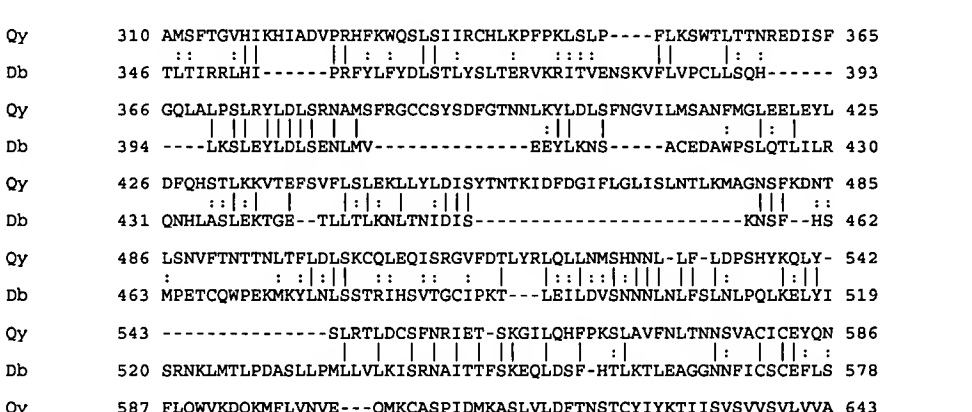


RESULT 5
US-09-949-016-8799
; Sequence 8799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8799

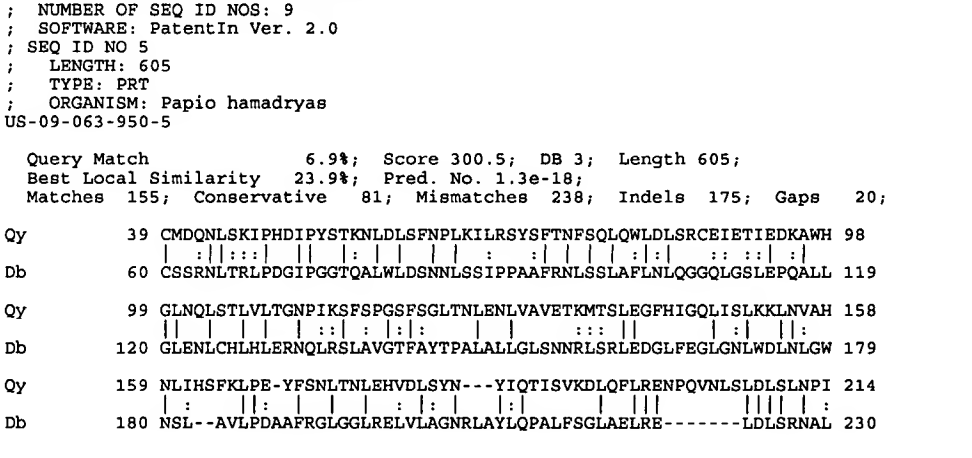
Query Match 10.1%; Score 439.5; DB 4; Length 775;
Best Local Similarity 24.7%; Pred. No. 3.5e-31;
Matches 201; Conservative 122; Mismatches 292; Indels 199; Gaps 32;





RESULT 6
US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-09-063-950-5

Query Match 6.9%; Score 300.5; DB 3; Length 605;
Best Local Similarity 23.9%; Pred. No. 1.3e-18;
Matches 155; Conservative 81; Mismatches 238; Indels 175; Gaps 20;



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Qy        215 DSIQAQAFQGI-RLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLESFDR 273
Db        231 RAIKANVFAQLPRLQKLYL------------------------------DRNL----- 253

Qy        274 SVMEGLCNVSIDEFRLTYINHFSDDIYNLNCLANISAMSFTGVHIKHIADVPRHFKWQSL 333
Db        254 -------------------------------IAAVAPGAFLGL---------KALRWLDL 273

Qy        334 SIIRCHLKPFPKLSLPFLKSWTLTTNR-----EDISFGQLALPSLRYLDLSRNAMSFRGC 388
Db        274 S----------------------HNRVAGLLEDTFPGLL---GLRVLRLSHNAIASLRP 307

Qy        389 CSYSDFGTNNLKYLDLSFNGV-ILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKL 447
Db        308 RTFEDL--HFLEELQLGHNRIRQLAERSFEGLGQLEVLTLDHNQLQEV-KVGAFLGLTNV 364

Qy        448 LYLDISYTNTKIDFDGIFLGLISLNTLKMAGNS------------------FKDNTLSN 488
Db        365 AVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFAGLSGLRRLFLKDNGLVG 424

Qy        489 V----FTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSL 544
Db        425 IEEQSLWGLAELLELDLTSNQLTHLPHQLFQGLGKLEYLLLSHNRLAELPADALGPLQRA 484

Qy        545 RTLDCSFNRIETSKGILQHFPKSLAVFNLTNNSVACICEYQNFLQ--WVKDQKMFLVNVE 602
Db        485 FWLDVSHNRLEALPGSLLASLGRLRYLNLRNNSLRTFTPQPPGLERLWLEG--------N 536

Qy        603 QMKCASPID-------MKASLVLDFTNSTC---------YIYKTIISVS 635
Db        537 PWDCSCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPVYTYNNITCAS 585
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RESULT 7
US-08-190-802A-50
; Sequence 50, Application US/08190802A
; Patent No. 5519003
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  P.O. Box 60850
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306-0850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/190,802A
;      FILING DATE:  01-FEB-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  8600-0139
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  603 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor bind.
;      INDIVIDUAL ISOLATE:  pro. complex-rat, Fig. 33
US-08-190-802A-50

  Query Match             6.7%;  Score 290.5;  DB 1;  Length 603;
  Best Local Similarity   22.4%;  Pred. No. 1.1e-17;
  Matches  152;  Conservative   99;  Mismatches  204;  Indels  223;  Gaps   26;

Qy         39 CMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWH 98
Db         60 CSSKNLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALL 119

Qy         99 GLNQLSTLVLTGNPIKSFSPGSFS---------------------------------- 122
Db        120 GLQNLYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGW 179

Qy        123 -----------GLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYF 170
Db        180 NSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSVK-ANVF 238

Qy        171 SNLTNLEHVDLSYNYIQTIS------VKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQG 224
Db        239 VHLPRLQKLYLDRNLITAVAPGAFLGMKALRW----------LDLSHNRVAGLMEDTFPG 288

Qy        225 -IRLHELTLRSNFNSSNVLKMCLQNMTGLH-VHRLILGEFK----NERNLESFDRSVMEG 278
Db        289 LLGLHVLRLAHN----AIASLRPRTFKDLHFLEELQLGHNRIRQLGERTFEGLGQLEVLT 344

Qy        279 LCNVSIDEFRL-TYINHFSDDIYNL--NCLANISAMSFTGVHIKHIADVPRHFKWQSLSI 335
Db        345 LNDNQITEVRVGAFSGLFNVAVMNLSGNCLRSLPERVFQGLDKLH----SLHLEHSCLGH 400

Qy        336 IRCHLKPFPKLS---LPFLKSWTLTTNREDISFGQLALPSLRYLDLSRNAMS------FR 386
Db        401 VRLH--TFAGLSGLRRLFLRDNSISSIEEQSLAG---LSELLELDLTTNRLTHLPRQLFQ 455

Qy        387 GCCSYSDFGTNNLKYLDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEK 446
Db        456 --------GLGHLEYLLLSYNQLTTLSAEVLG----------------------PLQR 483

Qy        447 LLYLDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQL 506
Db        484 AFWLDISHNH-----------------------------------------------L 494

Qy        507 EQISRGVFDTLYRLQLLNMSHNNL----------LFLDPSHYKQLYSLRTLDCSFNRIE 555
Db        495 ETLAEGLFSSLGRVRYLSLRNNSLQTFSPQPGLERLWLDANPW---------DCS----- 540

Qy        556 TSKGILQHFP-KSLAVFNLTNNSVACICEYQNFLQWVKD----QKMFLVNVEQMKCASPI 610
Db        541 --------CPLKALRDFALQNPGVV-----PRFVQTVCEGDDCQPVYTYN--NITCAGPA 585

Qy        611 DMKASLVLDFTNSTCYIY 628
Db        586 NV-SGLDLRDVSETHFVH 602
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RESULT 8
US-08-477-346-50
; Sequence 50, Application US/08477346
; Patent No. 6262023
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
```

```
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,346
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/487,072
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  603 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor bind.
;      INDIVIDUAL ISOLATE:  pro. complex-rat, Fig. 33
US-08-477-346-50

  Query Match             6.7%;  Score 290.5;  DB 3;  Length 603;
  Best Local Similarity   22.4%;  Pred. No. 1.1e-17;
  Matches  152;  Conservative   99;  Mismatches  204;  Indels  223;  Gaps   26;

Qy         39 CMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWH 98
              |  :||: :| ||| ||: | |  | |  : | :| | | | :|:|    : ::| :|
Db         60 CSSKNLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALL 119

Qy         99 GLNQLSTLVLTGNPIKSFSPGSFS---------------------------------- 122
              ||  |  | |  | ::: : | |:
Db        120 GLQNLYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGW 179

Qy        123 ------------GLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYF 170
                         || ||  ||    |:| |:       |  |::|::: | : | |    |
Db        180 NSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSVK-ANVF 238

Qy        171 SNLTNLEHVDLSYNYIQTIS------VKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQG 224
               :|  |: : |  | |  ::      :| |::          |||| | :  :    | |
Db        239 VHLPRLQKLYLDRNLITAVAPGAFLGMKALRW----------LDLSHNRVAGLMEDTFPG 288

Qy        225 -IRLHELTLRSNFNSSNVLKMCLQNMTGLH-VHRLILGEFK----NERNLESFDRSVMEG 278
               : || | |  |     :  :  :    || :  | ||  :      ||  |   :  :
Db        289 LLGLHVLRLAHN----AIASLRPRTFKDLHFLEELQLGHNRIRQLGERTFEGLGQLEVLT 344

Qy        279 LCNVSIDEFRL-TYINHFSDDIYNL--NCLANISAMSFTGVHIKHIADVPRHFKWQSLSI 335
              | :  | | |:  :   |:  : ||  ||| ::    | |:   |       | :   |
Db        345 LNDNQITEVRVGAFSGLFNVAVMNLSGNCLRSLPERVFQGLDKLH----SLHLEHSCLGH 400

Qy        336 IRCHLKPFPKLS---LPFLKSWTLTTNREDISFGQLALPSLRYLDLSRNAMS------FR 386
              :| |   |  ||     ||:  :::: |   |   |  | |||: | ::     |:
Db        401 VRLH--TFAGLSGLRRLFLRDNSISSIEEQSLAG---LSELLELDLTTNRLTHLPRQLFQ 455

Qy        387 GCCSYSDFGTNNLKYLDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEK 446
                  |  :|:|| ||:|  :  :||  :|                          |::
Db        456 --------GLGHLEYLLLSYNQLTTLSAEVLG----------------------PLQR 483

Qy        447 LLYLDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQL 506
                :||||: :                                              |

Db        484 AFWLDISHNH----------------------------------------------L 494

Qy        507 EQISRGVFDTLYRLQLLNMSHNNL----------LFLDPSHYKQLYSLRTLDCSFNRIE 555
              | :: |:| :| |:: |:: :|:|           |:|| : :          |||
Db        495 ETLAEGLFSSLGRVRYLSLRNNSLQTFSPQPGLERLWLDANPW---------DCS----- 540

Qy        556 TSKGILQHFP-KSLAVFNLTNNSVACICEYQNFLQWVKD----QKMFLVNVEQMKCASPI 610
                      | |:|  | | |  |         |:| | :    | ::  |   : || |
Db        541 --------CPLKALRDFALQNPGVV-----PRFVQTVCEGDDCQPVYTYN--NITCAGPA 585

Qy        611 DMKASLVLDFTNSTCYIY 628
              :: : | |   : | :::
Db        586 NV-SGLDLRDVSETHFVH 602


RESULT 9
US-08-473-089-50
; Sequence 50, Application US/08473089
; Patent No. 6342368
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/473,089
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  603 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor bind.
;      INDIVIDUAL ISOLATE:  pro. complex-rat, Fig. 33
US-08-473-089-50

  Query Match             6.7%;  Score 290.5;  DB 3;  Length 603;
  Best Local Similarity   22.4%;  Pred. No. 1.1e-17;
  Matches  152;  Conservative   99;  Mismatches  204;  Indels  223;  Gaps   26;

Qy         39 CMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWH 98
              |  :||: :| ||| ||: | |  | |  : | :| | | | :|:|    : ::| :|
Db         60 CSSKNLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALL 119

Qy         99 GLNQLSTLVLTGNPIKSFSPGSFS---------------------------------- 122
              ||  |  | |  | ::: : | |:
Db        120 GLQNLYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGW 179
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Qy        123 ------------GLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYF 170
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Db        180 NSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSVK-ANVF 238

Qy        171 SNLTNLEHVDLSYNYIQTIS------VKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQG 224
               :|  |: : |  | |  ::      :| |::           ||| | :  :    | |
Db        239 VHLPRLQKLYLDRNLITAVAPGAFLGMKALRW----------LDLSHNRVAGLMEDTFPG 288

Qy        225 -IRLHELTLRSNFNSSNVLKMCLQNMTGLH-VHRLILGEFK----NERNLESFDRSVMEG 278
              : || | |  |      :  :   || :  | ||  :      ||  |   :  :
Db        289 LLGLHVLRLAHN----AIASLRPRTFKDLHFLEELQLGHNRIRQLGERTFEGLGQLEVLT 344

Qy        279 LCNVSIDEFRL-TYINHFSDDIYNL--NCLANISAMSFTGVHIKHIADVPRHFKWQSLSI 335
              | :  | | |:  :   |:  : ||  ||| ::    | |:   |      | :   |
Db        345 LNDNQITEVRVGAFSGLFNVAVMNLSGNCLRSLPERVFQGLDKLH----SLHLEHSCLGH 400

Qy        336 IRCHLKPFPKLS---LPFLKSWTLTTNREDISFGQLALPSLRYLDLSRNAMS------FR 386
              :| |   |  ||     ||:  ::::  |    |   | |  |||: | ::      |:
Db        401 VRLH--TFAGLSGLRRLFLRDNSISSIEEQSLAG---LSELLELDLTTNRLTHLPRQLFQ 455

Qy        387 GCCSYSDFGTNNLKYLDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEK 446
                    |  :|:|| ||:|  :  :||  :|                          |::
Db        456 --------GLGHLEYLLLSYNQLTTLSAEVLG----------------------PLQR 483

Qy        447 LLYLDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQL 506
              :||||: :                                                 |
Db        484 AFWLDISHNH-----------------------------------------------L 494

Qy        507 EQISRGVFDTLYRLQLLNMSHNNL-----------LFLDPSHYKQLYSLRTLDCSFNRIE 555
              | :: |:| :| |:: |:: :|:|           |:|| : :         |||
Db        495 ETLAEGLFSSLGRVRYLSLRNNSLQTFSPQPGLERLWLDANPW---------DCS----- 540

Qy        556 TSKGILQHFP-KSLAVFNLTNNSVACICEYQNFLQWVKD----QKMFLVNVEQMKCASPI 610
                    | |:|  | | |  |        |:| | :    | ::  |   : || |
Db        541 --------CPLKALRDFALQNPGVV-----PRFVQTVCEGDDCQPVYTYN--NITCAGPA 585

Qy        611 DMKASLVLDFTNSTCYIY 628
              :: : | |    : | :::
Db        586 NV-SGLDLRDVSETHFVH 602


RESULT 10
US-08-487-072A-50
; Sequence 50, Application US/08487072A
; Patent No. 6423684
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,072A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  603 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor bind.
;      INDIVIDUAL ISOLATE:  pro. complex-rat, Fig. 33
US-08-487-072A-50

  Query Match             6.7%;  Score 290.5;  DB 4;  Length 603;
  Best Local Similarity   22.4%;  Pred. No. 1.1e-17;
  Matches  152;  Conservative   99;  Mismatches  204;  Indels  223;  Gaps   26;

Qy         39 CMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWH 98
              |  :||: :| ||| ||: | |  | |  : | :| | | | :|:|    : ::| :|
Db         60 CSSKNLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALL 119

Qy         99 GLNQLSTLVLTGNPIKSFSPGSFS---------------------------------- 122
              ||  |  | |  | ::: : | |:
Db        120 GLQNLYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGW 179

Qy        123 ------------GLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYF 170
                          || ||  ||    |:| |:      |  |::|::: | : | |    |
Db        180 NSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSVK-ANVF 238

Qy        171 SNLTNLEHVDLSYNYIQTIS------VKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQG 224
               :|  |: : |  | |  ::      :| |::           ||| | :  :    | |
Db        239 VHLPRLQKLYLDRNLITAVAPGAFLGMKALRW----------LDLSHNRVAGLMEDTFPG 288

Qy        225 -IRLHELTLRSNFNSSNVLKMCLQNMTGLH-VHRLILGEFK----NERNLESFDRSVMEG 278
              : || | |  |      :  :   || :  | ||  :      ||  |   :  :
Db        289 LLGLHVLRLAHN----AIASLRPRTFKDLHFLEELQLGHNRIRQLGERTFEGLGQLEVLT 344

Qy        279 LCNVSIDEFRL-TYINHFSDDIYNL--NCLANISAMSFTGVHIKHIADVPRHFKWQSLSI 335
              | :  | | |:  :   |:  : ||  ||| ::    | |:   |      | :   |
Db        345 LNDNQITEVRVGAFSGLFNVAVMNLSGNCLRSLPERVFQGLDKLH----SLHLEHSCLGH 400

Qy        336 IRCHLKPFPKLS---LPFLKSWTLTTNREDISFGQLALPSLRYLDLSRNAMS------FR 386
              :| |   |  ||     ||:  ::::  |    |   | |  |||: | ::      |:
Db        401 VRLH--TFAGLSGLRRLFLRDNSISSIEEQSLAG---LSELLELDLTTNRLTHLPRQLFQ 455

Qy        387 GCCSYSDFGTNNLKYLDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEK 446
                    |  :|:|| ||:|  :  :||  :|                          |::
Db        456 --------GLGHLEYLLLSYNQLTTLSAEVLG----------------------PLQR 483

Qy        447 LLYLDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQL 506
              :||||: :                                                 |
Db        484 AFWLDISHNH-----------------------------------------------L 494

Qy        507 EQISRGVFDTLYRLQLLNMSHNNL-----------LFLDPSHYKQLYSLRTLDCSFNRIE 555
              | :: |:| :| |:: |:: :|:|           |:|| : :         |||
Db        495 ETLAEGLFSSLGRVRYLSLRNNSLQTFSPQPGLERLWLDANPW---------DCS----- 540

Qy        556 TSKGILQHFP-KSLAVFNLTNNSVACICEYQNFLQWVKD----QKMFLVNVEQMKCASPI 610
                    | |:|  | | |  |        |:| | :    | ::  |   : || |
Db        541 --------CPLKALRDFALQNPGVV-----PRFVQTVCEGDDCQPVYTYN--NITCAGPA 585

Qy        611 DMKASLVLDFTNSTCYIY 628
              :: : | |    : | :::
Db        586 NV-SGLDLRDVSETHFVH 602


RESULT 11
US-09-353-585-2
; Sequence 2, Application US/09353585
; Patent No. 6287865
;  GENERAL INFORMATION:
;       APPLICANT: Dixon, Mark S
```

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;                  Jones, David A
;                  Jones, Jonathan DG
;       TITLE OF INVENTION: Plant pathogen resistance genes and uses
;                           thereof
;       NUMBER OF SEQUENCES: 15
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Nixon & Vanderhye PC
;            STREET: 8th Floor, 1100 No. 6287865th Glebe Road
;            CITY: Arlington
;            STATE: Virginia
;            COUNTRY: United States of America
;            ZIP: 22201-4714
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/353,585
;            FILING DATE: 15-Jul-1999
;            CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
;                            1/68
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/930,277
;            FILING DATE: 27-OCT-1997
;            APPLICATION NUMBER: PCT/GB96/00785
;            FILING DATE: 01-APR-1996
;            APPLICATION NUMBER: GB 9506658.5
;            FILING DATE: 31-MAR-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ms Mary J Wilson
;            REGISTRATION NUMBER: 32,955
;            REFERENCE/DOCKET NUMBER: 620-69
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (703) 816-4000
;            TELEFAX: (703) 816-4100
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1112 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       HYPOTHETICAL: YES
;       ORIGINAL SOURCE:
;            ORGANISM: Tomato
;            STRAIN: Cf2
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-353-585-2

  Query Match             6.7%;  Score 288.5;  DB 3;  Length 1112;
  Best Local Similarity   23.5%;  Pred. No. 4.4e-17;
  Matches  158;  Conservative   93;  Mismatches  243;  Indels  179;  Gaps   26;

Qy         23 GSLNPCIEVLPNIT--YQCMDQNLSKIPHDIPY--STKNLDLSFNPLKILRSYSFTNFSQ 78
              ||:   :  | |::  |   :|    || :| |  |   |||| | :      || | |
Db        397 GSIPASLGNLNNLSRLYLYNNQLSGSIPEEIGYLSSLTYLDLSNNSINGFIPASFGNMSN 456

Qy         79 LQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMT 138
              | :| |   :: :   :    |  |: | |: | :    | ||  | ||  |  |  :::
Db        457 LAFLFLYENQLASSVPEEIGYLRSLNVLDLSENALNGSIPASFGNLNNLSRLNLVNNQLS 516

Qy        139 SLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLR 198
                 || | ||  |::: | ::   :|  | || ||  ::|  | :     ::: :||
Db        517 GSIPEEIGYLRSLNVLDLSENALNG-SIPASFGNLNNLSRLNLVNNQLSGSIPEEIGYLR 575

Qy        199 ENPQVNLS-----------------------------------------------LDLSLNPI 214
                 : ||                                               | |  | :
Db        576 SLNDLGLSENALNGSIPASLGNLNNLSMLYLYNNQLSGSIPEEIGYLSSLTYLSLGNNSL 635

Qy        215 DSIQAQAFQGIR-LHELTLRS------------NFNSSNVLKM-----------CLQNMT 250
                 : :   :|  :| |  | |              |  |  || |           || |::
Db        636 NGLIPASFANMRNLQALILNDNNLIGEIPSSVCNLTSLEVLYMPRNNLKGKVPQCLGNIS 695

Qy        251 GLHVHRLILGEFKNE-----RNLES-----FDRSVMEGL---C--NVSIDEFRLTYINHF 295
                | | |  :    |  |       || |     | |: :||    |  |:|  |       |
Db        696 NLQVLSMSSNSFSGELPSSISNLTSLQILDFGRNNLEGAIPQCFGNISSLEVFDMQNNKL 755

Qy        296 SDDI---YNLNCLANISAMSFTGVHIKHIADVPRHF----KWQSLSIIRCHLK-PFPKL- 346
                |  :   ::: |  :: :::  |  ::   ::||       | | | :    |   ||
Db        756 SGTLPTNFSIGC--SLISLNLHGNELED--EIPRSLDNCKKLQVLDLGDNQLNDTFPMWL 811

Qy        347 -SLPFLKSWTLTTNRED----ISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKY 401
                :|| |:   ||:|:       |  ::  | || :|||||  |        |  |:  ::
Db        812 GTLPELRVLRLTSNKLHGPIRSSRAEIMFPDLRIIDLSRNAFS-------QDLPTSLFEH 864

Qy        402 LDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDF 461
                |     |:  :      :||  |  :   ::  ||:
Db        865 L----KGMRTVDKT---MEEPSYESYYDDSVVVVTK---------------------- 893

Qy        462 DGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQ 521
                |: | :: : :|                        | :|||  : |      |   |  ::
Db        894 -GLELEIVRILSL--------------------YTVIDLSSNKFEGHIPSVLGDLIAIR 931

Qy        522 LLNMSHNNLLFLDPSHYKQLYSLRTLDCSFNRIETSKGILQHFPKSLA------VFNLTN 575
                :||:||| |    ||    |  | :|| |||::          |: ||      ||::
Db        932 ILNVSHNALQGYIPSSLGSLSILESLDLSFNQLS------GEIPQQLASLTFLEFLNLSH 985

Qy        576 NSV-ACICEYQNF 587
                | :  || :   |
Db        986 NYLQGCIPQGPQF 998


RESULT 12
US-09-353-585-3
; Sequence 3, Application US/09353585
; Patent No. 6287865
;  GENERAL INFORMATION:
;       APPLICANT: Dixon, Mark S
;                  Jones, David A
;                  Jones, Jonathan DG
;       TITLE OF INVENTION: Plant pathogen resistance genes and uses
;                           thereof
;       NUMBER OF SEQUENCES: 15
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Nixon & Vanderhye PC
;            STREET: 8th Floor, 1100 No. 6287865th Glebe Road
;            CITY: Arlington
;            STATE: Virginia
;            COUNTRY: United States of America
;            ZIP: 22201-4714
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/353,585
;            FILING DATE: 15-Jul-1999
;            CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
;                            1/68
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/930,277
;            FILING DATE: 27-OCT-1997
;            APPLICATION NUMBER: PCT/GB96/00785
;            FILING DATE: 01-APR-1996
;            APPLICATION NUMBER: GB 9506658.5
;            FILING DATE: 31-MAR-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ms Mary J Wilson
;            REGISTRATION NUMBER: 32,955
;            REFERENCE/DOCKET NUMBER: 620-69
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (703) 816-4000
;            TELEFAX: (703) 816-4100
;   INFORMATION FOR SEQ ID NO: 3:
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;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 1112 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         HYPOTHETICAL: YES
;         ORIGINAL SOURCE:
;              ORGANISM: Tomato
;              STRAIN: Cf2
;         SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-353-585-3

  Query Match             6.7%;  Score 288.5;  DB 3;  Length 1112;
  Best Local Similarity   22.0%;  Pred. No. 4.4e-17;
  Matches  173;  Conservative  116;  Mismatches  282;  Indels  217;  Gaps   31;

Qy         23 GSLNPCIEVLPNIT--YQCMDQNLSKIPHDIPY--STKNLDLSFNPLKILRSYSFTNFSQ 78
Db        397 GSIPASLGNLNNLSRLYLYNNQLSGSIPEEIGYLSSLTYLDLSNNSINGFIPASFGNMSN 456

Qy         79 LQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMT 138
Db        457 LAFLFLYENQLASSVPEEIGYLRSLNVLDLSENALNGSIPASFGNLNNLSRLNLVNNQLS 516

Qy        139 SLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLR 198
Db        517 GSIPEEIGYLRSLNVLDLSENALNG-SIPASFGNLNNLSRLNLVNNQLSGSIPEEIGYLR 575

Qy        199 ENPQVNLS----------------------------------------------LDLSLNPI 214
Db        576 SLNDLGLSENALNGSIPASLGNLNNLSMLYLYNNQLSGSIPEEIGYLSSLTYLSLGNNSL 635

Qy        215 DSIQAQAFQGIR-LHELTLRS------------NFNSSNVLKM-----------CLQNMT 250
Db        636 NGLIPASFGNMRNLQALILNDNNLIGEIPSSVCNLTSLEVLYMPRNNLKGKVPQCLGNIS 695

Qy        251 GLHVHRLILGEFKNE-----RNLES-----FDRSVMEGL---C--NVSIDEFRLTYINHF 295
Db        696 NLQVLSMSSNSFSGELPSSISNLTSLQILDFGRNNLEGAIPQCFGNISSLEVFDMQNNKL 755

Qy        296 SDDI---YNLNCLANISAMSFTGVHIKHIADVPRHF----KWQSLSIIRCHLK-PFPKL- 346
Db        756 SGTLPTNFSIGC--SLISLNLHGNELED--EIPRSLDNCKKLQVLDLGDNQLNDTFPMWL 811

Qy        347 -SLPFLKSWTLTTNRED----ISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKY 401
Db        812 GTLPELRVLRLTSNKLHGPIRSSRAEIMFPDLRIIDLSRNAFS-------QDLPTSLFEH 864

Qy        402 LDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDF 461
Db        865 L----KGMRTVDKT---MEEPSYESYYDDSVVVVTK------------------------ 893

Qy        462 DGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQ 521
Db        894 -GLELEIVRILSL--------------------YTVIDLSSNKFEGHIPSVLGDLIAIR 931

Qy        522 LLNMSHNNLLFLDPSHYKQLYSLRTLDCSFNRIETSKGILQHFPKSLA------VFNLTN 575
Db        932 ILNVSHNALQGYIPSSLGSLSILESLDLSFNQLS------GEIPQQLASLTFLEFLNLSH 985

Qy        576 NSV-ACICEYQNFLQW----------------------VKDQKMFLVNVEQMKCASPI 610
Db        986 NYLQGCIPQGPQFRTFESNSYEGNDGLRGYPVSKGCGKDPVSEKNYTVSALEDQESNSEF 1045

Qy        611 --DMKASLVLDFTNSTCYIYKTIISVSVVSVLV----VATVAFLIYHFYFHLILIAGCKK 664
Db       1046 FNDFWKAALMGYGSGLC------IGISIIYILISTGNLRWLARIIEELEHKIIMQR--RK 1097

Qy        665 YSRGESIY 672
Db       1098 KQRGQRNY 1105
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RESULT 13
US-08-190-802A-49
; Sequence 49, Application US/08190802A
; Patent No. 5519003
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  P.O. Box 60850
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306-0850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/190,802A
;      FILING DATE:  01-FEB-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  8600-0139
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-190-802A-49

  Query Match             6.5%;  Score 281.5;  DB 1;  Length 605;
  Best Local Similarity   23.5%;  Pred. No. 7.4e-17;
  Matches  154;  Conservative   83;  Mismatches  242;  Indels  175;  Gaps   20;

Qy         39 CMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWH 98
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy         99 GLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAH 158
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        159 NLIHSFKLPE-YFSNLTNLEHVDLSYN---YIQTISVKDLQFLRENPQVNLSLDLSLNPI 214
Db        180 NSL--AVLPDAAFRGLGSLRELVLAGNRLAYLQPALFSGLAELRE-------LDLSRNAL 230

Qy        215 DSIQAQAF-QGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLESFDR 273
Db        231 RAIKANVFVQLPRLQKLYL-------------------------------DRNL----- 253

Qy        274 SVMEGLCNVSIDEFRLTYINHFSDDIYNLNCLANISAMSFTGVHIKHIADVPRHFKWQSL 333
Db        254 ------------------------------IAAVAPGAFLGL---------KALRWLDL 273

Qy        334 SIIRCHLKPFPKLSLPFLKSWTLTTNR-----EDISFGQLALPSLRYLDLSRNAMSFRGC 388
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Db        274 S----------------------HNRVAGLLEDTFPGLL---GLRVLRLSHNAIASLRP 307

Qy        389 CSYSDFGTNNLKYLDLSFNGV-ILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKL 447
              :: |   : |: | |  | :  |   :| || :|| |    |: |::| :   || |  :
Db        308 RTFKDL--HFLEELQLGHNRIRQLAERSFEGLGQLEVLTLDHNQLQEV-KAGAFLGLTNV 364

Qy        448 LYLDISYTNTKIDFDGIFLGLISLNTLKMAGNS------------------FKDNTLSN 488
              :::|    :   : :| ||  |::| : |:                    ||| |
Db        365 AVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVG 424

Qy        489 V----FTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSL 544
              :          |  |||:  ||  :   :|  | :|: | :| | |  |        |
Db        425 IEEQSLWGLAELLELDLTSNQLTHLPHRLFQGLGKLEYLLLSRNRLAELPADALGPLQRA 484

Qy        545 RTLDCSFNRIETSKGILQHFPKSLAVFNLTNNSVACICEYQNFLQ--WVKDQKMFLVNVE 602
              || | ||:|     |       |   :| |||:          |:  |::
Db        485 FWLDVSHNRLEALPNSLLAPLGRLRYLSLRNNSLRTFTPQPPGLERLWLEG--------N 536

Qy        603 QMKCASPID-------MKASLVLDFTNSTC---------YIYKTIISVSVVSVL 640
                  |  |:          | |  |  : |         | |  |   |   |:
Db        537 PWDCGCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPAYTYNNITCASPPEVV 590


RESULT 14
US-08-477-346-49
; Sequence 49, Application US/08477346
; Patent No. 6262023
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,346
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/487,072
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-477-346-49

  Query Match             6.5%;  Score 281.5;  DB 3;  Length 605;
  Best Local Similarity   23.5%;  Pred. No. 7.4e-17;
  Matches  154;  Conservative   83;  Mismatches  242;  Indels  175;  Gaps   20;

Qy         39 CMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWH 98
              |  :||:::|  :|  |:  | |  | |  :   :| | | | :|:|   :: ::| :|
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy         99 GLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAH 158
              ||  |  | |  | ::| : |:|:    | :|     ::: ||      | ||  ||:
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        159 NLIHSFKLPE-YFSNLTNLEHVDLSYN---YIQTISVKDLQFLRENPQVNLSLDLSLNPI 214
              | :    ||:  |  | :|  : |: |    |:|      |  |||       |||| | :
Db        180 NSL--AVLPDAAFRGLGSLRELVLAGNRLAYLQPALFSGLAELRE-------LDLSRNAL 230

Qy        215 DSIQAQAF-QGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLESFDR 273
              :|:|  | |  || :| |                                  :|||
Db        231 RAIKANVFVQLPRLQKLYL--------------------------------DRNL----- 253

Qy        274 SVMEGLCNVSIDEFRLTYINHFSDDIYNLNCLANISAMSFTGVHIKHIADVPRHFKWQSL 333
                                          :| ::  :| |:          :  :|  |
Db        254 ------------------------------IAAVAPGAFLGL---------KALRWLDL 273

Qy        334 SIIRCHLKPFPKLSLPFLKSWTLTTNR-----EDISFGQLALPSLRYLDLSRNAMSFRGC 388
                                          ||      ||   | |    || | || ||::
Db        274 S----------------------HNRVAGLLEDTFPGLL---GLRVLRLSHNAIASLRP 307

Qy        389 CSYSDFGTNNLKYLDLSFNGV-ILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKL 447
              :: |   : |: | |  | :  |   :| || :|| |    |: |::| :   || |  :
Db        308 RTFKDL--HFLEELQLGHNRIRQLAERSFEGLGQLEVLTLDHNQLQEV-KAGAFLGLTNV 364

Qy        448 LYLDISYTNTKIDFDGIFLGLISLNTLKMAGNS------------------FKDNTLSN 488
              :::|    :   : :| ||  |::| : |:                    ||| |
Db        365 AVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVG 424

Qy        489 V----FTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSL 544
              :          |  |||:  ||  :   :|  | :|: | :| | |  |        |
Db        425 IEEQSLWGLAELLELDLTSNQLTHLPHRLFQGLGKLEYLLLSRNRLAELPADALGPLQRA 484

Qy        545 RTLDCSFNRIETSKGILQHFPKSLAVFNLTNNSVACICEYQNFLQ--WVKDQKMFLVNVE 602
              || | ||:|     |       |   :| |||:          |:  |::
Db        485 FWLDVSHNRLEALPNSLLAPLGRLRYLSLRNNSLRTFTPQPPGLERLWLEG--------N 536

Qy        603 QMKCASPID-------MKASLVLDFTNSTC---------YIYKTIISVSVVSVL 640
                  |  |:          | |  |  : |         | |  |   |   |:
Db        537 PWDCGCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPAYTYNNITCASPPEVV 590


RESULT 15
US-08-473-089-49
; Sequence 49, Application US/08473089
; Patent No. 6342368
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/473,089
;      FILING DATE:  07-JUN-1995
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;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-473-089-49

  Query Match             6.5%;  Score 281.5;  DB 3;  Length 605;
  Best Local Similarity   23.5%;  Pred. No. 7.4e-17;
  Matches  154;  Conservative   83;  Mismatches  242;  Indels  175;  Gaps   20;

Qy         39 CMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWH 98
              |  :||:::|  :|  |: | |  | |  :   :| | | | :|:|   :: ::| :|
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy         99 GLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAH 158
              ||  |  | |  | ::| : |:|:    | :|     ::: ||       | ||  ||:
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        159 NLIHSFKLPE-YFSNLTNLEHVDLSYN---YIQTISVKDLQFLRENPQVNLSLDLSLNPI 214
              | :    ||:  |  | :|  : |: |   |:|      |  |||       |||| | :
Db        180 NSL--AVLPDAAFRGLGSLRELVLAGNRLAYLQPALFSGLAELRE-------LDLSRNAL 230

Qy        215 DSIQAQAF-QGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLESFDR 273
               :|:|  | |  || :| |                                  :|||
Db        231 RAIKANVFVQLPRLQKLYL--------------------------------DRNL----- 253

Qy        274 SVMEGLCNVSIDEFRLTYINHFSDDIYNLNCLANISAMSFTGVHIKHIADVPRHFKWQSL 333
                                        :| ::  :| |:         :  :|  |
Db        254 ------------------------------IAAVAPGAFLGL---------KALRWLDL 273

Qy        334 SIIRCHLKPFPKLSLPFLKSWTLTTNR-----EDISFGQLALPSLRYLDLSRNAMSFRGC 388
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Db        274 S----------------------HNRVAGLLEDTFPGLL---GLRVLRLSHNAIASLRP 307

Qy        389 CSYSDFGTNNLKYLDLSFNGV-ILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKL 447
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Db        308 RTFKDL--HFLEELQLGHNRIRQLAERSFEGLGQLEVLTLDHNQLQEV-KAGAFLGLTNV 364

Qy        448 LYLDISYTNTKIDFDGIFLGLISLNTLKMAGNS------------------FKDNTLSN 488
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Db        365 AVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVG 424

Qy        489 V----FTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSL 544
              :          |  |||:  ||  :   :|  | :|: | :| | |  |       |
Db        425 IEEQSLWGLAELLELDLTSNQLTHLPHRLFQGLGKLEYLLLSRNRLAELPADALGPLQRA 484

Qy        545 RTLDCSFNRIETSKGILQHFPKSLAVFNLTNNSVACICEYQNFLQ--WVKDQKMFLVNVE 602
               || | ||:|     |       |   :| |||:         |:  |::
Db        485 FWLDVSHNRLEALPNSLLAPLGRLRYLSLRNNSLRTFTPQPPGLERLWLEG--------N 536

Qy        603 QMKCASPID-------MKASLVLDFTNSTC---------YIYKTIISVSVVSVL 640
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Db        537 PWDCGCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPAYTYNNITCASPPEVV 590


Search completed: March 12, 2005, 19:59:02
Job time : 25.9539 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:55:29 ; Search time 73.8956 Seconds
(without alignments)
3727.157 Million cell updates/sec

Title: US-09-396-985B-6
Perfect score: 4335
Sequence: 1 MMPLLHLAGTLIMALFLSCL.....GKALNPDETSEEEQEATTLT 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2844	65.6	837	10	US-09-950-041-26	Sequence 26, Appl
2	2726	62.9	799	10	US-09-950-041-8	Sequence 8, Appli
3	2726	62.9	799	14	US-10-128-166-7	Sequence 7, Appli
4	2726	62.9	799	16	US-10-732-563-8	Sequence 8, Appli
5	2726	62.9	799	16	US-10-732-796A-8	Sequence 8, Appli
6	602.5	13.9	661	13	US-10-114-893-10	Sequence 10, Appl
7	602.5	13.9	661	15	US-10-038-854-134	Sequence 134, App
8	597.5	13.8	661	15	US-10-038-854-135	Sequence 135, App
9	597.5	13.8	661	15	US-10-037-417-107	Sequence 107, App
10	575	13.3	1032	10	US-09-954-987B-192	Sequence 192, App
11	575	13.3	1032	14	US-10-272-502A-31	Sequence 31, Appl
12	575	13.3	1032	15	US-10-407-952-32	Sequence 32, Appl
13	559	12.9	1050	10	US-09-954-987B-175	Sequence 175, App
14	559	12.9	1050	14	US-10-272-502A-22	Sequence 22, Appl
15	559	12.9	1050	15	US-10-407-952-26	Sequence 26, Appl
16	546	12.6	1059	10	US-09-954-987B-187	Sequence 187, App
17	546	12.6	1059	15	US-10-407-952-30	Sequence 30, Appl
18	546	12.6	1059	17	US-10-753-267-30	Sequence 30, Appl
19	541.5	12.5	859	14	US-10-125-692-6	Sequence 6, Appli
20	541	12.5	1041	9	US-09-168-978-3	Sequence 3, Appli
21	541	12.5	1041	9	US-09-978-295A-498	Sequence 498, App
22	541	12.5	1041	9	US-09-978-697-498	Sequence 498, App
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24	541	12.5	1041	9	US-09-999-832A-498	Sequence 498, App
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34	541	12.5	1041	10	US-09-918-585A-498	Sequence 498, App
35	541	12.5	1041	10	US-09-999-834A-498	Sequence 498, App
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37	541	12.5	1041	10	US-09-978-193A-498	Sequence 498, App
38	541	12.5	1041	10	US-09-999-830A-498	Sequence 498, App
39	541	12.5	1041	10	US-09-978-757A-498	Sequence 498, App
40	541	12.5	1041	10	US-09-978-187B-498	Sequence 498, App
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42	541	12.5	1041	10	US-09-978-375A-498	Sequence 498, App
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44	541	12.5	1041	10	US-09-978-188A-498	Sequence 498, App
45	541	12.5	1041	10	US-09-978-681A-498	Sequence 498, App

ALIGNMENTS

RESULT 1
US-09-950-041-26
; Sequence 26, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XK1
; CURRENT APPLICATION NUMBER: US/09/950,041
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-26

Query Match 65.6%; Score 2844; DB 10; Length 837;

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  Matches  558;  Conservative  114;  Mismatches  159;  Indels    8;  Gaps    6;

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Qy         61 SFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGS 120
              |||||: | |||| :| :|| |||||||||:|||| |:  |: ||||:||||||:| : |:
Db         60 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 119

Qy        121 FSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVD 180
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Qy        181 LSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRSNFNSSN 240
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Qy        241 VLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDIY 300
              |:| |:| : || ||||:||||:|| ||| ||:| :|||||::|:|||| |:::: |||
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Qy        301 NL-NCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTTN 359
              :| ||| |:|: |   | |: : |   :| || | :: |    || | |  ||  | |:|
Db        300 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 359

Qy        360 REDISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSANFMGL 419
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Qy        420 EELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAGN 479
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Db        480 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 539

Qy        540 QLYSLRTLDCSFNRIETS-KGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMFL 598
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RESULT 2
US-09-950-041-8
; Sequence 8, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
;  APPLICANT: Hardiman, Gerard T.
;  APPLICANT:  Rock, Fernando L.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  APPLICANT:  Ho, Stephen W.K.
;  APPLICANT:  Liu, Yong-Jun
;  TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
;  FILE REFERENCE: DX0724XK1
;  CURRENT APPLICATION NUMBER: US/09/950,041
;  CURRENT FILING DATE:  2002-05-06
;  PRIOR APPLICATION NUMBER: 09/728,540
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 60/207,558
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 09/073,363
;  PRIOR FILING DATE: 1999-06-05
;  PRIOR APPLICATION NUMBER: 60/044,293
;  PRIOR FILING DATE: 1997-05-07
;  PRIOR APPLICATION NUMBER: 60/072,212
;  PRIOR FILING DATE: 1998-01-22
;  PRIOR APPLICATION NUMBER: 60/076,947
;  PRIOR FILING DATE: 1998-03-05
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-950-041-8

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  Best Local Similarity   66.5%;  Pred. No. 5e-213;
  Matches  532;  Conservative  111;  Mismatches  151;  Indels    6;  Gaps    4;

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Qy        220 QAFQGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGL 279
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Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

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Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        459 IDFDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLY 518
              : |:||| || ||  |||||||::| | ::||   |||||||:|||||:|   |::|
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        519 RLQLLNMSHNNLLFLDPSHYKQLYSLRTLDCSFNRIETS-KGILQHFPKSLAVFNLTNNS 577
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Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        578 VACICEYQNFLQWVKDQKMFLVNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVV 637
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Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVL 599

Qy        638 SVLVVATVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEG 697
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Db        600 SVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEG 659

Qy        698 VPRFQLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQF 757
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Qy        758 LSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNALGRHIFWRRLKKALLDGK 817
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Db        780 SWNPEGTVGTGCNWQEATSI 799


RESULT 3
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US20030077279A1
; GENERAL INFORMATION:
;  APPLICANT: ARDITI, MOSHE
;  APPLICANT:  RAJAVASHISTH, TRIPATHI
;  APPLICANT:  SHAH, PREDIMAN K.
;  TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
;  TITLE OF INVENTION:  TOLL-LIKE RECEPTOR-4
;  FILE REFERENCE: 81476-0255398
;  CURRENT APPLICATION NUMBER: US/10/128,166
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-128-166-7

  Query Match             62.9%;  Score 2726;  DB 14;  Length 799;
  Best Local Similarity   66.5%;  Pred. No. 5e-213;
  Matches  532;  Conservative  111;  Mismatches  151;  Indels    6;  Gaps    4;

Qy         40 MDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWHG 99
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Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy        100 LNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHN 159
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Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        160 LIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQA 219
              || |||||||||||||||:||| | ||:|   ||: | : | :||||||||:: ||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        220 QAFQGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGL 279
              ||: ||||:||||:||:| ||:| |:| : || ||||:||||:|| ||| ||:| :|||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        280 CNVSIDEFRLTYINHFSDDIYNL-NCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRC 338
              ||::|:|||| |:::: ||| :| ||| |:|: |   | |: : |   :| || | :: |
Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        339 HLKPFPKLSLPFLKSWTLTTNREDISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNN 398
                 | |  ||  | |:|:   :| :: |||| :|||||| :||:|||| ||||| :
Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        399 LKYLDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTK 458
              |||||||||||| ||:||:|||:||:|||||| ||:::|||||||  |:|||||:|:|:
Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        459 IDFDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLY 518
              : |:||| || ||  |||||||::| | ::||   |||||||:|||||:|   |::|.
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        519 RLQLLNMSHNNLLFLDPSHYKQLYSLRTLDCSFNRIETS-KGILQHFPKSLAVFNLTNNS 577
               ||:|||||||   ||   || | ||: || | | | || |  |||| ||| | ||| |
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        578 VACICEYQNFLQWVKDQKMFLVNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVV 637
              || ||:|:||||:|||:  || ||:|:||:| | :   ||   | || : |||| |||:

Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVL 599

Qy        638 SVLVVATVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEG 697
              |||||: || |:| |||||:|:||| || |||:||||||||||:|||||||||||||||
Db        600 SVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEG 659

Qy        698 VPRFQLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQF 757
              || |||||||||||||||||||| ||||||||||||:|||||||||||||||||||||||
Db        660 VPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQF 719

Qy        758 LSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNALGRHIFWRRLKKALLDGK 817
              ||||:|||||||:||||:||||||||||||||||||||||: ||||||||||:|||||||
Db        720 LSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGK 779

Qy        818 ALNPD---ETSEEEQEATTL 834
              : ||:    |    ||||::
Db        780 SWNPEGTVGTGCNWQEATSI 799


RESULT 4
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
;  APPLICANT: Gupta, Shalley K.
;  APPLICANT:  Ghosh, Tarun K.
;  APPLICANT:  Fink, Jason R.
;  TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
;  FILE REFERENCE: 58183WO003
;  CURRENT APPLICATION NUMBER: US/10/732,563
;  CURRENT FILING DATE:  2003-12-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-732-563-8

  Query Match             62.9%;  Score 2726;  DB 16;  Length 799;
  Best Local Similarity   66.5%;  Pred. No. 5e-213;
  Matches  532;  Conservative  111;  Mismatches  151;  Indels    6;  Gaps    4;

Qy         40 MDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWHG 99
              |: |  ||| ::|:|||||||||||: | |||| :| :|| ||||||||:|||| |:
Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy        100 LNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHN 159
              |: ||||:||||||:| : |:||||::|: |||||| : ||| | || | :||:||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        160 LIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQA 219
              || |||||||||||||||:||| | ||:|   ||: | : | :||||||||:: ||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        220 QAFQGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGL 279
              ||: ||||:||||:||:| ||:| |:| : || ||||:||||:|| ||| ||:| :|||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        280 CNVSIDEFRLTYINHFSDDIYNL-NCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRC 338
              ||::|:|||| |:::: ||| :| ||| |:|: |   | |: : |   :| || | :: |
Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        339 HLKPFPKLSLPFLKSWTLTTNREDISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNN 398
                 | |  ||  | |:|:   :| :: |||| :|||||| :||:|||| ||||| :
Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        399 LKYLDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTK 458
              |||||||||||| ||:||:|||:||:|||||| ||:::|||||||  |:|||||:|:|:
Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        459 IDFDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLY 518
              : |:||| || ||  |||||||::| | ::||   |||||||:|||||:|   |::|
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Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        519 RLQLLNMSHNNLLFLDPSHYKQLYSLRTLDCSFNRIETS-KGILQHFPKSLAVFNLTNNS 577
              ||:|||||||    ||    || | ||: || | | | || |   ||||| |||  ||| |
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        578 VACICEYQNFLQWVKDQKMFLVNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVV 637
              || ||:|:||||:|||:  || ||:|:||:| | :   ||   | || : |||| |||:
Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVL 599

Qy        638 SVLVVATVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEG 697
              |||||: || |:| |||||:|:||| || |||:||||||||||:||||||||||||||||
Db        600 SVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEG 659

Qy        698 VPRFQLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQF 757
              || |||||||||||||||||| |||||||||||||:|||||||||||||||||||||||||
Db        660 VPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQF 719

Qy        758 LSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNALGRHIFWRRLKKALLDGK 817
              ||||:|||||||:||||:||||||||||||||||||||: ||||||||||:|||||||
Db        720 LSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGK 779

Qy        818 ALNPD---ETSEEEQEATTL 834
              : ||:    |    ||||::
Db        780 SWNPEGTVGTGCNWQEATSI 799


RESULT 5
US-10-732-796A-8
; Sequence 8, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
;  APPLICANT: Gupta, Shalley K.
;  APPLICANT:  Ghosh, Tarun K.
;  APPLICANT:  Fink, Jason R.
;  TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
;  FILE REFERENCE: S8182US004
;  CURRENT APPLICATION NUMBER: US/10/732,796A
;  CURRENT FILING DATE:  2003-12-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-732-796A-8

  Query Match            62.9%;  Score 2726;  DB 16;  Length 799;
  Best Local Similarity   66.5%;  Pred. No. 5e-213;
  Matches  532;  Conservative  111;  Mismatches  151;  Indels    6;  Gaps    4;

Qy         40 MDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWHG 99
              |: |  ||| ::|:|||||||||||||: | |||| :| :|| ||||||||:|||| |:
Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy        100 LNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHN 159
              |: ||||:||||||:| : |:||||::|: |||||| : ||| | || | :||:||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        160 LIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQA 219
              || ||||||||||||||:||| | ||:|    ||: | : | :|||||||||:: ||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        220 QAFQGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGL 279
              ||: ||||:||||:||:| ||:| |:| : || ||||:||||:|| ||| ||:| :|||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        280 CNVSIDEFRLTYINHFSDDIYNL-NCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRC 338
              ||::|:|||| |:::: ||| :| ||| |:|: |   | |: : |   :| || | :: |
Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        339 HLKPFPKLSLPFLKSWTLTTNREDISFGQLALPSLRYLDLSRNAMSFRGCCSYSDFGTNN 398
                  || | |  ||  | |:|:   :| :: |||| :|||||| :||:|||| ||||| :

Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        399 LKYLDLSFNGVILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTK 458
              |||||||||||| ||:||:|||:||:|||||| ||:::|||||||   |:|||||:|:|:
Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        459 IDFDGIFLGLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLY 518
              : |:||| || ||  |||||||::| | ::||   ||||||||:|||||:|    |::|
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        519 RLQLLNMSHNNLLFLDPSHYKQLYSLRTLDCSFNRIETS-KGILQHFPKSLAVFNLTNNS 577
              ||:|||||||    ||    || | ||: || | | | || |   ||||| |||  ||| |
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        578 VACICEYQNFLQWVKDQKMFLVNVEQMKCASPIDMKASLVLDFTNSTCYIYKTIISVSVV 637
              || ||:|:||||:|||:  || ||:|:||:| | :   ||   | || : |||| |||:
Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVL 599

Qy        638 SVLVVATVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEG 697
              |||||: || |:| |||||:|:||| || |||:||||||||||:||||||||||||||||
Db        600 SVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEG 659

Qy        698 VPRFQLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQF 757
              || |||||||||||||||||| |||||||||||||:|||||||||||||||||||||||||
Db        660 VPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQF 719

Qy        758 LSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNALGRHIFWRRLKKALLDGK 817
              ||||:|||||||:||||:||||||||||||||||||||: ||||||||||:|||||||
Db        720 LSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGK 779

Qy        818 ALNPD---ETSEEEQEATTL 834
              : ||:    |    ||||::
Db        780 SWNPEGTVGTGCNWQEATSI 799


RESULT 6
US-10-114-893-10
; Sequence 10, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
;  APPLICANT: Jacobs, Kenneth
;  APPLICANT: McCoy, John M.
;  APPLICANT: LaVallie, Edward R.
;  APPLICANT: Collins-Racie, Lisa A.
;  APPLICANT: Evans, Cheryl
;  APPLICANT: Merberg, David
;  APPLICANT: Treacy, Maurice
;  APPLICANT: Bowman, Michael R.
;  APPLICANT: Spaulding, Vikki
;  APPLICANT: Carlin-Duckett, McKeough
;  APPLICANT: Kelleher, Kerry S.
;  APPLICANT: Genetics Institute, Inc.
;  TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
;  FILE REFERENCE: GI 6000-10A
;  CURRENT APPLICATION NUMBER: US/10/114,893
;  CURRENT FILING DATE: 2002-04-02
;  EARLIER APPLICATION NUMBER: 09/413,232
;  EARLIER FILING DATE: 1999-10-06
;  NUMBER OF SEQ ID NOS: 321
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 661
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-114-893-10

  Query Match            13.9%;  Score 602.5;  DB 13;  Length 661;
  Best Local Similarity   28.2%;  Pred. No. 4.6e-40;
  Matches  185;  Conservative  127;  Mismatches  296;  Indels   47;  Gaps   18;

Qy         28 CIEVLPNITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRC 87
              |||   | || | :  ||:||  :| :|: |: ||| |  : : :|:    | :|||:||
Db         28 CIEKEANKTYNCENLGLSEIPDTLPNTTEFLEFSFNFLPTIHNRTFSRLMNLTFLDLTRC 87
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Qy         88 EIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQ 147
Db         88 QINWIHEDTFQSHHQLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEFIPVHN 147

Qy        148 LISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSL 207
Db        148 LENLESLYLGSNHISSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--AINLSL 204

Qy        208 DLSLNPIDSIQAQAFQGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERN 267
Db        205 NFNGNNVKGIELGAFDSTVFQSL----NFGGTPNLSVIFNGLQNSTTQSLWLGTFEDIDD 260

Qy        268 LESFDRSVMEGLCNVSIDEFRLTYINHFSD-DIYNLNCLANISAMSFTGVHIKHIADVPR 326
Db        261 -EDISSAMLKGLCEMSVESLNLQE-HRFSDISSTTFQCFTQLQELDLTATHLK---GLPS 315

Qy        327 HFKWQSLSIIR------------CHLKP--FPKLSLPFLKSWTLTTNREDISFGQL-ALP 371
Db        316 GMK--GLNLLKKLVLSVNHFDQLCQISAANFPSLTHLYIRG---NVKKLHLGVGCLEKLG 370

Qy        372 SLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVI-LMSANFMGLEELEYLDFQHS 430
Db        371 NLQTLDLSHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKECPQLELLDLAFT 430

Qy        431 TLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTL--SN 488
Db        431 RLHINAPQSPFQNLHFLQVLNLTYCFLDTSNQHLLAGLPVLRHLNLKGNHFQDGTITKTN 490

Qy        489 VFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLL--FLDP-SHYKQLYSLR 545
Db        491 LLQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHNSLTCDSIDSLSHLKGIY--- 547

Qy        546 TLDCSFNRIETSKGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMFLVNVEQMK 605
Db        548 -LNLAANSINIISPRLLPILSQQSTINLSHNPLDCTCSNIHFLTWYKENLHKLEGSEETT 606

Qy        606 CASPIDMKASLVLDFTNS----TCYIYKTIISVSVVSVLVVATVAFLIYHFYFHL 656
Db        607 CANPPSLRGVKLSDVKLSCGITAIGIFFLIVFLLLLAILLFFAVKYLLRWKYQHI 661
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RESULT 7
US-10-038-854-134
; Sequence 134, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-854-134

Query Match 13.9%; Score 602.5; DB 15; Length 661;
Best Local Similarity 28.2%; Pred. No. 4.6e-40;
Matches 185; Conservative 127; Mismatches 296; Indels 47; Gaps 18;

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Qy         28 CIEVLPNITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRC 87
Db         28 CIEKEANKTYNCENLGLSEIPDTLPNTTEFLEFSFNFLPTIHNRTFSRLMNLTFLDLTRC 87

Qy         88 EIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQ 147
Db         88 QINWIHEDTFQSHHQLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEFIPVHN 147

Qy        148 LISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSL 207
Db        148 LENLESLYLGSNHISSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--AINLSL 204

Qy        208 DLSLNPIDSIQAQAFQGIRLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERN 267
Db        205 NFNGNNVKGIELGAFDSTVFQSL----NFGGTPNLSVIFNGLQNSTTQSLWLGTFEDIDD 260

Qy        268 LESFDRSVMEGLCNVSIDEFRLTYINHFSD-DIYNLNCLANISAMSFTGVHIKHIADVPR 326
Db        261 -EDISSAMLKGLCEMSVESLNLQE-HRFSDISSTTFQCFTQLQELDLTATHLK---GLPS 315

Qy        327 HFKWQSLSIIR------------CHLKP--FPKLSLPFLKSWTLTTNREDISFGQL-ALP 371
Db        316 GMK--GLNLLKKLVLSVNHFDQLCQISAANFPSLTHLYIRG---NVKKLHLGVGCLEKLG 370

Qy        372 SLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVI-LMSANFMGLEELEYLDFQHS 430
Db        371 NLQTLDLSHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKECPQLELLDLAFT 430

Qy        431 TLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTL--SN 488
Db        431 RLHINAPQSPFQNLHFLQVLNLTYCFLDTSNQHLLAGLPVLRHLNLKGNHFQDGTITKTN 490

Qy        489 VFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLL--FLDP-SHYKQLYSLR 545
Db        491 LLQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHNSLTCDSIDSLSHLKGIY--- 547
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Qy        546 TLDCSFNRIETSKGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMFLVNVEQMK 605
              |: : | |      |       :  ||::| : | |   :|| | |:    |   |:
Db        548 -LNLAANSINIISPRLLPILSQQSTINLSHNPLDCTCSNIHFLTWYKENLHKLEGSEETT 606

Qy        606 CASPIDMKASLVLDFTNS----TCYIYKTIISVSVVSVLVVATVAFLIYHFYFHL 656
              ||:|  ::   : |   |       |:  |: : ::::|:   | :|:   | |:
Db        607 CANPPSLRGVKLSDVKLSCGITAIGIPFLIVFLLLLAILLFFAVKYLLRWKYQHI 661


RESULT 8
US-10-038-854-135
; Sequence 135, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
;  APPLICANT: Spytek, Kimberly A
;  APPLICANT:  Li, Li
;  APPLICANT:  Wolenc, Adam R
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Eisen, Andrew J
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Tchernev, Velizar
;  APPLICANT:  Spaderna, Steven K
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Gusev, Vladimir Y
;  APPLICANT:  Gangolli, Esha A
;  APPLICANT:  Guo, Xiaojia S
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  MacDougall, John R
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-230
;  CURRENT APPLICATION NUMBER: US/10/038,854
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 60/258,928
;  PRIOR FILING DATE: 2000-12-29
;  PRIOR APPLICATION NUMBER: 60/259,415
;  PRIOR FILING DATE: 2001-01-02
;  PRIOR APPLICATION NUMBER: 60/259,785
;  PRIOR FILING DATE: 2001-01-04
;  PRIOR APPLICATION NUMBER: 60/269,814
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/279,832
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/279,833
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/279,863
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/283,889
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,447
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: 60/286,683
;  PRIOR FILING DATE: 2001-04-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 411
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
;    LENGTH: 661
;    TYPE: PRT
;    ORGANISM: Mus musculus

US-10-038-854-135

  Query Match            13.8%;  Score 597.5;  DB 15;  Length 661;
  Best Local Similarity  27.9%;  Pred. No. 1.2e-39;
  Matches  187;  Conservative  125;  Mismatches  314;  Indels   45;  Gaps   15;

Qy         12 IMALFLSCLR--PGSLNPCIEVLPNITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILR 69
              ::||||: |    |   |||   | || | :  |::||  :| ||: |: ||| |  ::
Db         10 LVALFLASCRATTSSDQKCIEKEVNKTYNCENLGLNEIPGTLPNSTECLEFSFNVLPTIQ 69

Qy         70 SYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLEN 129
              : :|:    | :|||:||:|  | :  :   ::| ||||| ||:   :  : ||   |::
Db         70 NTTFSRLINLTFLDLTRCQIYWIHEDTFQSQHRLDTLVLTANPLIFMAETALSGPKALKH 129

Qy        130 LVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTI 189
              |  ::| ::|::   :    :|: | :  | | | |||: |     |: :|   | |  :
Db        130 LFFIQTGISSIDFIPLHNQKTLESLYLGSNHISSIKLPKGFPT-EKLKVLDFQNNAIHYL 188

Qy        190 SVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRSNFNSSNVLKMCLQNM 249
              | :|:  |::    ||||:|: | |  |:  ||      |    ||  :  | :  : :
Db        189 SKEDMSSLQQ--ATNLSLNLNGNDIAGIEPGAFDSAVFQSL----NFGGTQNLLVIFKGL 242

Qy        250 TGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDIYNLNCLANIS 309
                :  | || |: : : |    :| |||| :|::   |      |:       :| : :
Db        243 KNSTIQSLWLGTFE-DMDDEDISPAVFEGLCEMSVESINLQKHYFFNISSNTFHCFSGLQ 301

Qy        310 AMSFTGVHIKHIAD----------VPRHFKWQSLSIIRCHLKP--FPKLSLPFLKSWTL 356
              :  |  |:  :             |    |:::|    | :    || |:   :|
Db        302 ELDLTATHLSELPSGLVGLSTLKKLVLSANKFENL----CQISASNFPSLTHLSIKG--- 354

Qy        357 TTNREDISFGQLA-LPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVI-LMSA 414
              | | ::  | |  | :|| |||| : :    ||:      ::|: |:||:|  : | :
Db        355 NTKRLELGTGCLENLENLRELDLSHDDIETSDCCNLQLRNLSHLQSLNLSYNEPLSLKTE 414

Qy        415 NFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTL 474
              |    :|| ||   : ||     | | :|  |  |::|::   |  : :| || :|  |
Db        415 AFKECPQLELLDLAFTRLKVKDAQSPFQNLHLLKVLNLSHSLLDISSEQLFDGLPALQHL 474

Qy        475 KMAGNSFKDNTL--SNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLF 532
              : || |    :  :|       | | || | |  | :  | :|  :  :::||| |
Db        475 NLQGNHFPKGNIQKTNSLQTLGRLEILVLSFCDLSSIDQHAFTSLKMMNHVDLSHNRLTS 534

Qy        533 LD---PSHYKQLYSLRTLDCSFNRIETSKGILQHFPKSLAVFNLTNNSVACICEYQNFLQ 589
                  || | :|    |: : | |       |          ||  | : | |   ||:
Db        535 SSIEALSHLKGIY----LNLASNHISIILPSLLPILSQQRTINLRQNPLDCTCSNIYFLE 590

Qy        590 WVKDQKMFLVNVEQMKCASPIDMKASLVLDFTNSTCY----IYKTIISVSVVSVLVVATV 645
              | |:    | : |   | :|  ::   : | | |       |:  |: : | ::|::  |
Db        591 WYKENMQKLEDTEDTLCENPPLLRGVRLSDVTLSCSMAAVGIFFLIVFLLVFAILLIFAV 650

Qy        646 AFLIYHFYFHL 656
              : :   | |:
Db        651 KYFLRWKYQHI 661


RESULT 9
US-10-037-417-107
; Sequence 107, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
;  APPLICANT: Kekuda, Ramesh
;  APPLICANT:  Alsobrook II, John P
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Li, Li
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Edinger, Shlomit R
```

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;  APPLICANT:  Sciore, Paul
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Rothenberg, Mark
;  APPLICANT:  Stone, David J
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Anderson, David W
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Eisen, Andrew J
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-235
;  CURRENT APPLICATION NUMBER: US/10/037,417
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: 60/260,018
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: 60/260,360
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/272,411
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/272,817
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: 60/291,186
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: 60/303,231
;  PRIOR FILING DATE: 2001-07-05
;  PRIOR APPLICATION NUMBER: 60/305,060
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: 60/318,405
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/318,700
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
;   LENGTH: 661
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-037-417-107

  Query Match             13.8%;  Score 597.5;  DB 15;  Length 661;
  Best Local Similarity   27.9%;  Pred. No. 1.2e-39;
  Matches  187;  Conservative  125;  Mismatches  314;  Indels   45;  Gaps   15;

Qy         12 IMALFLSCLR--PGSLNPCIEVLPNITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILR 69
Db         10 LVALFLASCRATTSSDQKCIEKEVNKTYNCENLGLNEIPGTLPNSTECLEFSFNVLPTIQ 69

Qy         70 SYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLEN 129
Db         70 NTTFSRLINLTFLDLTRCQIYWIHEDTFQSQHRLDTLVLTANPLIFMAETALSGPKALKH 129

Qy        130 LVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTI 189
Db        130 LFFIQTGISSIDFIPLHNQKTLESLYLGSNHISSIKLPKGFPT-EKLKVLDFQNNAIHYL 188

Qy        190 SVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRSNFNSSNVLKMCLQNM 249
Db        189 SKEDMSSLQQ--ATNLSLNLNGNDIAGIEPGAFDSAVFQSL----NFGGTQNLLVIFKGL 242

Qy        250 TGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDIYNLNCLANIS 309
Db        243 KNSTIQSLWLGTFE-DMDDEDISPAVFEGLCEMSVESINLQKHYFFNISSNTFHCFSGLQ 301

Qy        310 AMSFTGVHIKHIAD-----------VPRHFKWQSLSIIRCHLKP--FPKLSLPFLKSWTL 356
Db        302 ELDLTATHLSELPSGLVGLSTLKKLVLSANKFENL----CQISASNFPSLTHLSIKG--- 354

Qy        357 TTNREDISFGQLA-LPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVI-LMSA 414
Db        355 NTKRLELGTGCLENLENLRELDLSHDDIETSDCCNLQLRNLSHLQSLNLSYNEPLSLKTE 414

Qy        415 NFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTL 474
Db        415 AFKECPQLELLDLAFTRLKVKDAQSPFQNLHLLKVLNLSHSLLDISSEQLFDGLPALQHL 474

Qy        475 KMAGNSFKDNTL--SNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLF 532
Db        475 NLQGNHFPKGNIQKTNSLQTLGRLEILVLSFCDLSSIDQHAFTSLKMMNHVDLSHNRLTS 534

Qy        533 LD---PSHYKQLYSLRTLDCSFNRIETSKGILQHFPKSLAVFNLTNNSVACICEYQNFLQ 589
Db        535 SSIEALSHLKGIY----LNLASNHISIILPSLLPILSQQRTINLRQNPLDCTCSNIYFLE 590

Qy        590 WVKDQKMFLVNVEQMKCASPIDMKASLVLDFTNSTCY----IYKTIISVSVVSVLVVATV 645
Db        591 WYKENMQKLEDTEDTLCENPPLLRGVRLSDVTLSCSMAAVGIFFLIVFLLVFAILLIFAV 650

Qy        646 AFLIYHFYFHL 656
Db        651 KYFLRWKYQHI 661


RESULT 10
US-09-954-987B-192
; Sequence 192, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
;  APPLICANT: Stefan Bauer
;  APPLICANT:  Grayson B. Lipford
;  APPLICANT:  Hermann Wagner
;  TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
;  TITLE OF INVENTION:  CpG-BASED IMMUNO-AGONIST/ANTAGONIST
;  FILE REFERENCE: C1041/7016 (AWS)
;  CURRENT APPLICATION NUMBER: US/09/954,987B
;  CURRENT FILING DATE:  2001-09-17
;  PRIOR APPLICATION NUMBER: US 60/233,035
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/263,657
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: US 60/291,726
;  PRIOR FILING DATE: 2001-05-17
;  PRIOR APPLICATION NUMBER: US 60/300,210
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 230
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 192
;   LENGTH: 1032
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-954-987B-192

  Query Match             13.3%;  Score 575;  DB 10;  Length 1032;
  Best Local Similarity   25.1%;  Pred. No. 1.5e-37;
  Matches  242;  Conservative  153;  Mismatches  318;  Indels  252;  Gaps   40;

Qy         32 LPNITYQCMDQN-LSKIPHDIPYSTKNLDLSFN---------------------------- 63
Db        120 LRNLTVLLLEDNQLYTIPAGLPESLKELSLIQNNIFQVTKNNTFGLRNLERLYLGWNCYF 179

Qy         64 -----------------PLKILRSYSFTNF--------SQLQWLDLSRCEIETIEDKAWH 98
Db        180 KCNQTFKVEDGAFKNLIHLKVL-SLSFNNLFYVPPKLPSSLRKLFLSNAKIMNITQEDFK 238

Qy         99 GLNQLSTLVLTGN------------PIKSFS-----PGSFSGLTNLENLVAVETKMTSLE 141
Db        239 GLENLTLLDLSGNCPRCYNAPFPCTPCKENSSIHIHPLAFQSLTQLLYLNLSSTSLRTIP 298

Qy        142 GFHIGQLISLKKLNVAHN-LIHSFKLPEYFSNLTNLEHVDLSYN-----YIQTISV---- 191
Db        299 STWFENLSNLKELHLEFNYLVQEIASGAFLTKLPSLQILDLSFNFQYKEYLQFINISSNF 358

Qy        192 --------------------KDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHEL 230
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Db        359 SKLRSLKKLHLRGYVFRELKKKHFEHLQSLPNL-ATINLGINFIEKIDFKAFQ------- 410

Qy        231 TLRSNFNSSNVLKMCLQNMTGLHVHRLILG-EFKNERNL---------ESFD-------- 272
Db        411 ----NFSKLDVI-----YLSGNRIASVLDGTDYSSWRNRLRKPLSTDDDEFDPHVNFYHS 461

Qy        273 -RSVMEGLCNVSIDEFRLTYINHF---------SDDIYNLNCLANISAMSFTGVHIKHIA 322
Db        462 TKPLIKPQCTAYGKALDLSLNNIFIIGKSQFEGFQDIACLNLSFNANTQVFNGTEFS--- 518

Qy        323 DVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTTNREDI----SFGQLALPSLRYLDL 378
Db        519 -----------------------SMPHIKYLDLTNNRLDFDDNNAFSD--LHDLEVLDL 552

Qy        379 SRNA--MSFRGCCSYSDFGTN--NLKYLDLSFNGVILMS----ANFMGLEELEYLDFQHS 430
Db        553 SHNAHYFSIAGVTHRLGFIQNLINLRVLNLSHNGIYTLTEESELKSISLKELVFSGNRLD 612

Qy        431 TLKKVTE---FSVFLSLEKLLYLDISYTNTKIDFDGIFLGL-ISLNTLKMAGNS--FKDN 484
Db        613 HLWNANDGKYWSIFKSLQNLIRLDLSYNNLQQIPNGAFLNLPQSLQELLISGNKLRFFNW 672

Qy        485 TLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSL 544
Db        673 TLLQYF---PHLHLLDLSRNELYFLPNCLSKFAHSLETLLLSHNHFSHLPSGFLSEARNL 729

Qy        545 RTLDCSFNRIE-TSKGILQHFPK-SLAVFNLTNNSVACICEYQNFLQWVKDQKMF----L 598
Db        730 VHLDLSFNTIKMINKSSLQTKMKTNLSILELHGNYFDCTCDISDFRSWLDENLNITIPKL 789

Qy        599 VNVEQMKCASPIDMKASLVLDFTNSTC--------YIYKTIISVSVVSVLVVATVAFLIY 650
Db        790 VNV---ICSNPGDQKSKSIMSLDLTTCVSDTTAAVLFFLTFLTTSM--VMLAALVHHLFY 844

Qy        651 ---HFYFHL--ILIAGCKKYSRGESIYDAFVIYSSQN---EDWVRNELVKNLEEGVPR-F 701
Db        845 WDVWFIYHMCSAKLKGYRTSSTSQTFYDAYISYDTKDASVTDWVINELRYHLEESEDKSV 904

Qy        702 QLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLS-- 759
Db        905 LLCLEERDWDPGLPIIDNLMQ-SINQSKKTIFVLTKKY-----------AKSWNFKTAF 951

Qy        760 ----------SRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNALGRHIFWRRL 809
Db        952 YLALQRLMDENMDVIIFILLEPVLQ--YSQYLRLRQRICKSSILQWPNNPKAENLFWQSL 1009

Qy        810 KKALL 814
Db       1010 KNVVL 1014
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RESULT 11
US-10-272-502A-31
; Sequence 31, Application US/10272502A
; Publication No. US20030139364A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Schetter, Christian
;  APPLICANT:  Bratzler, Robert L.
;  APPLICANT:  Vollmer, Jorg
;  APPLICANT:  Bauer, Stefan
;  APPLICANT:  Jurk, Marion
;  TITLE OF INVENTION: METHODS AND PRODUCTS FOR ENHANCING IMMUNE RESPONSES USING
;  TITLE OF INVENTION:  IMIDAZOQUINOLINE COMPOUNDS
;  FILE REFERENCE: C01039.70065.US
;  CURRENT APPLICATION NUMBER: US/10/272,502A
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/329,208
;  PRIOR FILING DATE: 2001-10-12
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;  LENGTH: 1032
;  TYPE: PRT
;  ORGANISM: Mus musculus
US-10-272-502A-31

  Query Match            13.3%;  Score 575;  DB 14;  Length 1032;
  Best Local Similarity  25.1%;  Pred. No. 1.5e-37;
  Matches  242;  Conservative  153;  Mismatches  318;  Indels  252;  Gaps   40;

Qy         32 LPNITYQCMDQN-LSKIPHDIPYSTKNLDLSFN------------------------- 63
Db        120 LRNLTVLLLEDNQLYTIPAGLPESLKELSLIQNNIFQVTKNNTFGLRNLERLYLGWNCYF 179

Qy         64 ----------------PLKILRSYSFTNF--------SQLQWLDLSRCEIETIEDKAWH 98
Db        180 KCNQTFKVEDGAFKNLIHLKVL-SLSFNNLFYVPPKLPSSLRKLFLSNAKIMNITQEDFK 238

Qy         99 GLNQLSTLVLTGN-----------PIKSFS-----PGSFSGLTNLENLVAVETKMTSLE 141
Db        239 GLENLTLLDLSGNCPRCYNAPFPCTPCKENSSIHIHPLAFQSLTQLLYLNLSSTSLRTIP 298

Qy        142 GFHIGQLISLKKLNVAHN-LIHSFKLPEYFSNLTNLEHVDLSYN-----YIQTISV---- 191
Db        299 STWFENLSNLKELHLEFNYLVQEIASGAFLTKLPSLQILDLSFNFQYKEYLQFINISSNF 358

Qy        192 --------------------KDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHEL 230
Db        359 SKLRSLKKLHLRGYVFRELKKKHFEHLQSLPNL-ATINLGINFIEKIDFKAFQ------- 410

Qy        231 TLRSNFNSSNVLKMCLQNMTGLHVHRLILG-EFKNERNL---------ESFD-------- 272
Db        411 ----NFSKLDVI-----YLSGNRIASVLDGTDYSSWRNRLRKPLSTDDDEFDPHVNFYHS 461

Qy        273 -RSVMEGLCNVSIDEFRLTYINHF---------SDDIYNLNCLANISAMSFTGVHIKHIA 322
Db        462 TKPLIKPQCTAYGKALDLSLNNIFIIGKSQFEGFQDIACLNLSFNANTQVFNGTEFS--- 518

Qy        323 DVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTTNREDI----SFGQLALPSLRYLDL 378
Db        519 -----------------------SMPHIKYLDLTNNRLDFDDNNAFSD--LHDLEVLDL 552

Qy        379 SRNA--MSFRGCCSYSDFGTN--NLKYLDLSFNGVILMS----ANFMGLEELEYLDFQHS 430
Db        553 SHNAHYFSIAGVTHRLGFIQNLINLRVLNLSHNGIYTLTEESELKSISLKELVFSGNRLD 612

Qy        431 TLKKVTE---FSVFLSLEKLLYLDISYTNTKIDFDGIFLGL-ISLNTLKMAGNS--FKDN 484
Db        613 HLWNANDGKYWSIFKSLQNLIRLDLSYNNLQQIPNGAFLNLPQSLQELLISGNKLRFFNW 672

Qy        485 TLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSL 544
Db        673 TLLQYF---PHLHLLDLSRNELYFLPNCLSKFAHSLETLLLSHNHFSHLPSGFLSEARNL 729

Qy        545 RTLDCSFNRIE-TSKGILQHFPK-SLAVFNLTNNSVACICEYQNFLQWVKDQKMF----L 598
Db        730 VHLDLSFNTIKMINKSSLQTKMKTNLSILELHGNYFDCTCDISDFRSWLDENLNITIPKL 789

Qy        599 VNVEQMKCASPIDMKASLVLDFTNSTC--------YIYKTIISVSVVSVLVVATVAFLIY 650
Db        790 VNV---ICSNPGDQKSKSIMSLDLTTCVSDTTAAVLFFLTFLTTSM--VMLAALVHHLFY 844

Qy        651 ---HFYFHL--ILIAGCKKYSRGESIYDAFVIYSSQN---EDWVRNELVKNLEEGVPR-F 701
Db        845 WDVWFIYHMCSAKLKGYRTSSTSQTFYDAYISYDTKDASVTDWVINELRYHLEESEDKSV 904

Qy        702 QLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLS-- 759
Db        905 LLCLEERDWDPGLPIIDNLMQ-SINQSKKTIFVLTKKY-----------AKSWNFKTAF 951

Qy        760 ----------SRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNALGRHIFWRRL 809
Db        952 YLALQRLMDENMDVIIFILLEPVLQ--YSQYLRLRQRICKSSILQWPNNPKAENLFWQSL 1009
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Qy        810 KKALL 814
              |  :|
Db       1010 KNVVL 1014


RESULT 12
US-10-407-952-32
; Sequence 32, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
;  APPLICANT: Lipford, Grayson
;  APPLICANT:  Bauer, Stefan
;  TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligoribonucleotides
;  FILE REFERENCE: C01041.70037.US
;  CURRENT APPLICATION NUMBER: US/10/407,952
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: US 60/421,966
;  PRIOR FILING DATE: 2002-10-29
;  PRIOR APPLICATION NUMBER: US 60/370,515
;  PRIOR FILING DATE: 2002-04-04
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 1032
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-407-952-32

  Query Match             13.3%;  Score 575;  DB 15;  Length 1032;
  Best Local Similarity   25.1%;  Pred. No. 1.5e-37;
  Matches  242;  Conservative  153;  Mismatches  318;  Indels  252;  Gaps   40;

Qy         32 LPNITYQCMDQN-LSKIPHDIPYSTKNLDLSFN---------------------------- 63
              | |:|   ::  | |  ||  :| | | | |  |
Db        120 LRNLTVLLLEDNQLYTIPAGLPESLKELSLIQNNIFQVTKNNTFGLRNLERLYLGWNCYF 179

Qy         64 -----------------PLKILRSYSFTNF--------SQLQWLDLSRCEIETIEDKAWH 98
                              ||:| | || |          | |: | ||  :|  |  : :
Db        180 KCNQTFKVEDGAFKNLIHLKVL-SLSFNNLFYVPPKLPSSLRKLFLSNAKIMNITQEDFK 238

Qy         99 GLNQLSTLVLTGN------------PIKSFS-----PGSFSGLTNLENLVAVETKMTSLE 141
              ||  |: | |:||             | |  |      | :|  || |  |     | : ::
Db        239 GLENLTLLDLSGNCPRCYNAPFPCTPCKENSSIHIHPLAFQSLTQLLYLNLSSTSLRTIP 298

Qy        142 GFHIGQLISLKKLNVAHN-LIHSFKLPEYFSNLTNLEHVDLSYN-----YIQTISV---- 191
                  | :||:|::  | |:        : : | :|: :|||:|     |:|  |::
Db        299 STWFENLSNLKELHLEFNYLVQEIASGAFLTKLPSLQILDLSFNFQYKEYLQFINISSNF 358

Qy        192 ---------------------KDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHEL 230
                                  |  : |:  | :  :::| :| |: |  :|||
Db        359 SKLRSLKKLHLRGYVFRELKKKHFEHLQSLPNL-ATINLGINFIEKIDFKAFQ------- 410

Qy        231 TLRSNFNSSNVLKMCLQNMTGLHVHRLILG-EFKNERNL---------ESFD-------- 272
                ||:  :|:      ::|  :  :: | :: : ||          : ||
Db        411 ----NFSKLDVI-----YLSGNRIASVLDGTDYSSWRNRLRKPLSTDDDEFDPHVNFYHS 461

Qy        273 -RSVMEGLCNVSIDEFRLTYINHF---------SDDIYNLNCLANISAMSFTGVHIKHIA 322
               : :::  |         |:  | |           ||  ||   |  :   | |
Db        462 TKPLIKPQCTAYGKALDLSLNNIFIIGKSQFEGFQDIACLNLSFNANTQVFNGTEFS--- 518

Qy        323 DVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTTNREDI----SFGQLALPSLRYLDL 378
                                  |:| :|   || || |     :|    |  |  |||
Db        519 ----------------------SMPHIKYLDLTNNRLDFDDNNAFSD--LHDLEVLDL 552

Qy        379 SRNA--MSFRGCCSYSDFGTN--NLKYLDLSFNGVILMS----ANFMGLEELEYLDFQHS 430
              | ||   |  |       |  |  ||: |:|| ||:  ::       : |:|| :   :
Db        553 SHNAHYFSIAGVTHRLGFIQNLINLRVLNLSHNGIYTLTEESELKSISLKELVFSGNRLD 612

Qy        431 TLKKVTE---FSVFLSLEKLLYLDISYTNTKIDFDGIFLGL-ISLNTLKMAGNS--FKDN 484
               |    :  :|:| ||: |: ||:|| | :   :| || |  ||  | ::||    | :
Db        613 HLWNANDGKYWSIFKSLQNLIRLDLSYNNLQQIPNGAFLNLPQSLQELLISGNKLRFFNW 672

Qy        485 TLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSL 544
                ||   |   :|  ||||: :|  :   :   : |: | :|||:   |      : :|
Db        673 TLLQYF---PHLHLLDLSRNELYFLPNCLSKFAHSLETLLLSHNHFSHLPSGFLSEARNL 729

Qy        545 RTLDCSFNRIE-TSKGILQHFPK-SLAVFNLTNNSVACICEYQNFLQWVKDQKMF----L 598
                || ||| |:  :|  ||   | :|::  |  |   | |:  :|  |: :        |
Db        730 VHLDLSFNTIKMINKSSLQTKMKTNLSILELHGNYFDCTCDISDFRSWLDENLNITIPKL 789

Qy        599 VNVEQMKCASPIDMKASLVLDFTNSTC--------YIYKTIISVSVVSVLVVATVAFLIY 650
              |||    |::| | |:  ::    :||          : | :: |:  |:: | |  | |
Db        790 VNV---ICSNPGDQKSKSIMSLDLTTCVSDTTAAVLFFLTFLTTSM--VMLAALVHHLFY 844

Qy        651 ---HFYFHL--ILIAGCKKYSRGESIYDAFVIYSSQN---EDWVRNELVKNLEEGVPR-F 701
                  | :|:    : | :  |  :: |||:: | :::    ||| |||  :|||   :
Db        845 WDVWFIYHMCSAKLKGYRTSSTSQTFYDAYISYDTKDASVTDWVINELRYHLEESEDKSV 904

Qy        702 QLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLS-- 759
               |||  ||: ||: |  |::|   ::|:| | |::: :             |::| | :
Db        905 LLCLEERDWDPGLPIIDNLMQ-SINQSKKTIFVLTKKY------------AKSWNFKTAF 951

Qy        760 ----------SRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNALGRHIFWRRL 809
                       :  ||||:|| | :    | : | : : ::: |:| :|    ::||: |
Db        952 YLALQRLMDENMDVIIFILLEPVLQ--YSQYLRLRQRICKSSILQWPNNPKAENLFWQSL 1009

Qy        810 KKALL 814
              |  :|
Db       1010 KNVVL 1014


RESULT 13
US-09-954-987B-175
; Sequence 175, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
;  APPLICANT: Stefan Bauer
;  APPLICANT:  Grayson B. Lipford
;  APPLICANT:  Hermann Wagner
;  TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
;  TITLE OF INVENTION:  CpG-BASED IMMUNO-AGONIST/ANTAGONIST
;  FILE REFERENCE: C1041/7016 (AWS)
;  CURRENT APPLICATION NUMBER: US/09/954,987B
;  CURRENT FILING DATE:  2001-09-17
;  PRIOR APPLICATION NUMBER: US 60/233,035
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/263,657
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: US 60/291,726
;  PRIOR FILING DATE: 2001-05-17
;  PRIOR APPLICATION NUMBER: US 60/300,210
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 230
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 175
;   LENGTH: 1050
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-954-987B-175

  Query Match             12.9%;  Score 559;  DB 10;  Length 1050;
  Best Local Similarity   24.4%;  Pred. No. 3.1e-36;
  Matches  265;  Conservative  153;  Mismatches  327;  Indels  342;  Gaps   52;

Qy          4 LLHLAGTLIMALFLSCLRPGSLNPCIEVLPNI-----TYQCMDQNLSKIPHDIPYSTKNL 58
              |: |   |:  :|      | :| || ||  ||         | |::|::||  || :| ||
Db         13 LIFLNMLLVSRVFGFRWFPKTL-PC-EVKVNIPEAHVIVDCTDKHLTEIPEGIPTNTTNL 70

Qy         59 DLSFNPLKILRSYSFTNFSQLQWLDL----------SRCEIET----IEDKAWHGLNQLS 104
               |: | :  :    ||   : |: :||          |:  : |    |   :: ||: |
Db         71 TLTINHIPSISPDSFRRLNHLEEIDLRCNCVPVLLGSKANVCTKRLQIRPGSFSGLSDLK 130

Qy        105 TLVLTGNPIKSFS---PGSFSGLTNLE--NLVAVE----TKMTSLEGFHIGQ-------- 147
               | | || :       | |   | :||  |: ::     |:: ::|  ::||
Db        131 ALYLDGNQLLEIPQDLPSSLH-LLSLEANNIFSITKENLTELVNIETLYLGQNCYYRNPC 189
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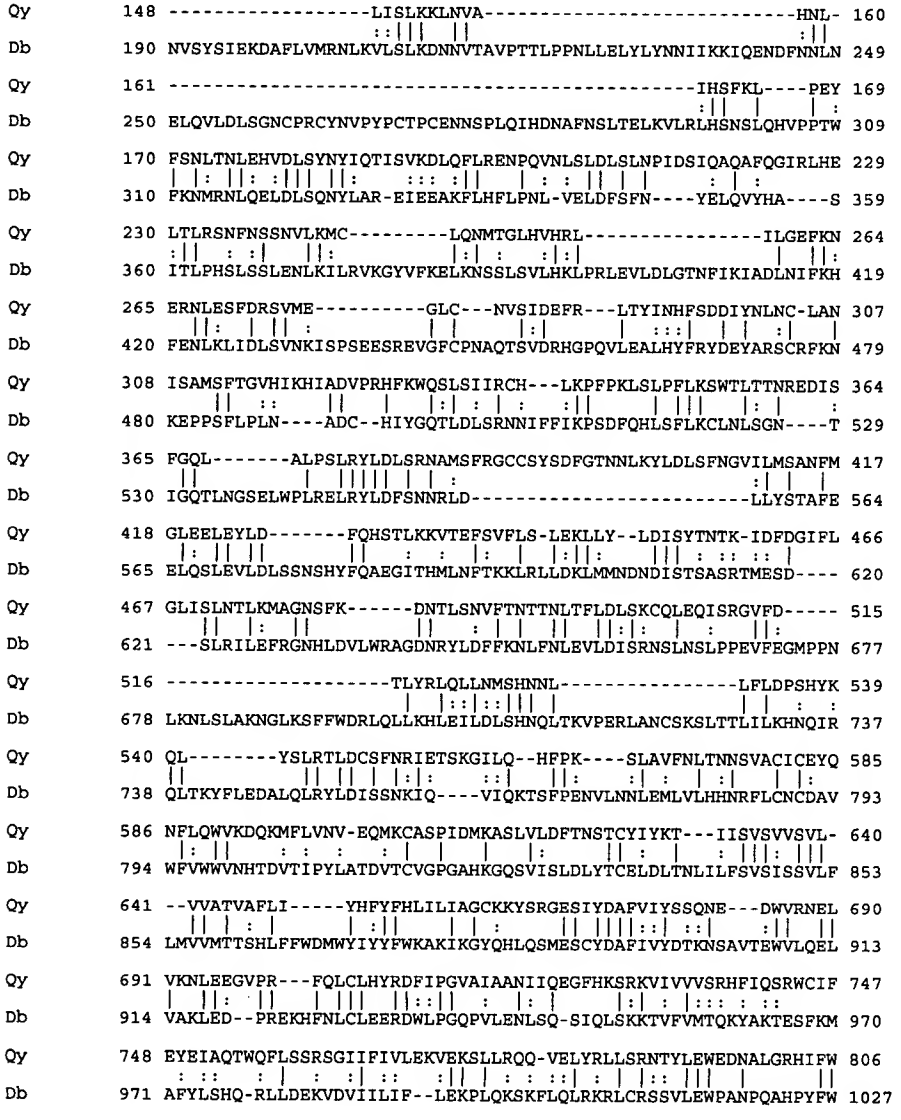
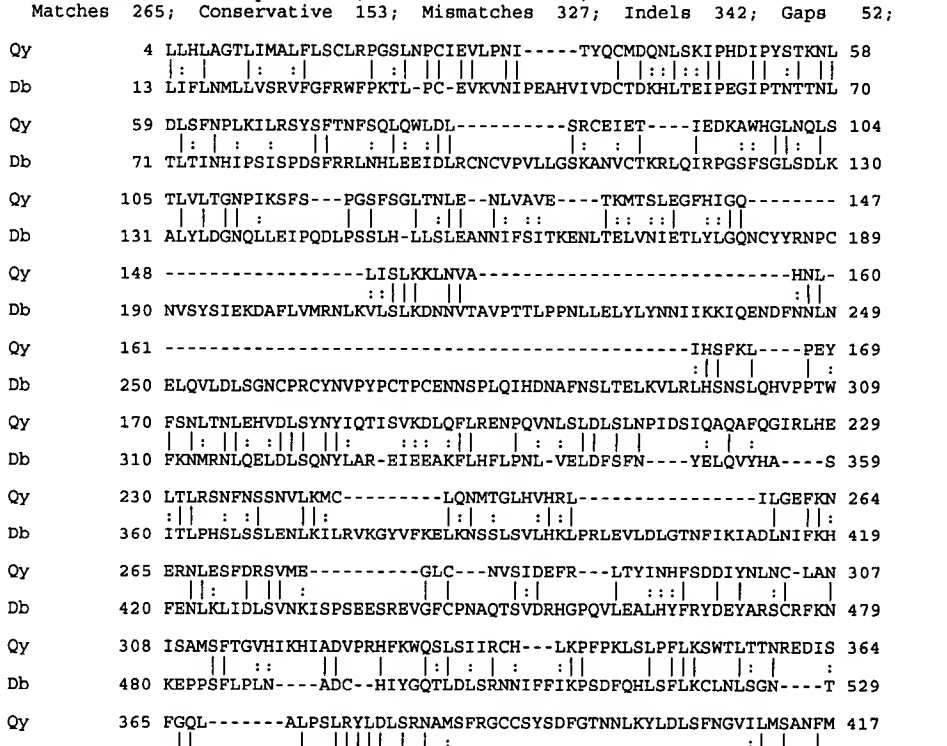


RESULT 14
US-10-272-502A-22
; Sequence 22, Application US/10272502A
; Publication No. US20030139364A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Vollmer, Jorg
; APPLICANT: Bauer, Stefan
; APPLICANT: Jurk, Marion
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ENHANCING IMMUNE RESPONSES USING
; TITLE OF INVENTION: IMIDAZOQUINOLINE COMPOUNDS
; FILE REFERENCE: C01039.70065.US
; CURRENT APPLICATION NUMBER: US/10/272,502A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,208
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1050
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-272-502A-22

Query Match 12.9%; Score 559; DB 14; Length 1050;
Best Local Similarity 24.4%; Pred. No. 3.1e-36;
Matches 265; Conservative 153; Mismatches 327; Indels 342; Gaps 52;



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Qy        540 QL--------YSLRTLDCSFNRIETSKGILQ--HFPK----SLAVFNLTNNSVACICEYQ 585
Db        738 QLTKYFLEDALQLRYLDISSNKIQ----VIQKTSFPENVLNNLEMLVLHHNRFLCNCDAV 793

Qy        586 NFLQWVKDQKMFLVNV-EQMKCASPIDMKASLVLDFTNSTCYIYKT---IISVSVVSVL- 640
Db        794 WFVWWVNHTDVTIPYLATDVTCVGPGAHKGQSVISLDLYTCELDLTNLILFSVSISSVLF 853

Qy        641 --VVATVAFLI-----YHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNE---DWVRNEL 690
Db        854 LMVVMTTSHLFFWDMWYIYYFWKAKIKGYQHLQSMESCYDAFIVYDTKNSAVTEWVLQEL 913

Qy        691 VKNLEEGVPR---FQLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIF 747
Db        914 VAKLED--PREKHFNLCLEERDWLPGQPVLENLSQ-SIQLSKKTVFVMTQKYAKTESFKM 970

Qy        748 EYEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQ-VELYRLLSRNTYLEWEDNALGRHIFW 806
Db        971 AFYLSHQ-RLLDEKVDVIILIF--LEKPLQKSKFLQLRKRLCRSSVLEWPANPQAHPYFW 1027

Qy        807 RRLKKAL 813
Db       1028 QCLKNAL 1034
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RESULT 15
US-10-407-952-26
; Sequence 26, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Bauer, Stefan
; TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligoribonucleotides
; FILE REFERENCE: C01041.70037.US
; CURRENT APPLICATION NUMBER: US/10/407,952
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 1050
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-407-952-26

Query Match 12.9%; Score 559; DB 15; Length 1050;
Best Local Similarity 24.4%; Pred. No. 3.1e-36;
Matches 265; Conservative 153; Mismatches 327; Indels 342; Gaps 52;

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Qy          4 LLHLAGTLIMALFLSCLRPGSLNPCIEVLPNI-----TYQCMDQNLSKIPHDIPYSTKNL 58
Db         13 LIFLNMLLVSRVFGFRWFPKTL-PC-EVKVNIPEAHVIVDCTDKHLTEIPEGIPTNTTNL 70

Qy         59 DLSFNPLKILRSYSFTNFSQLQWLDL----------SRCEIET----IEDKAWHGLNQLS 104
Db         71 TLTINHIPSISPDSFRRLNHLEEIDLRCNCVPVLLGSKANVCTKRLQIRPGSFSGLSDLK 130

Qy        105 TLVLTGNPIKSFS---PGSFSGLTNLE--NLVAVE----TKMTSLEGFHIGQ-------- 147
Db        131 ALYLDGNQLLEIPQDLPSSLH-LLSLEANNIFSITKENLTELVNIETLYLGQNCYYRNPC 189

Qy        148 ------------------LISLKKLNVA----------------------------HNL- 160
Db        190 NVSYSIEKDAFLVMRNLKVLSLKDNNVTAVPTTLPPNLLELYLYNNIIKKIQENDFNNLN 249

Qy        161 ------------------------------------------------IHSFKL----PEY 169
Db        250 ELQVLDLSGNCPRCYNVPYPCTPCENNSPLQIHDNAFNSLTELKVLRLHSNSLQHVPPTW 309

Qy        170 FSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHE 229
Db        310 FKNMRNLQELDLSQNYLAR-EIEEAKFLHFLPNL-VELDFSFN----YELQVYHA----S 359

Qy        230 LTLRSNFNSSNVLKMC---------LQNMTGLHVHRL----------------ILGEFKN 264
Db        360 ITLPHSLSSLENLKILRVKGYVFKELKNSSLSVLHKLPRLEVLDLGTNFIKIADLNIFKH 419

Qy        265 ERNLESFDRSVME----------GLC---NVSIDEFR---LTYINHFSDDIYNLNC-LAN 307
Db        420 FENLKLIDLSVNKISPSEESREVGFCPNAQTSVDRHGPQVLEALHYFRYDEYARSCRFKN 479

Qy        308 ISAMSFTGVHIKHIADVPRHFKWQSLSIIRCH---LKPFPKLSLPFLKSWTLTTNREDIS 364
Db        480 KEPPSFLPLN----ADC--HIYGQTLDLSRNNIFFIKPSDFQHLSFLKCLNLSGN----T 529

Qy        365 FGQL-------ALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSANFM 417
Db        530 IGQTLNGSELWPLRELRYLDFSNNRLD------------------------LLYSTAFE 564

Qy        418 GLEELEYLD-------FQHSTLKKVTEFSVFLS-LEKLLY--LDISYTNTK-IDFDGIFL 466
Db        565 ELQSLEVLDLSSNSHYFQAEGITHMLNFTKKLRLLDKLMMNDNDISTSASRTMESD---- 620

Qy        467 GLISLNTLKMAGNSFK------DNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFD----- 515
Db        621 ---SLRILEFRGNHLDVLWRAGDNRYLDFFKNLFNLEVLDISRNSLNSLPPEVFEGMPPN 677

Qy        516 --------------------TLYRLQLLNMSHNNL----------------LFLDPSHYK 539
Db        678 LKNLSLAKNGLKSFFWDRLQLLKHLEILDLSHNQLTKVPERLANCSKSLTTLILKHNQIR 737

Qy        540 QL--------YSLRTLDCSFNRIETSKGILQ--HFPK----SLAVFNLTNNSVACICEYQ 585
Db        738 QLTKYFLEDALQLRYLDISSNKIQ----VIQKTSFPENVLNNLEMLVLHHNRFLCNCDAV 793

Qy        586 NFLQWVKDQKMFLVNV-EQMKCASPIDMKASLVLDFTNSTCYIYKT---IISVSVVSVL- 640
Db        794 WFVWWVNHTDVTIPYLATDVTCVGPGAHKGQSVISLDLYTCELDLTNLILFSVSISSVLF 853

Qy        641 --VVATVAFLI-----YHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNE---DWVRNEL 690
Db        854 LMVVMTTSHLFFWDMWYIYYFWKAKIKGYQHLQSMESCYDAFIVYDTKNSAVTEWVLQEL 913

Qy        691 VKNLEEGVPR---FQLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIF 747
Db        914 VAKLED--PREKHFNLCLEERDWLPGQPVLENLSQ-SIQLSKKTVFVMTQKYAKTESFKM 970

Qy        748 EYEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQ-VELYRLLSRNTYLEWEDNALGRHIFW 806
Db        971 AFYLSHQ-RLLDEKVDVIILIF--LEKPLQKSKFLQLRKRLCRSSVLEWPANPQAHPYFW 1027

Qy        807 RRLKKAL 813
Db       1028 QCLKNAL 1034
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Search completed: March 12, 2005, 20:27:59
Job time : 80.8956 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:01 ; Search time 21.5445 Seconds
(without alignments)
3729.074 Million cell updates/sec

Title: US-09-396-985B-6
Perfect score: 4335
Sequence: 1 MMPLLHLAGTLIMALFLSCL.....GKALNPDETSEEEQEATTLT 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	597.5	13.8	661	2	I56258	RP105 - mouse
2	465.5	10.7	786	2	T08664	Toll protein-like
3	397	9.2	1097	2	A29943	Toll protein precu
4	374	8.6	1389	2	T13852	gene wheeler prote
5	371	8.6	1385	2	T13887	tlr protein - frui
6	320.5	7.4	1134	1	A29944	chaoptin precursor
7	303	7.0	1066	2	T15864	hypothetical prote
8	301.5	7.0	603	2	JC6128	insulin-like growt
9	300.5	6.9	605	2	JC5239	insulin-like growt
10	290.5	6.7	603	2	JC1282	insulin-like growt
11	287.5	6.6	1112	2	T10504	disease resistance
12	285.5	6.6	1051	2	T13174	gp150 protein - fr
13	281.5	6.5	605	2	A41915	insulin-like growt
14	279	6.4	1469	2	B36665	slit protein 2 pre
15	279	6.4	1480	2	A36665	slit protein 1 pre
16	274	6.3	1692	2	A33988	adenylate cyclase
17	270.5	6.2	1143	2	T10636	hypothetical prote
18	270	6.2	907	2	JG0193	G protein-coupled
19	266.5	6.1	1523	2	T13953	MEGF5 protein - ra
20	266	6.1	1531	2	T42218	slit-1 protein hom
21	265.5	6.1	1016	2	T30553	disease resistance
22	264.5	6.1	1027	2	B85089	receptor protein k
23	261	6.0	1232	2	T05322	hypothetical prote
24	259	6.0	910	2	G84648	probable disease r
25	256	5.9	560	2	A60164	platelet membrane
26	253	5.8	907	2	JE0176	orphan G protein-c
27	252	5.8	1120	2	B86479	hypothetical prote
28	250	5.8	1068	2	H96769	hypothetical prote
29	249	5.7	662	2	S42799	garp precursor - h
30	249	5.7	855	2	T17460	disease resistance
31	247.5	5.7	1778	2	AF1116	internalin protein
32	247	5.7	890	2	T00800	disease resistance
33	246.5	5.7	853	2	T17461	disease resistance
34	246.5	5.7	910	2	B96770	hypothetical prote
35	243.5	5.6	738	2	T19938	hypothetical prote
36	243	5.6	1091	2	A58532	glial cell membran
37	243	5.6	1784	2	C96615	hypothetical prote
38	242.5	5.6	603	2	T24315	hypothetical prote
39	242.5	5.6	800	2	H84740	hypothetical prote
40	242.5	5.6	951	2	A96770	hypothetical prote
41	239	5.5	855	2	T07015	Cf-4A protein - to
42	237	5.5	994	2	H96510	probable disease r
43	236.5	5.5	622	2	JC7973	synleurin - human
44	235.5	5.4	983	2	G84524	probable disease r
45	235.5	5.4	2026	1	OYBY	adenylate cyclase

ALIGNMENTS

RESULT 1
I56258
RP105 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56258
R;Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995
A;Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a m
A;Reference number: I56258; MUID:95204928; PMID:7897216
A;Accession: I56258
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-661 <RES>
A;Cross-references: UNIPROT:Q62192; GB:D37797; NID:g761711; PIDN:BAA07043.1; PID:g761712

Query Match 13.8%; Score 597.5; DB 2; Length 661;
Best Local Similarity 27.9%; Pred. No. 1.8e-29;
Matches 187; Conservative 125; Mismatches 314; Indels 45; Gaps 15;

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Qy         12 IMALFLSCLR--PGSLNPCIEVLPNITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILR 69
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Db         10 LVALFLASCRATTSSDQKCIEKEVNKTYNCENLGLNEIPGTLPNSTECLEFSFNVLPTIQ 69

Qy         70 SYSFTNFSQLQWLDLSRCEIETIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLEN 129
              : :|:   | :|||:||:|  | :  :   ::| ||||| ||:   :  : ||   |::
Db         70 NTTFSRLINLTFLDLTRCQIYWIHEDTFQSQHRLDTLVLTANPLIFMAETALSGPKALKH 129

Qy        130 LVAVETKMTSLEGFHIGQLISLKKLNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTI 189
              |  ::| ::|::   :    :|: | :  | | | |||: |     |: :|   | |  :
Db        130 LFFIQTGISSIDFIPLHNQKTLESLYLGSNHISSIKLPKGFPT-EKLKVLDFQNNAIHYL 188

Qy        190 SVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRSNFNSSNVLKMCLQNM 249
              | :|:  |::    ||||:|: | |  |:  ||      |    ||  :  | :  : :
Db        189 SKEDMSSLQQ--ATNLSLNLNGNDIAGIEPGAFDSAVFQSL----NFGGTQNLLVIFKGL 242

Qy        250 TGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDIYNLNCLANIS 309
              :  | || |: : : |    :| |||| :|::   |      |:      :| : :
Db        243 KNSTIQSLWLGTFE-DMDDEDISPAVFEGLCEMSVESINLQKHYFFNISSNTFHCFSGLQ 301

Qy        310 AMSFTGVHIKHIAD----------VPRHFKWQSLSIIRCHLKP--FPKLSLPFLKSWTL 356
              :  | |:  :              |    |:::|    | :    || |:   :|
Db        302 ELDLTATHLSELPSGLVGLSTLKKLVLSANKFENL----CQISASNFPSLTHLSIKG--- 354

Qy        357 TTNREDISFGQLA-LPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVI-LMSA 414
              | | ::  | |  | :|| |||| : :    ||:      ::|: |:||:|  : | :
Db        355 NTKRLELGTGCLENLENLRELDLSHDDIETSDCCNLQLRNLSHLQSLNLSYNEPLSLKTE 414

Qy        415 NFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTL 474
              |    :|| ||   : ||     | | :|  |  |::|::   |  : :| || :|  |
Db        415 AFKECPQLELLDLAFTRLKVKDAQSPFQNLHLLKVLNLSHSLLDISSEQLFDGLPALQHL 474
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Qy        475 KMAGNSFKDNTL--SNVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLF 532
Db        475 NLQGNHFPKGNIQKTNSLQTLGRLEILVLSFCDLSSIDQHAFTSLKMMNHVDLSHNRLTS 534

Qy        533 LD---PSHYKQLYSLRTLDCSFNRIETSKGILQHFPKSLAVFNLTNNSVACICEYQNFLQ 589
Db        535 SSIEALSHLKGIY----LNLASNHISIILPSLLPILSQQRTINLRQNPLDCTCSNIYFLE 590

Qy        590 WVKDQKMFLVNVEQMKCASPIDMKASLVLDFTNSTCY----IYKTIISVSVVSVLVVATV 645
Db        591 WYKENMQKLEDTEDTLCENPPLLRGVRLSDVTLSCSMAAVGIFFLIVFLLVFAILLIFAV 650

Qy        646 AFLIYHFYFHL 656
Db        651 KYFLRWKYQHI 661
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RESULT 2
T08664
Toll protein-like receptor DKFZp547I0610.1 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08664
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16466
A;Accession: T08664
A;Molecule type: mRNA
A;Residues: 1-786 <POU>
A;Cross-references: UNIPROT:Q15399; EMBL:AL050262
A;Experimental source: fetal brain; clone DKFZp547I0610
C;Genetics:
A;Note: DKFZp547I0610.1

Query Match 10.7%; Score 465.5; DB 2; Length 786;
Best Local Similarity 24.8%; Pred. No. 3.6e-21;
Matches 203; Conservative 131; Mismatches 287; Indels 197; Gaps 33;

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Qy        120 SFSGLTNLENLVAVETKMTSLEGFHIGQL-----ISLKKLN---VAHNLIHSFKLPEYFS 171
Db         32 SKNGLIHVPKDLSQKTTILNISQNYISELWTSDILSLSKLRILIISHNRIQYLDISVFKF 91

Qy        172 NLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLS-LDLSLNPIDSIQ-AQAFQGI-RLH 228
Db         92 N-QELEYLDLSHNKLVKISC--------HPTVNLKHLDLSFNAFDALPICKEFGNMSQLK 142

Qy        229 ELTL-RSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEF 287
Db        143 FLGLSTTHLEKSSVLPIAHLNISKV---LLVLGETYGEKEDPG-------GLQDFNTESL 192

Qy        288 RLTYIN----HFSDDIYNLNCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRCHLKPF 343
Db        193 HIVFPTNKEFHF---------ILDVSVKTVANLELSNIKCVLEDSKCSYFLSILAKLQTN 243

Qy        344 PKLSLPFLKS----------------WTLTTNREDIS----FGQLALPSLRYLDLSRNAMS 384
Db        244 PKLSSLTLNNIETTWNSFIRILQLVWHTTVWYSSISNVKLQGQLDFRDFDYSGTSLKALS 303

Qy        385 FRGCCS----------YSDFGTNNLK--------------------YLDLSFNGVILMSA 414
Db        304 IHQVVSDVFGFPQSYIYEIFSNMNIKNFTVSGTRMVHMLCPSKISPFLHLDFSNNLLTDT 363

Qy        415 NFMG---LEELEYLDFQHSTLKKVTEFS-VFLSLEKLLYLDISYTNTKID-FDGIFLGLI 469
Db        364 VFENCGHLTELETLILQMNQLKELSKIAEMTTQMKSLQQLDISQNSVSYDEKKGDCSWTK 423

Qy        470 SLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTL-YRLQLLNMSHN 528
Db        424 SLLSLNMS---------SNILTDT------------------IFRCLPPRIKVLDL-HS 454

Qy        529 NLLFLDPSHYKQLYSLRTLDCSFNRIETSKGILQHFPKSLAVFNLTNNSVA--------- 579
Db        455 NKIKSIPKQVVKLEALQELNVAFNSLTDLPGCGSF--SSLSVLIIDHNSVSHPSADFFQS 512

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Qy        580 ---------------CICEYQNFLQWVKDQKMFLVNVEQM-----------KCASPIDM 612
Db        513 CQKMRSIKAGDNPFQCTCELGEFVK----------NIDQVSSEVLEGWPDSYKCDYPESY 562

Qy        613 KASLVLDFTNSTCYIYKTIISVSVVSVLVVATVAFLIYHFYFHL-----ILIAGCKKYSR 667
Db        563 RGTLLKDFHMSELSCNITLLIVTIVATMLVLAVTVTSLCIYLDLPWYLRMVCQWTQTRRR 622

Qy        668 GESI----------YDAFVIYSSQNEDWVRNELVKNLE-EGVPRFQLCLHYRDFIPGVAI 716
Db        623 ARNIPLEELQRNLQFHAFISYSGHDSFWVKNELLPNLEKEGM---QICLHERNFVPGKSI 679

Qy        717 AANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKV-EKS 775
Db        680 VENII-TCIEKSYKSIFVLSPNFVQSEWCHYELYFAHHNLFHEGSNSLILILLEPIPQYS 738

Qy        776 LLRQQVELYRLLSRNTYLEWEDNALGRHIFWRRLKKAL 813
Db        739 IPSSYHKLKSLMARRTYLEWPKEKSKRGLFWANLRAAI 776
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RESULT 3
A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A29943
R;Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A;Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, ap
A;Reference number: A29943; MUID:88135760; PMID:2449285
A;Accession: A29943
A;Molecule type: DNA
A;Residues: 1-1097 <HAS>
A;Cross-references: UNIPROT:P08953; GB:M19969; GB:J02682; NID:g158640; PIDN:AAA28941.1;
C;Genetics:
A;Gene: FlyBase:Tl
A;Cross-references: FlyBase:FBgn0003717
C;Keywords: transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-1097/Product: Toll protein #status predicted <MAT>

Query Match 9.2%; Score 397; DB 2; Length 1097;
Best Local Similarity 23.4%; Pred. No. 1e-16;
Matches 196; Conservative 119; Mismatches 302; Indels 222; Gaps 30;

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Qy         33 PNITYQCMDQNLSKIPHDI-PYSTK--NLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEI 89
Db        319 PELQILRLRAELQSLPGDLFEHSTQITNISLGDNLLKTLPATLLEHQVNLLSLDLSNNRL 378

Qy         90 ETIEDKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEG------- 142
Db        379 THLPDSLFAHTTNLTDLRLEDNLLTGISGDIFSNLGNLVTLVMSRNRLRTIDSRAFVSTN 438

Qy        143 ----FHI-----------------------GQLISLKKLNVAHNLIHSFKLPEYFSNLT 174
Db        439 GLRHLHLDHNDIDLQQPLLDIMLQTQINSPFGYMHGLLTLNLRNNSI-IFVYNDWKNTML 497

Qy        175 NLEHVDLSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGIRLHELTLRS 234
Db        498 QLRELDLSYNNISSLGYEDLAFLSQN-------------------------RLH------ 526

Qy        235 NFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINH 294
Db        527 ------------VNMTHNKIRRIALPE----------DVHLGEGYNN------NLVHVD- 557

Qy        295 FSDDIYNLNCLANISAMSFTGVHIKHIADVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSW 354
Db        558 LNDNPLVCDCTILWFIQLVRGVHKPQYS---RQFKLRTDRLV---------CSQPNVLEG 605

Qy        355 TLTTNREDISFGQLALPSLRYLDLSRNAMSFRGC-CSYSDFGTNNLKYLDLSFNGVILMS 413
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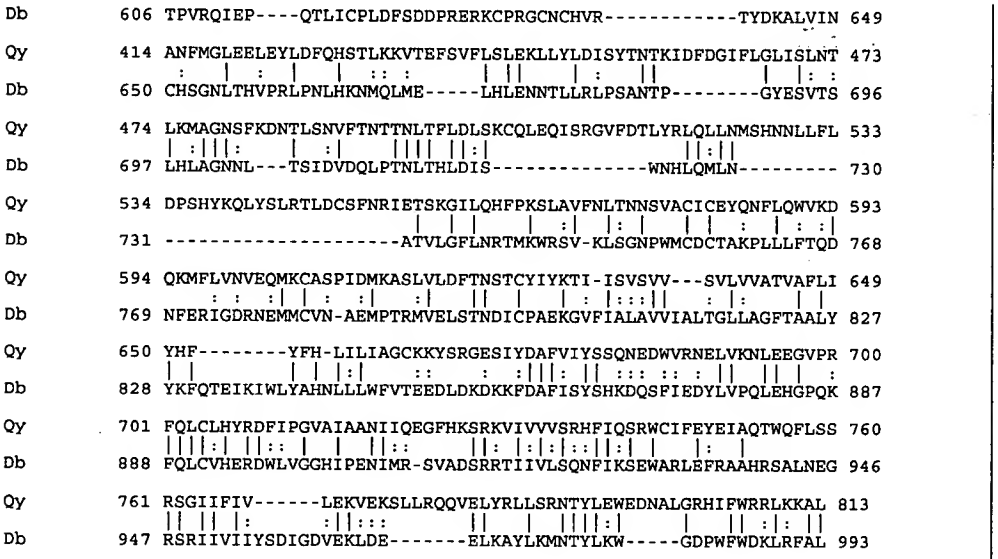
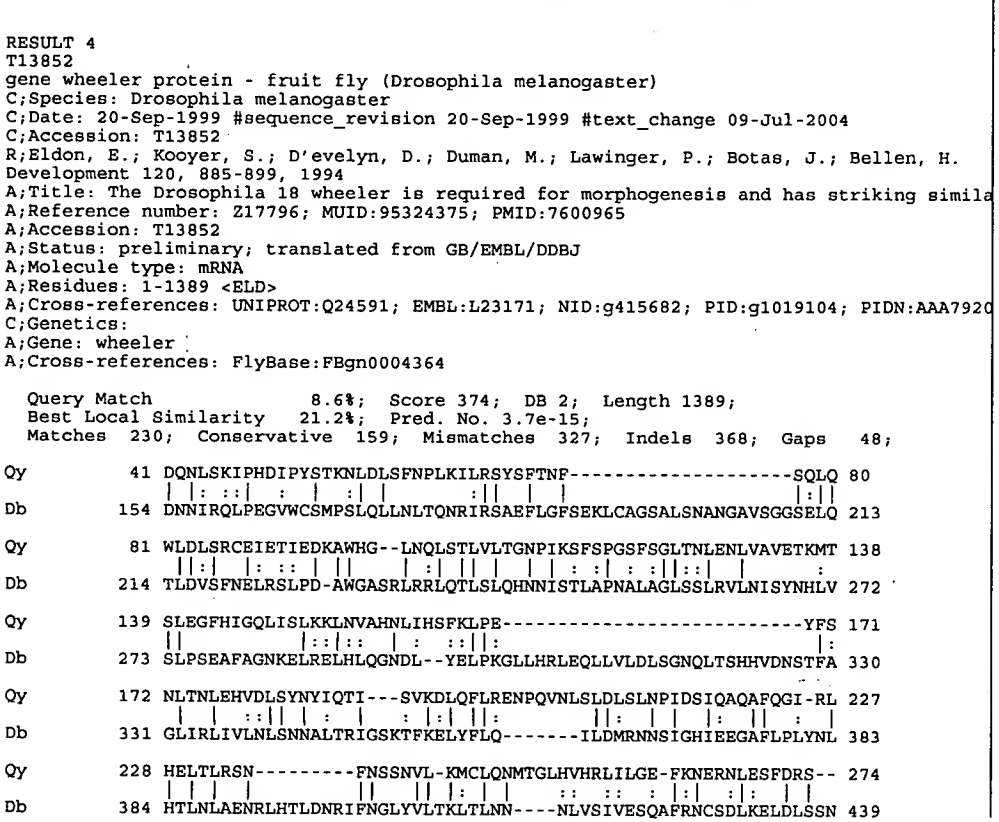
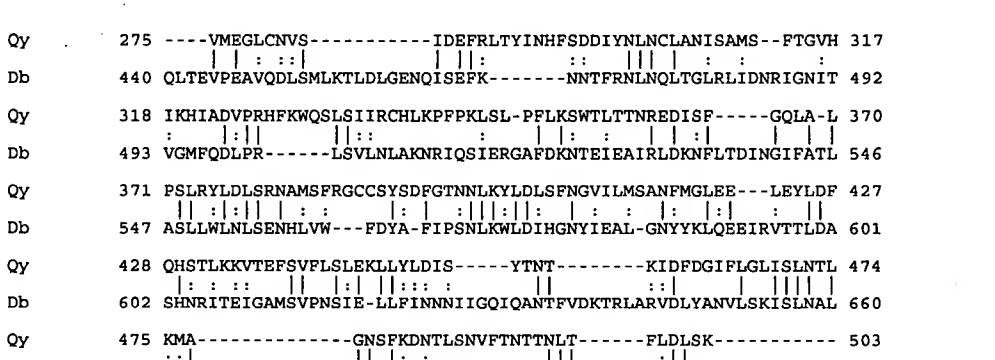


RESULT 4
T13852
gene wheeler protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13852
R;Eldon, E.; Kooyer, S.; D'evelyn, D.; Duman, M.; Lawinger, P.; Botas, J.; Bellen, H.
Development 120, 885-899, 1994
A;Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simila
A;Reference number: Z17796; MUID:95324375; PMID:7600965
A;Accession: T13852
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1389 <ELD>
A;Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:g415682; PID:g1019104; PIDN:AAA7920
C;Genetics:
A;Gene: wheeler
A;Cross-references: FlyBase:FBgn0004364

Query Match 8.6%; Score 374; DB 2; Length 1389;
Best Local Similarity 21.2%; Pred. No. 3.7e-15;
Matches 230; Conservative 159; Mismatches 327; Indels 368; Gaps 48;





RESULT 5
T13887
tlr protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13887
R;Chiang, C.; Beachy, P.A.
Mech. Dev. 47, 225-239, 1994
A;Title: Expression of a novel Toll-like gene spans the parasegment boundary and contrib
A;Reference number: Z17805; MUID:95151581; PMID:7848870
A;Accession: T13887
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1385 <CHI>
A;Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PIDN:AAB33383

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C;Genetics:
A;Cross-references: FlyBase:FBgn0004364
A;Note: tlr

  Query Match             8.6%;  Score 371;  DB 2;  Length 1385;
  Best Local Similarity   21.2%;  Pred. No. 5.6e-15;
  Matches  230;  Conservative  157;  Mismatches  329;  Indels  368;  Gaps   48;

Qy         41 DQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNF--------------------SQLQ  80
              | |: ::|  :  |  :| |        :||  |  |                      |:||
Db        154 DNNIRQLPEGVWCSMPSLQLLNLTQNRIRSAEFLGFSEKLCAGSALSNANGAVSGGSELQ  213

Qy         81 WLDLSRCEIETIEDKAWHG--LNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMT  138
               ||:|  |: :: | ||    | :| || |  | | : :| : :||::|  |     :
Db        214 TLDVSFNELRSLPD-AWGASRLRRLQTLSLQHNNISTLAPNALAGLSSLRVLNISYNHLV  272

Qy        139 SLEGFHIGQLISLKKLNVAHN--------LIHSF-----------KLPEY------FSNL  173
              ||          |::|::  |        |:|           :| ::      |: |
Db        273 SLPSEAPAGNKELRELHLQGNDLYELPKGLLHRLEQLLVLDLSGNQLTDHHVDNSTFAGL  332

Qy        174 TNLEHVDLSYNYIQTI---SVKDLQFLRENPQVNLSLDLSLNPIDSIQAQAFQGI-RLHE  229
              |  ::|| | :  |    : |:| ||:          ||:  | |  |:  ||  :  ||
Db        333 IRLIVLNLSNNALTRIGSKTFKELYFLQ-------ILDMRNNSIGHIEEGAFLPLYNLHT  385

Qy        230 LTLRSN---------FNSSNVL-KMCLQNMTGLHVHRLILGE-FKNERNLESFDRS----  274
              | |  |          ||   || |: | |     ::  ::  : |:|  :|:  | |
Db        386 LNLAENRLHTLDNRIFNGLYVLTKLTLNN----NLVSIVESQAFRNCSDLKELDLSSNQL  441

Qy        275 --VMEGLCNVS-----------IDEFRLTYINHFSDDIYNLNCLANISAMS--FTGVHIK  319
                | |   ::|           | ||:       ::   ||| |  :  :      : :
Db        442 TEVPEAAQDLSMLKTLDLGENQISEFK-------NNTFRNLNQLTGLRLIDNRIGNITVG  494

Qy        320 HIADVPRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTTNRE-----------DISFGQ  367
               |:||      ||::        |  :  ::      | |             ||:
Db        495 MFQDLPR------LSVLN-----LAKNRIQSIERGAFDKNTEIEAIRLDKKFLTDINGIF  543

Qy        368 LALPSLRYLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSANFMGLEE---LEY  424
              | || :|:|| | : :     |: |  :|||:||:  | :  :  |:  |:|   :
Db        544 ATLASLLWLNLSENHLVW---FDYA-FIPSNLKWLDIHGNYIEAL-GNYYKLQEEIRVTT  598

Qy        425 LDFQHSTLKKVTEFSVFLSLEKLLYLDIS-----YTNT--------KIDFDGIFLGLISL  471
              ||  |: : ::   ||  |:| ||::: :       ||        ::|     |  |||
Db        599 LDASHNRITEIGAMSVPNSIE-LLFINNNIIGQIQANTFVDKTRLARVDLYANVLSKISL  657

Qy        472 NTLKMA-------------GNSFKDNTLSNVFTNTTNLT------FLDLSK--------  503
              | |::|                || |: :           |||       :||
Db        658 NALRVAPVSAEKPVPEFYLGGNPFECDCSMEWLQRINNLTTRQHPHVVDLGNIECLMPHS  717

Qy        504 ------------------------------CQLEQ------------------------  508
                                           |: ||
Db        718 RSAPLRPLASLSASDFVCKYESHCPPTCHCCEYEQCECEVICPGNCSCFHDATWATNIVD  777

Qy        509 ------------ISRGVFDTLY-----------------RLQLLNMSHNNLLFLDPSHY  538
                         | : | | ||                 |: | :: :||: |
Db        778 CGRQDLAALPNRIPQDVSD-LYLDGNNMPELEVGHLTGRRNLRALYLNASNLMTLQNGSL  836

Qy        539 KQLYSLRTLDCSFNRIETSKG-----------------ILQHFPK-------SLAVFNLT  574
               || :|| |     |::   :|                :| |           || |  |
Db        837 AQLVNLRVLHLENNKLTALEGTEFRSLGLLRELYLHNNMLTHISNATFEPLVSLEVLRLD  896

Qy        575 NNSV---------------------ACIC-EYQNFLQWVKDQKMFLVNVEQMKCA-SPI  610
              || :                     :| | : :   |:| |  | : :   : |  : |
Db        897 NNRLSSLPHLQYRHSLQGLTLGRNAWSCRCQQLRELAQFVSDNAMVVRDAHDIYCLDAGI  956

Qy        611 DMKASLVLDFTNS-TC--------------------YIYKTIISVSVVSVLVVATVAFLI  649
                :  |: :  |   |                    |    : :| |:  | |  :   :
Db        957 KRELELIGNLANGPDCSDLLDASASNISSSQDLAGGYRLPLLAAVLVLIFLDVVLIIVFV 1016

Qy        650 YHFYFHLILIAG-----CK-KYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFQL  703
              :    : | |      |: ::     :||| :::| :: ::|   :   || | | |:|
Db       1017 FRESVRMWLFAHYGVRVCEPRFEDAGKLYDAIILHSEKDYEFVCRNIAAELEHGRPPFRL 1076

Qy        704 CLHYRDFIPGVAIAANIIQ--EGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSR  761
```

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              |:  ||  |     |: :|  ||   |||:|:|::|: : : |   |:  |    |  |
Db       1077 CIQQRDLPP----QASHLQLVEGARASRKIILVLTRNLLATEWNRIEFRNA----FHESL 1128

Qy        762 SGII--FIVLEK----------VEKSLLRQQVELYRLLSRNTYLEWEDNALGRHIFWRRL  809
               |:    :::|:          | |   : |   |||: : |            || :|
Db       1129 RGLAQKLVIIEETSVSAEAEDVAELSPYLKSVPSNRLLTCDRY-----------FWEKL 1176

Qy        810 KKAL 813
              : |:
Db       1177 RYAI 1180


RESULT 6
A29944
chaoptin precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: photoreceptor cell-specific membrane protein
C;Species: Drosophila melanogaster
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29944; A21123
R;Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
Cell 52, 291-301, 1988
A;Title: Chaoptin, a cell surface glycoprotein required for Drosophila photoreceptor cel
A;Reference number: A29944; MUID:88135762; PMID:3124963
A;Accession: A29944
A;Molecule type: DNA
A;Residues: 1-1134 <REI>
A;Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M1901
R;Zipursky, S.L.; Venkatesh, T.R.; Teplow, D.B.; Benzer, S.
Cell 36, 15-26, 1984
A;Title: Neuronal development in the Drosophila retina: monoclonal antibodies as molecul
A;Reference number: A21123; MUID:84106810; PMID:6420071
A;Accession: A21123
A;Molecule type: protein
A;Residues: 31-43,'HX',46-49,'H' <ZIP>
C;Genetics:
A;Gene: FlyBase:chp
A;Cross-references: FlyBase:FBgn0000313
A;Introns: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
C;Superfamily: chaoptin; leucine-rich alpha-2-glycoprotein repeat homology
C;Keywords: cell adhesion; glycoprotein; membrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-1134/Product: chaoptin #status predicted <MAT>
F;80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR
F;103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
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F;326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
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F;453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F;551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
F;577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
F;601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>
F;625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR23>
F;649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>
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F;708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>
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F;854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
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F;949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
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F;996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
F;1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
F;1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Query Match 7.4%; Score 320.5; DB 1; Length 1134;
Best Local Similarity 22.0%; Pred. No. 5.9e-12;
Matches 165; Conservative 111; Mismatches 236; Indels 237; Gaps 29;

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Qy         42 QNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNF-SQLQWLDLSRCEIETIEDKAWHGL 100
Db        148 RHLQKLRH--------LDLGYNHITHIQHDSFRGLEDSLQTLILRENCISQLMSHSFSGL 199

Qy        101 NQLSTLVLTGNPIKSFSPGSF-SGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAHN 159
Db        200 LILETLDLSGNNLFEIDPNVFVDGMPRLTRLLLTDNILSEIPYDALGPLKSLRTLDISHN 259

Qy        160 LIHSFKLPEYF----SNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPID 215
Db        260 VIWSLSGNETYEIKASTKLNLDNLHLEYNHIEVLPPNSFKYF---DTVNRTF-FDGNPIH 315

Qy        216 SIQAQAFQGIRLHELTLR----------SNFNSSNVLKMCLQNMTGLHVHRL----- 257
Db        316 TLREDAFKPARIREIYMRYCGLTNISPVAFDSLVNSLQILDLSGNNLTKLH-HKLFNNFD 374

Qy        258 IL-------GEFKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDIYNLNCLANISA 310
Db        375 VLRVISMRDNKIKIQKPTETFN-AVHYTLLKLDLSGDR--------NDPTNLQTLRNMTR 425

Qy        311 M-SFTGVHIKHIADV---PRHFK-----WQSLSIIRC-----------HLKPFPKLSLPF 350
Db        426 MRNMRSLSISRLGSSSVGPEDFKDFGVELEDLQITRASLSGIQSHAFKHVRGLKRLDF-- 483

Qy        351 LKSWTLTTNREDISFGQL----------------ALP--------SLRYLDLSRNAMSFR 386
Db        484 --SENGISSIENDAFHEIGHSLISLKMSHGYSGSALPAEPLRHLTSLQELDFSNNHISSM 541

Qy        387 GCCSYSDF-----------------GT------NNLKYLDLSFNGVILMSAN------- 415
Db        542 SDTSFHFLKNLRLLELHDNRIEQVLKGTFQGDIHSKLEEISLRFNHLTSISQHTFFDLEA 601

Qy        416 ------------------FMGLEELEYLDFQHSTLKKVTEFSVFLSLEKL---------- 447
Db        602 LRKLHLDDNKIDKIERRAFMNLDELEYLSLRGNKINNLADES-FQNLPKLEILDMAFNQL 660

Qy        448 ----------------------------------------LY------LDISYTNTK 458
Db        661 PNFNFDYFDQVGTLSNLNVNVSHNQIRQLMYNSSWSGRNEHGGMYHSNIKILDLSHNNIS 720

Qy        459 IDFDGIFL-GLISLNTLKMAGNSFKDNTLSNVFTNTTNLTFLDLSKCQLEQISRGVFDTL 517
Db        721 IIHPGYFRPAEISLTHLHLGYNSLM-NTTRDVFGNMPHLQWLDLSYNWIHELDFDAFKNT 779

Qy        518 YRLQLLNMSHNNLLFLDPSHYKQLYSLRTLDCSFN----------------RIETSKGIL 561
Db        780 KQLQLVFFGHNYLSDIPQDIFKPVQGLRIVDFSHNHLRGLPDNLFYNGGMEKLDVSHNMM 839

Qy        562 QHFPKS---------LAVFNLTNNSVACI 581
Db        840 LKIPSSSLSSLAALTLCELHLSNNFISTI 868
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RESULT 7
T15864
hypothetical protein C56E6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15864
R;Fulton, L.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C56E6.
A;Reference number: S69019
A;Accession: T15864
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1066 <FUL>
A;Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:g1055114; PID:g1055120; PIDN:AAA810
C;Genetics:
A;Gene: CESP:C56E6.6
A;Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3; 9

Query Match 7.0%; Score 303; DB 2; Length 1066;
Best Local Similarity 22.8%; Pred. No. 6.6e-11;
Matches 145; Conservative 110; Mismatches 260; Indels 120; Gaps 23;

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Qy         34 NITYQCMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIE 93
Db        131 NITH-LMDTNEVTFESEMKVILRN-----NKVRRLDKHSFRSFRKIRELDISYNQIQTVE 184

Qy         94 DKAWHGLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLISLKK 153
Db        185 DSSFETVGHMQSLDLSYNRIAYLPRGM------LKNFAK----------------TLKT 221

Qy        154 LNVAHNLIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSLDLSLNP 213
Db        222 LKLAENMIHA--TPEALRDLRNLTHLNLNGNKLNRI---DGDVLKGCTDTLVELFIANNY 276

Qy        214 IDSIQAQAFQGIR-LHELTLRSNFNSSNVLKMCLQNMTGL---------HVHRLIL--GE 261
Db        277 LEHIPHGVLSGMKQLEHLDISKN------KIMSLKKPTSLLSITKEETSTVRRLNLAGNR 330

Qy        262 FKNERNLESFDRSVMEGLCNVSIDEFRLTYINHFSDDIYNLNCLANISAMSFTGVHIKHI 321
Db        331 INNMSDYLIFEHMPLLTYVDVSFNRIRFISPRVFEK-------LKNLESLFLQNNQLAHF 383

Qy        322 ADVPRHFKWQSLSIIRCHLKPFPKLS---LPFLKSWTLTTNREDI----SFGQLALPSLR 374
Db        384 PSLFRLDKLRHLMLDNNQIQKIDNFSLADLPKLQHLSLAGNQLDIITENMFGSSSSSELK 443

Qy        375 YLDLSRNAMSFRGCCSYSDFGTNNLKYLDLSFNGV-ILMSANFMGLEELEYLDFQHSTLK 433
Db        444 SLNLAHNKIHSISSRSFSDL--DNLQQLRLSHNNIRTITSMTFSNLRNLRYLDLSHNRII 501

Qy        434 KVTEFSVF-LSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAGNSFK---------- 482
Db        502 KILPSALYQLPALDVLHLDHNNLN-EIDRDA-FRSFSDLQSLKLSHNAFRRFSCEFLGSI 559

Qy        483 ---------DNTLS--NVFTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLL 531
Db        560 SQVHQLDLSSNQINEIDIFCIARGIRKLSLASNSVEKINRKLLQDATELTSIDISHNGII 619

Qy        532 FLDPSHYKQLYSLRTLDCSFNRIETSKGILQHFPKSLAVFNLTNNSVACICEYQNFLQWV 591
Db        620 DVDSDAFCECRKLSHIKLSHNYIR---------------NLWKGTRVCI-------PWI 656

Qy        592 KDQKMFLV----NVEQMKCASPIDMKASLVLDFTN 622
Db        657 SHLTTFCFFTKEHLERTISFSYIIVDSSQLTSFGN 691
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RESULT 8
JC6128
insulin-like growth factor binding complex acid labile chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: JC6128
R;Boisclair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T.
Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996
A;Title: Organization and chromosomal localization of the gene encoding the mouse acid l
A;Reference number: JC6128; MUID:96413591; PMID:8816745
A;Accession: JC6128

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A;Molecule type: DNA
A;Residues: 1-603 <BOI>
A;Cross-references: UNIPROT:P70389; GB:U66900; NID:g1621612; PIDN:AAB17270.1; PID:g16216
C;Comment: This protein is a serum protein and it is of the ternary complex in the physi
C;Genetics:
A;Gene: als
A;Map position: 17

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  Best Local Similarity   24.9%;  Pred. No. 3.8e-11;
  Matches  160;  Conservative   87;  Mismatches  240;  Indels  155;  Gaps   25;

Qy         39 CMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWH 98
Db         60 CSSRNLTQLPDGIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALL 119

Qy         99 GLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAH 158
Db        120 GLQNLYHLHLERNLLRSLAAGLFRHTPSLASLSLGNNLLGRLEEGLFRGLSHLWDLNLGW 179

Qy        159 NLIHSFKLPE-YFSNLTNLEHVDLSYN---YIQTISVKDLQFLRENPQVNLSLDLSLNPI 214
Db        180 NSL--VVLPDTVFQGLGNLHELVLAGNKLTYLQPALLCGLGELRE-------LDLSRNAL 230

Qy        215 DSIQAQAFQGI-RLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLESFDR 273
Db        231 RSVKANVFIHLPRLQKLYLD------------RNLITAVAPRAFLG------------ 264

Qy        274 SVMEGLCNVSIDEFRLTYINHFSDDIYNLNCLANISAMSF---TGVHIKHIAD------V 324
Db        265 --MKAL--------RWLDLSH--------NRVAGLLEDTFPGLLGLHVLRLAHNAITSLR 306

Qy        325 PRHFKWQSLSIIRCHLKPFPKLSLPFLKSWTLTTNREDISFGQL------ALPSLRYLDL 378
Db        307 PRTFK----------------DLHFLEELQLGHNR----IRQLGEKTFEGLGQLEVLTL 345

Qy        379 SRNAMSFRGCCSYSDFGTNNLKYLDLSFNGVILMSAN-FMGLEELEYLDFQHSTLKKVTE 437
Db        346 NDNQIHEVKVGAF--FGLFNVAVMNLSGNCLRSLPEHVFQGLGRLHSLHLEHSCLGRIRL 403

Qy        438 FSVFLSLEKLLYLDISYTNTKIDFDGIFLGLISLNTLKMAGNSFKDNTLSNV----FTNT 493
Db        404 HT------------------------FAGLSGLRRLFL-----RDNSISSIEEQSLAGL 433

Qy        494 TNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSLRTLDCSFNR 553
Db        434 SELLELDLTANQLTHLPRQLFQGLGQLEYLLLSNNQLTMLSEDVLGPLQRAFWLDLSHNR 493

Qy        554 IET-SKGILQHFPKSLAVFNLTNNSVACICEYQNFLQWVKDQKMFLVNVEQMKCASPIDM 612
Db        494 LETPAEGLFSSLGR-LRYLNLRNNSL------QTFVPQPGLERLWL-DANPWDCSCPLKA 545

Qy        613 KASLVLD-------FTNSTC--------YIYKTIISVSVVSV 639
Db        546 LRDFALQNPGVVPRFVQTVCEGDDCQPVYTYNNITCAGPANV 587


RESULT 9
JC5239
insulin-like growth factor acid-labile chain - baboon
C;Species: Papio sp. (baboon)
C;Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C;Accession: JC5239
R;Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-lik
A;Reference number: JC5239; MUID:97040714; PMID:8886027
A;Contents: liver
A;Accession: JC5239
A;Molecule type: mRNA
A;Residues: 1-605 <DEL>
C;Comment: This factor is structurally related to proinsulin and have insuline-like meta

  Query Match             6.9%;  Score 300.5;  DB 2;  Length 605;
  Best Local Similarity   23.9%;  Pred. No. 4.4e-11;
  Matches  155;  Conservative   81;  Mismatches  238;  Indels  175;  Gaps   20;

Qy         39 CMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWH 98
Db         60 CSSRNLTRLPDGIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGSLEPQALL 119

Qy         99 GLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAH 158
Db        120 GLENLCHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLEDGLFEGLGNLWDLNLGW 179

Qy        159 NLIHSFKLPE-YFSNLTNLEHVDLSYN---YIQTISVKDLQFLRENPQVNLSLDLSLNPI 214
Db        180 NSL--AVLPDAAFRGLGGLRELVLAGNRLAYLQPALFSGLAELRE-------LDLSRNAL 230

Qy        215 DSIQAQAFQGI-RLHELTLRSNFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLESFDR 273
Db        231 RAIKANVFAQLPRLQKLYL------------------------------DRNL----- 253

Qy        274 SVMEGLCNVSIDEFRLTYINHFSDDIYNLNCLANISAMSFTGVHIKHIADVPRHFKWQSL 333
Db        254 ------------------------------IAAVAPGAFLGL---------KALRWLDL 273

Qy        334 SIIRCHLKPFPKLSLPFLKSWTLTTNR-----EDISFGQLALPSLRYLDLSRNAMSFRGC 388
Db        274 S----------------------HNRVAGLLEDTFPGLL---GLRVLRLSHNAIASLRP 307

Qy        389 CSYSDFGTNNLKYLDLSFNGV-ILMSANFMGLEELEYLDFQHSTLKKVTEFSVFLSLEKL 447
Db        308 RTFEDL--HFLEELQLGHNRIRQLAERSFEGLGQLEVLTLDHNQLQEV-KVGAFLGLTNV 364

Qy        448 LYLDISYTNTKIDFDGIFLGLISLNTLKMAGNS------------------FKDNTLSN 488
Db        365 AVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFAGLSGLRRLFLKDNGLVG 424

Qy        489 V----FTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSHNNLLFLDPSHYKQLYSL 544
Db        425 IEEQSLWGLAELLELDLTSNQLTHLPHQLFQGLGKLEYLLLSHNRLAELPADALGPLQRA 484

Qy        545 RTLDCSFNRIETSKGILQHFPKSLAVFNLTNNSVACICEYQNFLQ--WVKDQKMFLVNVE 602
Db        485 FWLDVSHNRLEALPGSLLASLGRLRYLNLRNNSLRTFTPQPPGLERLWLEG--------N 536

Qy        603 QMKCASPID-------MKASLVLDFTNSTC---------YIYKTIISVS 635
Db        537 PWDCSCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPVYTYNNITCAS 585


RESULT 10
JC1282
insulin-like growth factor-binding protein acid labile chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1282
R;Dai, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A;Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A;Reference number: JC1282; MUID:93038676; PMID:1384485
A;Accession: JC1282
A;Molecule type: mRNA
A;Residues: 1-603 <DAI>
A;Cross-references: UNIPROT:P35859; GB:S46785; NID:g258002; PIDN:AAB23770.2; PID:g570593
A;Experimental source: liver
A;Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205 a
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-603/Product: insulin-like growth factor binding protein, acid labile chain #status p
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

  Query Match             6.7%;  Score 290.5;  DB 2;  Length 603;
  Best Local Similarity   22.4%;  Pred. No. 1.8e-10;
  Matches  152;  Conservative   99;  Mismatches  204;  Indels  223;  Gaps   26;
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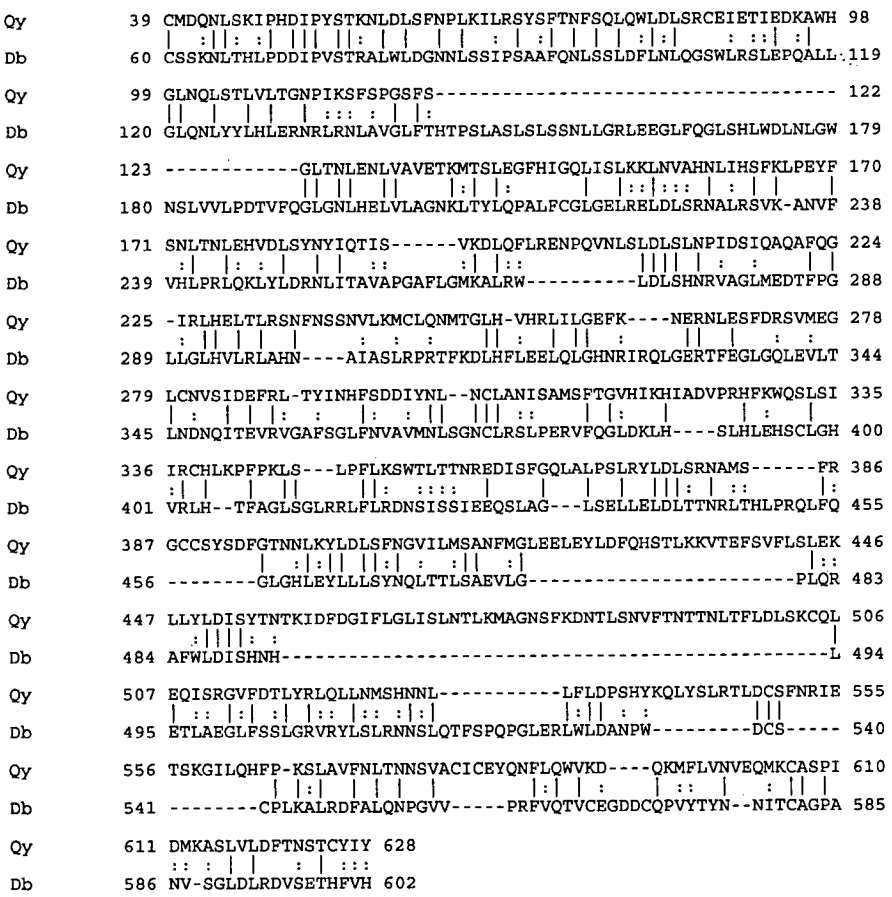
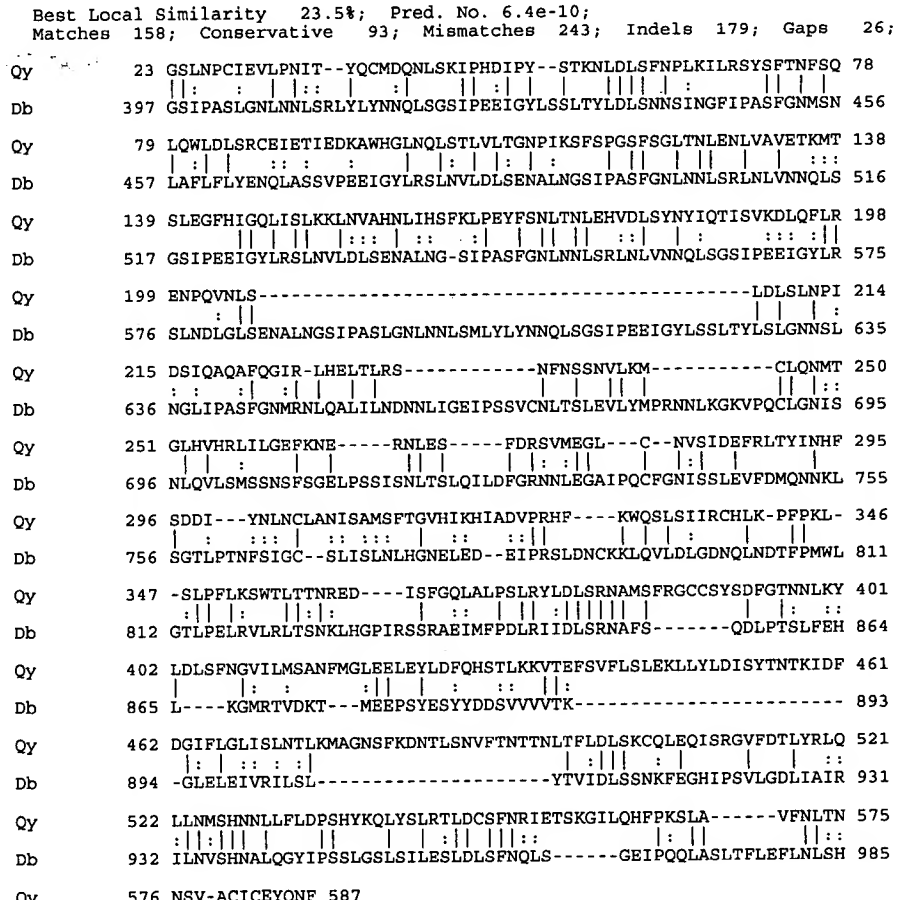


RESULT 11
T10504
disease resistance protein Cf-2.1 - currant tomato
C;Species: Lycopersicon pimpinellifolium (currant tomato)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10504; T10515
R;Dixon, M.S.; Jones, D.A.; Keddie, J.S.; Thomas, C.M.; Harrison, K.; Jones, J.D.
Cell 84, 451-459, 1996
A;Title: The tomato Cf-2 disease resistance locus comprises two functional genes encodin
A;Reference number: Z17062; MUID:96190812; PMID:8608599
A;Accession: T10504
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1112 <DIX>
A;Cross-references: UNIPROT:Q41397; EMBL:U42444; NID:g1184074; PIDN:AAC15779.1; PID:g118
A;Experimental source: cultivar Cf 2
A;Accession: T10515
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1066,'I',1068-1085,'E',1087-1110,'R',1112 <DI2>
A;Cross-references: EMBL:U42445; NID:g1184076; PIDN:AAC15780.1; PID:g1184077
A;Experimental source: cultivar Cf 2

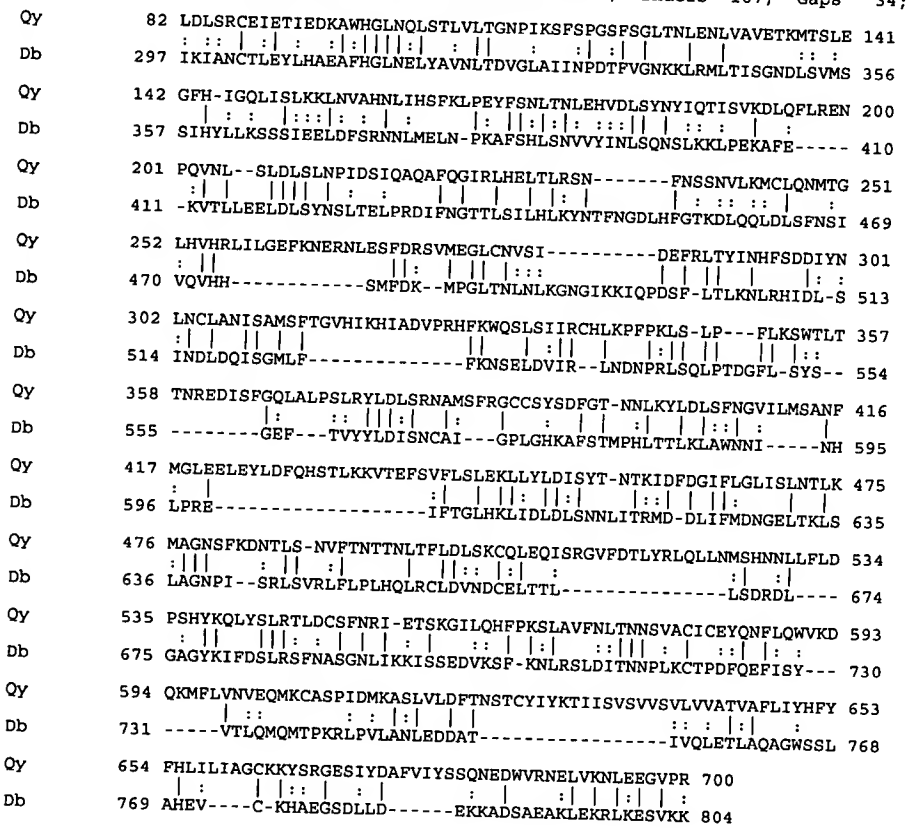
Query Match 6.6%; Score 287.5; DB 2; Length 1112;



RESULT 12
T13174
gp150 protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13174
R;Tian, S.S.; Zinn, K.
J. Biol. Chem. 269, 28478-28486, 1994
A;Title: An adhesion molecule-like protein that interacts with and is a substrate for
A;Reference number: Z17630; MUID:95050638; PMID:7961789
A;Accession: T13174
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1051 <TIA>
A;Cross-references: UNIPROT:Q24007; EMBL:U15220; NID:g595859; PID:g595860; PIDN:AAA617
A;Experimental source: strain Oregon R
C;Genetics:
A;Cross-references: FlyBase:FBgn0013272
A;Map position: 2

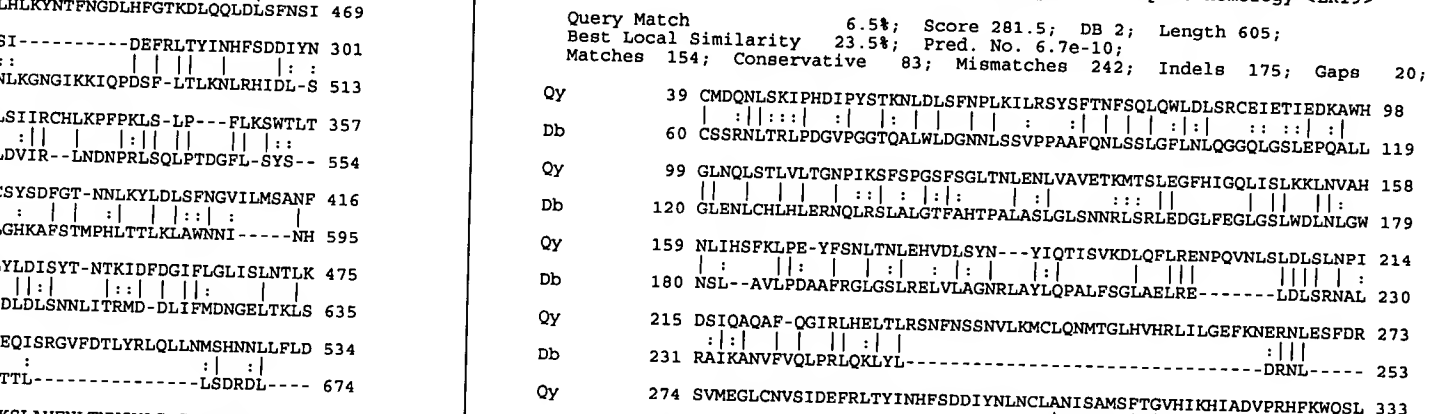
Query Match 6.6%; Score 285.5; DB 2; Length 1051;

Best Local Similarity 24.0%; Pred. No. 7.9e-10;
Matches 155; Conservative 114; Mismatches 211; Indels 167; Gaps 34;



RESULT 13
A41915
insulin-like growth factor-binding complex acid-labile chain precursor - human
N;Alternate names: Acid-Labile Subunit (ALS)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A41915
R;Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
Mol. Endocrinol. 6, 870-876, 1992
A;Title: Structure and functional expression of the acid-labile subunit of the insulin-l
A;Reference number: A41915; MUID:92357025; PMID:1379671
A;Accession: A41915
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-605 <LEO>
A;Cross-references: UNIPROT:P35858; GB:M86826; NID:g184807; PIDN:AAA36047.1; PID:g184808
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:110171)
F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F;339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F;363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F;387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F;435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F;459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
F;483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>
F;507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>

Query Match 6.5%; Score 281.5; DB 2; Length 605;
Best Local Similarity 23.5%; Pred. No. 6.7e-10;
Matches 154; Conservative 83; Mismatches 242; Indels 175; Gaps 20;



RESULT 14
B36665
slit protein 2 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
C;Accession: B36665
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and con
A;Reference number: A36665; MUID:91099665; PMID:2176636
A;Accession: B36665

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1469 <ROT>
A;Cross-references: GB:X53959
C;Genetics:
A;Gene: FlyBase:sli
A;Cross-references: FlyBase:FBgn0003425
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F;1028-1061/Domain: EGF homology <EGF>
F;1068-1099/Domain: EGF homology <EGF2>
F;1115-1148/Domain: EGF homology <EGF1>

  Query Match             6.4%;  Score 279;  DB 2;  Length 1469;
  Best Local Similarity   21.6%;  Pred. No. 3.1e-09;
  Matches  151;  Conservative   85;  Mismatches  238;  Indels  224;  Gaps   21;

Qy        39 CMDQNLSKIPHDIPYSTKNLDLSFNPLKILRSYSFTNFSQLQWLDLSRCEIETIEDKAWH 98
             | :::|: :|  :|  | :: |  | :  |   ||::| :|: :|||   |  |    |
Db       308 CREKSLTSVPVTLPDDTTDVRLEQNFITELPPKSFSSFRRLRRIDLSNNNISRIAHDALS 367

Qy        99 GLNQLSTLVLTGNPIKSFSPGSFSGLTNLENLVAVETKMTSLEGFHIGQLISLKKLNVAH 158
             || ||:|||| || ||    | | || :|  |:   ::: :        | ||  |::
Db       368 GLKQLTTLVLYGNKIKDLPSGVFKGLGSLRLLLLNANEISCIRKDAFRDLHSLSLLSLYD 427

Qy       159 NLIHSFKLPEYFSNLTNLEHVDLSYNYIQTISVKDLQFLRENPQVNLSLDLSLNPIDSIQ 218
             | | |      |  : ::: | |: |    |   :|::| :        |  |||::
Db       428 NNIQSL-ANGTFDAMKSMKTVHLAKN--PFICDCNLRWLADY--------LHKNPIETSG 476

Qy       219 AQAFQGIRLHELTLRS----NFNSSNVLKMCLQNMTGLHVHRLILGEFKNERNLESFDRS 274
             |:     |:|   : |     | |                        ||          |
Db       477 ARCESPKRMHRRRIESLREEKFKCS-----------------WGEL----------RM 507

Qy       275 VMEGLCNVSIDEFRLTYINHFSDDIYNLNCLANISAMSFTGVHIKHI-ADVPRHFKWQSL 333
              : | | :  |                |     : :  ||  :| |  |:| |
Db       508 KLSGECRMDSD-------------CPAMCHCEGTTVDCTGRRLKEIPRDIPLH------ 547

Qy       334 SIIRCHLKPFPKLSLPFLKSWTLTTNREDIS-------FGQLALPSLRYLDLSRNAMSFR 386
                          :  |  |  ::         ||:  || |  |:| || ::
Db       548 ------------------TTELLLNDNELGRISSDGLFGR--LPHLVKLELKRNQLT-- 584

Qy       387 GCCSYSDFGTNNLKYLDLSFNGVILMSAN-FMGLEELEYLDFQHSTLKKVTEFSVFLSLE 445
                              |:     | | |   :: |    : :|:::  :|| | |
Db       585 --------------------GI---EPNAFEGASHIQELQLGENKIKEISN-KMFLGLH 619

Qy       446 KLLYLDISYTNTKIDFDGIFLGLISLNTLKMAGNSF---------------------- 481
              :|  |::          | |  | || :| :| | |
Db       620 QLKTLNLYDNQISCVMPGSFEHLNSLTSLNLASNPFNCNCHLAWFAECVRKKSLNGGAAR 679

Qy       482 ------------KD-----------------------------------NTLSNV--- 489
                                                                  | | :
Db       680 CGAPSKVRDVQIKDLPHSEFKCSSENSEGCLGDGYCPPSCTCTGTVVACSRNQLKEIPRG 739

Qy       490 ----------------------FTNTTNLTFLDLSKCQLEQISRGVFDTLYRLQLLNMSH 527
                                  :  :|| |||| |:  :|   |  | :|  | :|:
Db       740 IPAETSELYLESNEIEQIHYERIRHLRSLTRLDLSNNQITILSNYTFANLTKLSTLIISY 799

Qy       528 NNLLFLDPSHYKQLYSLRTLDCSFNRIE-TSKGILQHFPKSLAVFNLTNNSVACICEYQN 586
             | |  |        | :|| :    |||    :|  :   |||     | :| : | |  :
Db       800 NKLQCLQRHALSGLNNLRVVSLHGNRISMLPEGSFEDL-KSLTHIALGSNPLYCDCGLKW 858

Qy       587 FLQWVKDQKMFLVNVEQMKCASPIDMKASLVLDFTNST 624
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Db       859 FSDWI---KLDYVEPGIARCAEPEQMKDKLILSTPSSS 893


RESULT 15
A36665
slit protein 1 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
C;Accession: A36665; A31640; S13523
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and
A;Reference number: A36665; MUID:91099665; PMID:2176636
A;Accession: A36665
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1480 <ROT>
A;Cross-references: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g8615
R;Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
Cell 55, 1047-1059, 1988
A;Title: slit: An EGF-homologous locus of D. melanogaster involved in the development
A;Reference number: A31640; MUID:89077533; PMID:3144436
A;Accession: A31640
A;Molecule type: DNA
A;Residues: 881-1182,'G',1185-1404,'GT',1463-1464,'YHA' <RO2>
A;Cross-references: GB:M23543; NID:g340939; PID:g514357
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A;Gene: FlyBase:sli
A;Cross-references: FlyBase:FBgn0003425
A;Introns: 1351/3
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotei
C;Keywords: alternative splicing; growth factor
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F;1028-1061/Domain: EGF homology <EGF>
F;1068-1099/Domain: EGF homology <EGF2>
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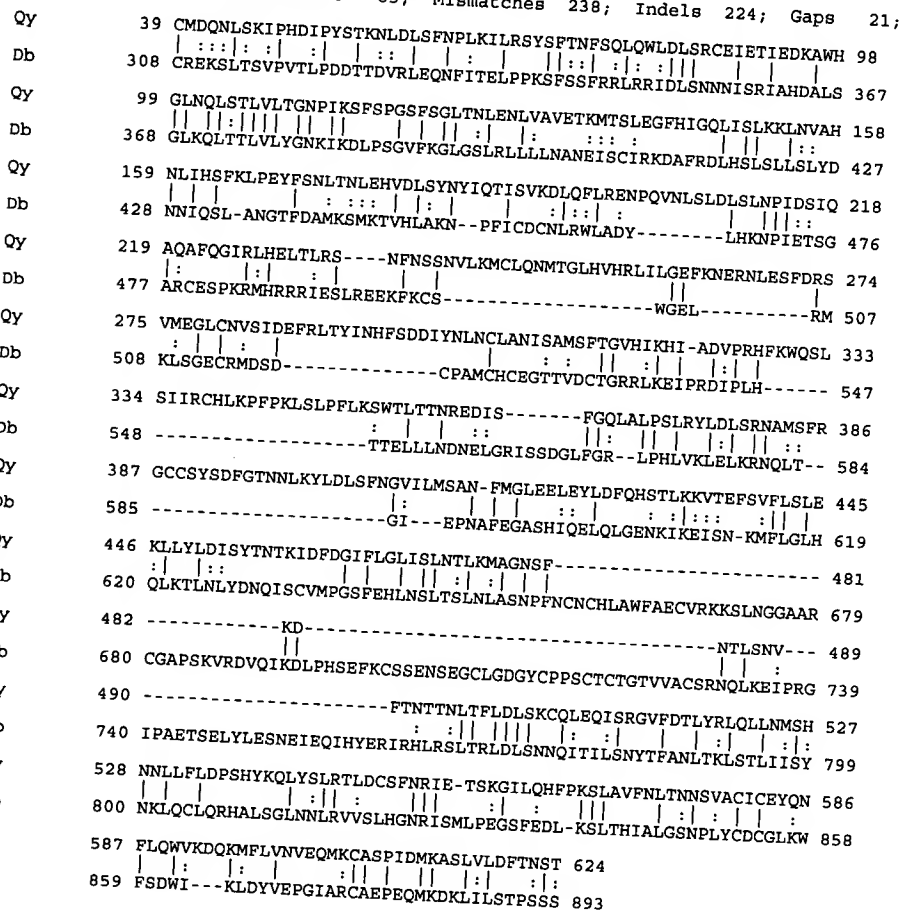
F;1115-1148/Domain: EGF homology <EGF1>

Query Match 6.4%; Score 279; DB 2; Length 1480;
Best Local Similarity 21.6%; Pred. No. 3.2e-09;
Matches 151; Conservative 85; Mismatches 238; Indels 224; Gaps 21;



Search completed: March 12, 2005, 19:57:06
Job time : 27.5445 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:15:31 ; Search time 87.4 Seconds
(without alignments)
3712.721 Million cell updates/sec

Title: US-09-396-985B-98
Perfect score: 4355
Sequence: 1 MMSASRLAGTLIPAMAFLSC.....SWNPEGTVGTGCNWQEATSI 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4355	100.0	839	6	ABU04773	Abu04773 Human exp
2	4355	100.0	839	6	ABU04774	Abu04774 Human exp
3	4355	100.0	839	6	ABU04775	Abu04775 Human exp
4	4355	100.0	839	7	ADC78785	Adc78785 Human PRO
5	4355	100.0	839	7	ADD48826	Add48826 Human Pro
6	4335.5	99.6	837	2	AAW86361	Aaw86361 Human DNA
7	4335.5	99.6	837	5	AAE16102	Aae16102 Human DNA
8	4335.5	99.6	837	6	ABU04776	Abu04776 Human exp
9	4328.5	99.4	837	5	AAE16116	Aae16116 Human DNA
10	4178	95.9	808	8	ADO57782	Ado57782 Chimpanze
11	4167	95.7	808	8	ADO57785	Ado57785 Gorilla t
12	4164	95.6	808	8	ADO57803	Ado57803 Chimpanze
13	4141	95.1	799	2	AAW86352	Aaw86352 Human DNA
14	4141	95.1	799	5	AAE16093	Aae16093 Human DNA
15	4141	95.1	799	5	ABB83162	Abb83162 Human Tol
16	4141	95.1	799	6	ABR42963	Abr42963 Human Tol
17	4141	95.1	799	7	ADB39121	Adb39121 Human tol
18	4141	95.1	799	8	ADP56656	Adp56656 Human Tol
19	4141	95.1	799	8	ADP48597	Adp48597 Human Tol
20	4040	92.8	801	8	ADO57788	Ado57788 Gibbon to
21	3918	90.0	795	8	ADO57791	Ado57791 Rhesus mo
22	3892	89.4	795	8	ADO57800	Ado57800 Hamadryas
23	3819	87.7	801	8	ADO57797	Ado57797 Squirrel
24	3683.5	84.6	738	8	ADP29455	Adp29455 Human sec
25	3501	80.4	745	8	ADO57794	Ado57794 White-fac
26	1090	25.0	208	3	AAY88059	Aay88059 Human Tol
27	919	21.1	178	8	ADN12270	Adn12270 IL-1R/TLR
28	785	18.0	179	7	ADC42707	Adc42707 Murine To
29	629.5	14.5	661	2	AAW28510	Aaw28510 Product o
30	629.5	14.5	661	2	AAW87556	Aaw87556 B cell su
31	629.5	14.5	661	7	ADC38652	Adc38652 Human sec
32	629.5	14.5	661	7	ADF69098	Adf69098 Human MP5
33	628.5	14.4	650	3	AAY82527	Aay82527 Human RP1
34	615.5	14.1	661	2	AAW47274	Aaw47274 Human B-c
35	603.5	13.9	784	2	AAW86350	Aaw86350 Human DNA
36	603.5	13.9	784	5	AAE16091	Aae16091 Human DNA
37	603.5	13.9	784	5	ABB83161	Abb83161 Human Tol
38	603.5	13.9	784	8	ADN02005	Adn02005 Human inf
39	602.5	13.8	784	2	AAY05869	Aay05869 Human Tol
40	602.5	13.8	784	6	ABU61956	Abu61956 Human Tol
41	602.5	13.8	784	7	ADL15005	Adl15005 Human Tol
42	602.5	13.8	784	8	ADP56652	Adp56652 Human Tol
43	602.5	13.8	784	8	ADP48593	Adp48593 Human Tol
44	602.5	13.8	784	8	ADP23787	Adp23787 PRO polyp
45	602.5	13.8	784	8	ADQ39727	Adq39727 Human myo

ALIGNMENTS

RESULT 1
ABU04773
ID ABU04773 standard; protein; 839 AA.
XX
AC ABU04773;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1439.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1439; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a

```
CC   mammal an immunogenic response directed against any of the purified
CC   polypeptide. The purified polypeptide, or the antibody that binds to this
CC   polypeptide, is useful for treating cancer. The polypeptide is also
CC   useful for identifying compounds that binds to a naturally processed
CC   class I or class II MHC-binding polypeptide. The polypeptides and
CC   polynucleotides are particularly useful for treating or preventing
CC   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC   lymphoma or leukaemia. These are also useful for screening agents for
CC   treating the above mentioned diseases. This sequence represents an
CC   expressed protein tag (EPT) isolated from human tissue for translational
CC   profiling. Note: This sequence does not appear in the printed
CC   specification but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 839 AA;

  Query Match             100.0%;  Score 4355;  DB 6;  Length 839;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180
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Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480
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Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540
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Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600
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Qy        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720

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Qy        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
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RESULT 2
ABU04774
ID   ABU04774 standard; protein; 839 AA.
XX
AC   ABU04774;
XX
DT   29-JAN-2003  (first entry)
XX
DE   Human expressed protein tag (EPT) #1440.
XX
KW   Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW   protease; protease inhibitor; transporter; cytoskeletal protein;
KW   receptor; transcription factor; cancer; MHC;
KW   major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW   adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200278524-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US009671.
XX
PR   28-MAR-2001; 2001US-0279495P.
PR   21-MAY-2001; 2001US-0292544P.
PR   08-AUG-2001; 2001US-0310801P.
PR   01-OCT-2001; 2001US-0326370P.
PR   04-DEC-2001; 2001US-0336780P.
PR   20-FEB-2002; 2002US-0358985P.
XX
PA   (ZYCO-) ZYCOS INC.
XX
PI   Chicz RM,  Tomlinson AJ,  Urban RG;
XX
DR   WPI; 2003-040607/03.
XX
PT   New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT   cytoskeletal proteins, receptors or transcription factors), useful for
PT   treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT   leukemia.
XX
PS   Example 2; SEQ ID NO 1440; 134pp; English.
XX
CC   The invention describes a purified polypeptide, which comprises a
CC   fragment of a kinase, phosphatase, protease, protease inhibitor,
CC   transporter, cytoskeletal protein, receptor or transcription factor. The
CC   polypeptide is useful as an immunogenic composition for eliciting in a
CC   mammal an immunogenic response directed against any of the purified
CC   polypeptide. The purified polypeptide, or the antibody that binds to this
CC   polypeptide, is useful for treating cancer. The polypeptide is also
CC   useful for identifying compounds that binds to a naturally processed
CC   class I or class II MHC-binding polypeptide. The polypeptides and
CC   polynucleotides are particularly useful for treating or preventing
CC   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC   lymphoma or leukaemia. These are also useful for screening agents for
CC   treating the above mentioned diseases. This sequence represents an
CC   expressed protein tag (EPT) isolated from human tissue for translational
CC   profiling. Note: This sequence does not appear in the printed
CC   specification but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 839 AA;

  Query Match             100.0%;  Score 4355;  DB 6;  Length 839;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60
```

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Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420
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Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

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Qy        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540
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Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660

Qy        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720

Qy        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780

Qy        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
```

```
RESULT 3
ABU04775
ID   ABU04775 standard; protein; 839 AA.
XX
AC   ABU04775;
XX
DT   29-JAN-2003  (first entry)
XX
DE   Human expressed protein tag (EPT) #1441.
XX
KW   Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW   protease; protease inhibitor; transporter; cytoskeletal protein;
KW   receptor; transcription factor; cancer; MHC;
KW   major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW   adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200278524-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US009671.
XX
PR   28-MAR-2001; 2001US-0279495P.
PR   21-MAY-2001; 2001US-0292544P.
PR   08-AUG-2001; 2001US-0310801P.
PR   01-OCT-2001; 2001US-0326370P.
PR   04-DEC-2001; 2001US-0336780P.
PR   20-FEB-2002; 2002US-0358985P.
XX
PA   (ZYCO-) ZYCOS INC.
XX
PI   Chicz RM,  Tomlinson AJ,  Urban RG;
XX
DR   WPI; 2003-040607/03.
XX
PT   New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT   cytoskeletal proteins, receptors or transcription factors), useful for
PT   treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT   leukemia.
XX
PS   Example 2; SEQ ID NO 1441; 134pp; English.
XX
CC   The invention describes a purified polypeptide, which comprises a
CC   fragment of a kinase, phosphatase, protease, protease inhibitor,
CC   transporter, cytoskeletal protein, receptor or transcription factor. The
CC   polypeptide is useful as an immunogenic composition for eliciting in a
CC   mammal an immunogenic response directed against any of the purified
CC   polypeptide. The purified polypeptide, or the antibody that binds to this
CC   polypeptide, is useful for treating cancer. The polypeptide is also
CC   useful for identifying compounds that binds to a naturally processed
CC   class I or class II MHC-binding polypeptide. The polypeptides and
CC   polynucleotides are particularly useful for treating or preventing
CC   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC   lymphoma or leukaemia. These are also useful for screening agents for
CC   treating the above mentioned diseases. This sequence represents an
CC   expressed protein tag (EPT) isolated from human tissue for translational
CC   profiling. Note: This sequence does not appear in the printed
CC   specification but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 839 AA;
```

```
  Query Match           100.0%;  Score 4355;  DB 6;  Length 839;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660

Qy        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720

Qy        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780

Qy        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
```

RESULT 4
ADC78785
ID ADC78785 standard; protein; 839 AA.
XX
AC ADC78785;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human PRO protein #7.
XX
KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease.
XX
OS Homo sapiens.
XX
PN WO2003034984-A2.
XX
PD 01-MAY-2003.
XX
PF 15-OCT-2002; 2002WO-US033070.
XX
PR 19-OCT-2001; 2001US-0340083P.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Gurney AL;
XX
DR WPI; 2003-481990/45.
DR N-PSDB; ADC78784.
XX
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
PT medicament for diagnosing or treating cancer or inflammatory bowel
PT disorder e.g., ulcerative colitis or Crohn's disease.
XX
PS Claim 12; SEQ ID NO 14; 327pp; English.
XX
CC The invention comprises the amino acid and coding sequences of human PRO
CC proteins. The DNA and protein sequences of the invention are useful for
CC the diagnosis and treatment of cancer and inflammatory bowel disease
CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
CC sequence represents a human PRO protein of the invention.
XX
SQ Sequence 839 AA;

```
  Query Match            100.0%;  Score 4355;  DB 7;  Length 839;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660

Qy        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720

Qy        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780

Qy        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
```

RESULT 5
ADD48826
ID ADD48826 standard; protein; 839 AA.
XX
AC ADD48826;
XX

```
DT   02-DEC-2004  (revised)
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein AAF05316, SEQ ID NO 14536.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; AAF05316.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Example 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (described in Table 3
CC   of the specification) which is differentially expressed during pain.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 839 AA;

  Query Match             100.0%;  Score 4355;  DB 7;  Length 839;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLML 660

Qy        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720

Qy        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLR 780

Qy        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839


RESULT 6
AAW86361
ID   AAW86361 standard; protein; 837 AA.
XX
AC   AAW86361;
XX
DT   15-MAR-1999  (first entry)
XX
DE   Human DNAX toll-like receptor DTLR4.
XX
KW   DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KW   interleukin 1 receptor; phosphate metabolism; innate immunity response;
KW   modulate inflammatory function; morphological effect;
KW   immunological disorder.
XX
OS   Homo sapiens.
XX
PN   WO9850547-A2.
XX
PD   12-NOV-1998.
```

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XX
PF   07-MAY-1998;   98WO-US008979.
XX
PR   07-MAY-1997;   97US-0044293P.
PR   22-JAN-1998;   98US-0072212P.
PR   05-MAR-1998;   98US-0076947P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Hardiman GT,  Rock FL,  Bazan JF,  Kastelein RA;
XX
DR   WPI; 1999-059670/05.
DR   N-PSDB; AAV80675.
XX
PT   Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
PT   metabolism, modulate inflammatory function or innate immunity responses.
XX
PS   Claim 3; Page 147-149; 171pp; English.
XX
CC   The present invention specifically describes human DNAX toll-like
CC   receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
CC   in the present invention. Also described are: (1) a fusion protein
CC   comprising a DTLR protein or peptide; (2) a binding compound, preferably
CC   an antibody or antibody fragment which specifically binds to a DTLR
CC   protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
CC   ; (4) an expression vector comprising the nucleic acid of (3); and (5) a
CC   host cell comprising the vector of (4). The host cell of (5) can be used
CC   to produce the DTLR proteins. The DTLR proteins can be used to alter
CC   phosphate metabolism, to modulate inflammatory function, innate immunity
CC   responses or morphological effects. The DTLR proteins can be used in the
CC   treatment of conditions exhibiting abnormal expression of the receptors
CC   of their ligands. These abnormalities are typically manifested by
CC   immunological disorders
XX
SQ   Sequence 837 AA;

  Query Match             99.6%;  Score 4335.5;  DB 2;  Length 837;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  837;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 MSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDL 61
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 MSASRLAGTLIPAMAFLSCVRPESWEPCVE-VPNITYQCMELNFYKIPDNLPFSTKNLDL 59

Qy         62 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 119

Qy        122 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 179

Qy        182 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 239

Qy        242 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 299

Qy        302 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 359

Qy        362 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 419

Qy        422 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 479

Qy        482 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 539

Qy        542 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 599

Qy        602 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 659

Qy        662 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 719

Qy        722 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 779

Qy        782 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 837


RESULT 7
AAE16102
ID   AAE16102 standard; protein; 837 AA.
XX
AC   AAE16102;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human DNAX Toll like receptor (DTLR) 4 #2.
XX
KW   Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW   interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS   Homo sapiens.
XX
PN   WO200190151-A2.
XX
PD   29-NOV-2001.
XX
PF   23-MAY-2001; 2001WO-US016766.
XX
PR   25-MAY-2000; 2000US-0207558P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Hardiman GT,  Rock FL,  Bazan JF,  Kastelein RA,  Ho SWK,  Liu Y;
XX
DR   WPI; 2002-083085/11.
DR   N-PSDB; AAD26292.
XX
PT   New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT   conditions exhibiting abnormal expression of the receptors of their
PT   ligands, particularly abnormalities manifested by immunological
PT   disorders.
XX
PS   Claim 3; Page 41; 297pp; English.
XX
CC   The invention relates to mammalian receptor proteins, e.g., primate,
CC   human DNAX Toll like receptor (DTLR) protein and their corresponding
CC   nucleic acids. The DTLR is useful for treating conditions exhibiting
CC   abnormal expression of the receptors of their ligands. Such abnormality
CC   is manifested by immunological disorders. In particular, the DTLR is
CC   useful for treating various disease or disorders associated with abnormal
CC   expression or abnormal triggering of response to a ligand. The DTLR is
CC   also useful as an immunogen for the production of antisera or antibodies
CC   specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC   receptor family members, for the DTLR or its various fragments. The
CC   purified DTLR can be used to screen monoclonal antibodies or antigen-
CC   binding fragments. The antibodies are useful for screening expression
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CC   libraries for particular expression products. These are useful for
CC   detecting or diagnosing various immunological conditions related to
CC   expression of DTLR or cells that express it. The present sequence is
CC   human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33.
CC   Note: The present sequence SEQ ID NO 26 is stated to be similar to the
CC   sequence shown in page 240-243 (AAE16116). However these sequences differ
CC   at several locations
XX
SQ   Sequence 837 AA;

  Query Match             99.6%;  Score 4335.5;  DB 5;  Length 837;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  837;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 MSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDL 61
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 MSASRLAGTLIPAMAFLSCVRPESWEPCVE-VPNITYQCMELNFYKIPDNLPFSTKNLDL 59

Qy         62 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 119

Qy        122 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 179

Qy        182 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 239

Qy        242 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 299

Qy        302 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 359

Qy        362 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 419

Qy        422 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 479

Qy        482 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 539

Qy        542 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 599

Qy        602 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 659

Qy        662 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 719

Qy        722 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 779

Qy        782 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 837

RESULT 8
ABU04776
ID   ABU04776 standard; protein; 837 AA.
XX
AC   ABU04776;
XX
DT   29-JAN-2003  (first entry)
XX
DE   Human expressed protein tag (EPT) #1442.
XX
KW   Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW   protease; protease inhibitor; transporter; cytoskeletal protein;
KW   receptor; transcription factor; cancer; MHC;
KW   major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW   adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200278524-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US009671.
XX
PR   28-MAR-2001; 2001US-0279495P.
PR   21-MAY-2001; 2001US-0292544P.
PR   08-AUG-2001; 2001US-0310801P.
PR   01-OCT-2001; 2001US-0326370P.
PR   04-DEC-2001; 2001US-0336780P.
PR   20-FEB-2002; 2002US-0358985P.
XX
PA   (ZYCO-) ZYCOS INC.
XX
PI   Chicz RM,  Tomlinson AJ,  Urban RG;
XX
DR   WPI; 2003-040607/03.
XX
PT   New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT   cytoskeletal proteins, receptors or transcription factors), useful for
PT   treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT   leukemia.
XX
PS   Example 2; SEQ ID NO 1442; 134pp; English.
XX
CC   The invention describes a purified polypeptide, which comprises a
CC   fragment of a kinase, phosphatase, protease, protease inhibitor,
CC   transporter, cytoskeletal protein, receptor or transcription factor. The
CC   polypeptide is useful as an immunogenic composition for eliciting in a
CC   mammal an immunogenic response directed against any of the purified
CC   polypeptide. The purified polypeptide, or the antibody that binds to this
CC   polypeptide, is useful for treating cancer. The polypeptide is also
CC   useful for identifying compounds that binds to a naturally processed
CC   class I or class II MHC-binding polypeptide. The polypeptides and
CC   polynucleotides are particularly useful for treating or preventing
CC   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC   lymphoma or leukaemia. These are also useful for screening agents for
CC   treating the above mentioned diseases. This sequence represents an
CC   expressed protein tag (EPT) isolated from human tissue for translational
CC   profiling. Note: This sequence does not appear in the printed
CC   specification but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 837 AA;

  Query Match             99.6%;  Score 4335.5;  DB 6;  Length 837;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  837;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 MSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDL 61
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 MSASRLAGTLIPAMAFLSCVRPESWEPCVE-VPNITYQCMELNFYKIPDNLPFSTKNLDL 59

Qy         62 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 119
```

```
Qy        122 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 179

Qy        182 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 239

Qy        242 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 299

Qy        302 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 359

Qy        362 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 419

Qy        422 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 479

Qy        482 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 539

Qy        542 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 599

Qy        602 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 659

Qy        662 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 719

Qy        722 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 779

Qy        782 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 837


RESULT 9
AAE16116
ID   AAE16116 standard; protein; 837 AA.
XX
AC   AAE16116;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human DNAX Toll like receptor (DTLR) 4 #2, alternative version.
XX
KW   Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW   interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 211
FT                   /label= Unknown
FT                   /note= "Encoded by AAY"
XX
PN   WO200190151-A2.
XX
PD   29-NOV-2001.
XX
PF   23-MAY-2001; 2001WO-US016766.
XX
PR   25-MAY-2000; 2000US-0207558P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Hardiman GT,  Rock FL,  Bazan JF,  Kastelein RA,  Ho SWK,  Liu Y;
XX
DR   WPI; 2002-083085/11.
DR   N-PSDB; AAD26306.
XX
PT   New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT   conditions exhibiting abnormal expression of the receptors of their
PT   ligands, particularly abnormalities manifested by immunological
PT   disorders.
XX
PS   Claim 3; Page 240-243; 297pp; English.
XX
CC   The invention relates to mammalian receptor proteins, e.g., primate,
CC   human DNAX Toll like receptor (DTLR) protein and their corresponding
CC   nucleic acids. The DTLR is useful for treating conditions exhibiting
CC   abnormal expression of the receptors of their ligands. Such abnormality
CC   is manifested by immunological disorders. In particular, the DTLR is
CC   useful for treating various disease or disorders associated with abnormal
CC   expression or abnormal triggering of response to a ligand. The DTLR is
CC   also useful as an immunogen for the production of antisera or antibodies
CC   specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC   receptor family members, for the DTLR or its various fragments. The
CC   purified DTLR can be used to screen monoclonal antibodies or antigen-
CC   binding fragments. The antibodies are useful for screening expression
CC   libraries for particular expression products. These are useful for
CC   detecting or diagnosing various immunological conditions related to
CC   expression of DTLR or cells that express it. The present sequence is
CC   human DTLR4 protein, alternative version. The DTLR4 gene is located on
CC   chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
CC   be similar to the sequence shown in page 41 (AAE16102). However these
CC   sequences differ at several locations
XX
SQ   Sequence 837 AA;

  Query Match             99.4%;  Score 4328.5;  DB 5;  Length 837;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  836;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          2 MSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDL 61
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 MSASRLAGTLIPAMAFLSCVRPESWEPCVE-VPNITYQCMELNFYKIPDNLPFSTKNLDL 59

Qy         62 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 SFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGA 119

Qy        122 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 FSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLD 179

Qy        182 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLN 241
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        180 LSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLXPMNFIQPGAFKEIRLHKLTLRNNFDSLN 239

Qy        242 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 VMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDII 299

Qy        302 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 DLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSN 359

Qy        362 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGL 419
```

```
Qy        422 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 EQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGN 479

Qy        482 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 SFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYK 539

Qy        542 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 599

Qy        602 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 VEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLL 659

Qy        662 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 AGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAAN 719

Qy        722 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 IIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQ 779

Qy        782 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 QVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTGCNWQEATSI 837
```

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RESULT 10
ADO57782
ID   ADO57782 standard; protein; 808 AA.
XX
AC   ADO57782;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Chimpanzee toll-like receptor 4 SEQ ID NO:3.
XX
KW   toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW   immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW   sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS   Pan troglodytes.
XX
PN   WO2004042365-A2.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-US036247.
XX
PR   01-NOV-2002; 2002US-0423113P.
XX
PA   (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI   Messier W;
XX
DR   WPI; 2004-400726/37.
DR   N-PSDB; ADO57780, ADO57781.
XX
PT   Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT   in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT   sequence of the Old World monkey with that of a human.
XX
PS   Example 1; SEQ ID NO 3; 111pp; English.
XX
CC   The invention relates to a novel method for identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an old world monkey
CC   comprising comparing the TLR4 polynucleotide sequence of the Old World
CC   monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC   method of the invention has antibacterial, immunosuppressive, and
CC   antiasthmatic activity. The method is useful in identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC   change may be associated with reduced sensitivity to Gram-negative
CC   bacterial infection. The methods, agents and composition are useful in
CC   treating sepsis, severe sepsis or septic shock and asthma. The present
CC   sequence represents chimpanzee TLR4.
XX
SQ   Sequence 808 AA;
```

```
  Query Match             95.9%;  Score 4178;  DB 8;  Length 808;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches  805;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         32 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 60

Qy         92 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        152 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 180

Qy        212 LNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEK 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEK 240

Qy        272 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFG 331
              ||||||||||||||||||||||||||||||||||||||||||||||||: |||||||||
Db        241 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIKSVKDFSYNFG 300

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        392 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 420

Qy        452 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 480

Qy        512 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 540

Qy        572 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNK 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNK 600

Qy        632 TIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNE 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNE 660

Qy        692 LVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEY 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEY 720

Qy        752 EIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRL 811
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        721 EIAQTWQFLSSRAGIIFIVLQKVEKTLLRRQVELYRLLSRNTYLEWEDSVLGRHIFWRRL 780

Qy        812 RKALLDGKSWNPEGTVGTGCNWQEATSI 839
              ||||||||||||||||||||||||||||
Db        781 RKALLDGKSWNPEGTVGTGCNWQEATSI 808
```

```
RESULT 11
ADO57785
ID   ADO57785 standard; protein; 808 AA.
XX
AC   ADO57785;
```

```
XX
DT   12-AUG-2004  (first entry)
XX
DE   Gorilla toll-like receptor 4 SEQ ID NO:6.
XX
KW   toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW   immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW   sepsis; severe sepsis; septic shock; asthma; gorilla.
XX
OS   Gorilla gorilla.
XX
PN   WO2004042365-A2.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-US036247.
XX
PR   01-NOV-2002; 2002US-0423113P.
XX
PA   (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI   Messier W;
XX
DR   WPI; 2004-400726/37.
DR   N-PSDB; ADO57783, ADO57784.
XX
PT   Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT   in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT   sequence of the Old World monkey with that of a human.
XX
PS   Example 1; SEQ ID NO 6; 111pp; English.
XX
CC   The invention relates to a novel method for identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an old world monkey
CC   comprising comparing the TLR4 polynucleotide sequence of the Old World
CC   monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC   method of the invention has antibacterial, immunosuppressive, and
CC   antiasthmatic activity. The method is useful in identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC   change may be associated with reduced sensitivity to Gram-negative
CC   bacterial infection. The methods, agents and composition are useful in
CC   treating sepsis, severe sepsis or septic shock and asthma. The present
CC   sequence represents gorilla TLR4.
XX
SQ   Sequence 808 AA;

  Query Match             95.7%;  Score 4167;  DB 8;  Length 808;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches  803;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         32 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 60

Qy         92 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        152 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 211
              ||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEYLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 180

Qy        212 LNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEK 271
              |||| ||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db        181 LNPMTFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVRRLVLGEFRNEGNLEK 240

Qy        272 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFG 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFG 300

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        392 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 420

Qy        452 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 480

Qy        512 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 571
              ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db        481 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLRVLDYSLNHIMTSKKQELQHFPSSL 540

Qy        572 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNK 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNK 600

Qy        632 TIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNE 691
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db        601 TIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENVYDAFVIYSSQDEDWVRNE 660

Qy        692 LVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEY 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEY 720

Qy        752 EIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRL 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 EIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRL 780

Qy        812 RKALLDGKSWNPEGTVGTGCNWQEATSI 839
              ||||||||||||||||||||||||||||
Db        781 RKALLDGKSWNPEGTVGTGCNWQEATSI 808


RESULT 12
ADO57803
ID   ADO57803 standard; protein; 808 AA.
XX
AC   ADO57803;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Chimpanzee toll-like receptor 4 SEQ ID NO:24.
XX
KW   toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW   immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW   sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS   Pan troglodytes.
XX
PN   WO2004042365-A2.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-US036247.
XX
PR   01-NOV-2002; 2002US-0423113P.
XX
PA   (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI   Messier W;
XX
DR   WPI; 2004-400726/37.
DR   N-PSDB; ADO57801, ADO57802.
XX
PT   Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT   in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT   sequence of the Old World monkey with that of a human.
XX
PS   Disclosure; SEQ ID NO 24; 111pp; English.
XX
CC   The invention relates to a novel method for identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an old world monkey
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CC   comprising comparing the TLR4 polynucleotide sequence of the Old World
CC   monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC   method of the invention has antibacterial, immunosuppressive, and
CC   antiasthmatic activity. The method is useful in identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC   change may be associated with reduced sensitivity to Gram-negative
CC   bacterial infection. The methods, agents and composition are useful in
CC   treating sepsis, severe sepsis or septic shock and asthma. The present
CC   sequence represents chimpanzee TLR4.
XX
SQ   Sequence 808 AA;

  Query Match             95.6%;  Score 4164;  DB 8;  Length 808;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches  803;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         32 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 60

Qy         92 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        152 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 180

Qy        212 LNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEK 271
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        181 LNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEENLEK 240

Qy        272 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFG 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||: |||||||||
Db        241 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIKSVKDFSYNFG 300

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 391
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 WQHLELVKCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        392 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 420

Qy        452 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 480

Qy        512 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 540

Qy        572 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNK 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNK 600

Qy        632 TIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNE 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNE 660

Qy        692 LVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEY 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEY 720

Qy        752 EIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRL 811
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        721 EIAQTWQFLSSRAGIIFIVLQKVEKTLLRRQVELYRLLSRNTYLEWEDSVLGRHIFWRRL 780

Qy        812 RKALLDGKSWNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||||||||||
Db        781 RKALLDGKSWNPEGTVGTGCNWQEATSI 808
```

```
RESULT 13
AAW86352
ID   AAW86352 standard; protein; 799 AA.
XX
AC   AAW86352;
XX
DT   15-MAR-1999  (first entry)
XX
DE   Human DNAX toll-like receptor DTLR4.
XX
KW   DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KW   interleukin 1 receptor; phosphate metabolism; innate immunity response;
KW   modulate inflammatory function; morphological effect;
KW   immunological disorder.
XX
OS   Homo sapiens.
XX
PN   WO9850547-A2.
XX
PD   12-NOV-1998.
XX
PF   07-MAY-1998;   98WO-US008979.
XX
PR   07-MAY-1997;   97US-0044293P.
PR   22-JAN-1998;   98US-0072212P.
PR   05-MAR-1998;   98US-0076947P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Hardiman GT,  Rock FL,  Bazan JF,  Kastelein RA;
XX
DR   WPI; 1999-059670/05.
DR   N-PSDB; AAV80666.
XX
PT   Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
PT   metabolism, modulate inflammatory function or innate immunity responses.
XX
PS   Example; Page 115-117; 171pp; English.
XX
CC   The present invention specifically describes human DNAX toll-like
CC   receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
CC   in the present invention. Also described are: (1) a fusion protein
CC   comprising a DTLR protein or peptide; (2) a binding compound, preferably
CC   an antibody or antibody fragment which specifically binds to a DTLR
CC   protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
CC   ; (4) an expression vector comprising the nucleic acid of (3); and (5) a
CC   host cell comprising the vector of (4). The host cell of (5) can be used
CC   to produce the DTLR proteins. The DTLR proteins can be used to alter
CC   phosphate metabolism, to modulate inflammatory function, innate immunity
CC   responses or morphological effects. The DTLR proteins can be used in the
CC   treatment of conditions exhibiting abnormal expression of the receptors
CC   of their ligands. These abnormalities are typically manifested by
CC   immunological disorders
XX
SQ   Sequence 799 AA;

  Query Match             95.1%;  Score 4141;  DB 2;  Length 799;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  799;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         41 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy        101 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        161 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        221 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 280
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        281 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        341 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        401 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        461 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 520
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        521 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 580
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        581 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 640
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600

Qy        641 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 700
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

Qy        701 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 760
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720

Qy        761 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 820
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Qy        821 WNPEGTVGTGCNWQEATSI 839
                |||||||||||||||||||
Db        781 WNPEGTVGTGCNWQEATSI 799


RESULT 14
AAE16093
ID   AAE16093 standard; protein; 799 AA.
XX
AC   AAE16093;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human DNAX Toll like receptor (DTLR) 4 #1.
XX
KW   Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW   interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS   Homo sapiens.
XX
PN   WO200190151-A2.
XX
PD   29-NOV-2001.
XX
PF   23-MAY-2001; 2001WO-US016766.
XX
PR   25-MAY-2000; 2000US-0207558P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Hardiman GT,  Rock FL,  Bazan JF,  Kastelein RA,  Ho SWK,  Liu Y;
XX
DR   WPI; 2002-083085/11.
DR   N-PSDB; AAD26283.
XX
PT   New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT   conditions exhibiting abnormal expression of the receptors of their
PT   ligands, particularly abnormalities manifested by immunological
PT   disorders.
XX
PS   Claim 1; Page 35; 297pp; English.
XX
CC   The invention relates to mammalian receptor proteins, e.g., primate,
CC   human DNAX Toll like receptor (DTLR) protein and their corresponding
CC   nucleic acids. The DTLR is useful for treating conditions exhibiting
CC   abnormal expression of the receptors of their ligands. Such abnormality
CC   is manifested by immunological disorders. In particular, the DTLR is
CC   useful for treating various disease or disorders associated with abnormal
CC   expression or abnormal triggering of response to a ligand. The DTLR is
CC   also useful as an immunogen for the production of antisera or antibodies
CC   specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC   receptor family members, for the DTLR or its various fragments. The
CC   purified DTLR can be used to screen monoclonal antibodies or antigen-
CC   binding fragments. The antibodies are useful for screening expression
CC   libraries for particular expression products. These are useful for
CC   detecting or diagnosing various immunological conditions related to
CC   expression of DTLR or cells that express it. The present sequence is
CC   human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33
XX
SQ   Sequence 799 AA;

  Query Match             95.1%;  Score 4141;  DB 5;  Length 799;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  799;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          41 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 100
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Db           1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy         101 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy         161 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy         221 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy         281 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy         341 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy         401 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy         461 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 520
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy         521 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 580
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy         581 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 640
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 600

Qy         641 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 700
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

Qy        701 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 720

Qy        761 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Qy        821 WNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||
Db        781 WNPEGTVGTGCNWQEATSI 799


RESULT 15
ABB83162
ID   ABB83162 standard; protein; 799 AA.
XX
AC   ABB83162;
XX
DT   09-AUG-2002  (first entry)
XX
DE   Human Toll-like receptor-4, Tlr4.
XX
KW   Human; virucide; antibacterial; fungicide; parasiticide; receptor;
KW   cytostatic; immunostimulatory; scavenger receptor; Toll receptor;
KW   respiratory tract infection; Toll-like receptor; Tlr4.
XX
OS   Homo sapiens.
XX
PN   WO200235236-A1.
XX
PD   02-MAY-2002.
XX
PF   26-OCT-2001; 2001WO-FR003352.
XX
PR   27-OCT-2000; 2000FR-00013883.
XX
PA   (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
PI   Jeannin P,  Magistrelli G,  Herbault N,  Bonnefoy J;
XX
DR   WPI; 2002-383586/41.
DR   N-PSDB; ABN83318.
XX
PT   Identifying agent that binds to scavenger receptors and signals through a
PT   Toll receptor, useful as carrier or adjuvant in vaccines, promotes a
PT   cytotoxic T cell response.
XX
PS   Disclosure; Page 58-60; 71pp; French.
XX
CC   The present invention relates to a method for identifying new therapeutic
CC   compounds (I) by selecting molecules that bind to scavenger receptors and
CC   signal through a Toll receptor. The present sequence is the protein
CC   sequence for human Toll-like receptor-4, Tlr4, which was used to
CC   illustrate the method of the invention. (I) are useful as carriers and/or
CC   adjuvants in prophylactic or therapeutic vaccines, particularly where the
CC   antigen is derived from a virus, bacterium, yeast, fungus, parasite or
CC   tumour cell, especially a pathogen that causes respiratory tract
CC   infection, also more generally for inducing an immune response. (I) can
CC   also be used for specific targeting of active agents (antigens etc.) to
CC   antigen-presenting cells (especially immature dendritic cells), for
CC   subsequent internalisation by these cells
XX
SQ   Sequence 799 AA;

  Query Match             95.1%;  Score 4141;  DB 5;  Length 799;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  799;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         41 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 100
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Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy        101 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 160
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Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        161 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        221 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        281 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 340
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Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        341 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 400
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Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        401 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 460
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Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        461 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 520
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Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        521 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 580
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Qy        581 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLS 640
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Qy        641 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 700
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Db        601 VLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGV 660

Qy        701 PPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFL 760
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Qy        761 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 820
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Db        721 SSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKS 780

Qy        821 WNPEGTVGTGCNWQEATSI 839
              |||||||||||||||||||
Db        781 WNPEGTVGTGCNWQEATSI 799


Search completed: March 12, 2005, 19:55:07
Job time : 90.4 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:46 ; Search time 23.0639 Seconds
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Title: US-09-396-985B-98
Perfect score: 4355
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4197	96.4	844	4	US-09-949-016-9438	Sequence 9438, Ap
2	629.5	14.5	661	1	US-08-514-014-4	Sequence 4, Appli
3	629.5	14.5	661	2	US-08-833-823-4	Sequence 4, Appli
4	599.5	13.8	784	4	US-09-982-308B-23	Sequence 23, Appl
5	539	12.4	775	4	US-09-949-016-8799	Sequence 8799, Ap
6	316	7.3	605	3	US-09-063-950-5	Sequence 5, Appli
7	305	7.0	623	4	US-09-949-016-10995	Sequence 10995, A
8	303	7.0	605	1	US-08-190-802A-49	Sequence 49, Appl
9	303	7.0	605	3	US-08-477-346-49	Sequence 49, Appl
10	303	7.0	605	3	US-08-473-089-49	Sequence 49, Appl
11	303	7.0	605	4	US-08-487-072A-49	Sequence 49, Appl
12	303	7.0	605	4	US-09-538-092-1087	Sequence 1087, Ap
13	299.5	6.9	662	4	US-09-538-092-1325	Sequence 1325, Ap
14	299.5	6.9	662	4	US-09-949-016-6619	Sequence 6619, Ap
15	299.5	6.9	665	4	US-09-949-016-10710	Sequence 10710, A
16	299	6.9	1525	3	US-09-191-647-2	Sequence 2, Appli
17	299	6.9	1525	3	US-09-540-245A-2	Sequence 2, Appli
18	299	6.9	1525	3	US-09-540-153-2	Sequence 2, Appli
19	296	6.8	603	1	US-08-190-802A-50	Sequence 50, Appl
20	296	6.8	603	3	US-08-477-346-50	Sequence 50, Appl
21	296	6.8	603	3	US-08-473-089-50	Sequence 50, Appl
22	296	6.8	603	4	US-08-487-072A-50	Sequence 50, Appl
23	292.5	6.7	907	4	US-09-170-496D-264	Sequence 264, App
24	292.5	6.7	907	4	US-09-170-496D-278	Sequence 278, App
25	289.5	6.6	1112	3	US-09-353-585-3	Sequence 3, Appli
26	289	6.6	1529	4	US-09-312-283C-396	Sequence 396, App
27	286	6.6	1112	3	US-09-353-585-2	Sequence 2, Appli
28	285	6.5	1523	3	US-09-182-024A-2	Sequence 2, Appli
29	283.5	6.5	1166	4	US-10-101-464A-900	Sequence 900, App
30	281	6.5	1101	3	US-08-986-485-2	Sequence 2, Appli
31	278	6.4	1091	3	US-08-986-485-5	Sequence 5, Appli
32	275	6.3	620	4	US-09-907-794A-73	Sequence 73, Appl
33	275	6.3	620	4	US-09-905-125A-73	Sequence 73, Appl
34	275	6.3	620	4	US-09-902-775A-73	Sequence 73, Appl
35	275	6.3	620	4	US-09-906-700-73	Sequence 73, Appl
36	275	6.3	620	4	US-09-903-603A-73	Sequence 73, Appl
37	275	6.3	620	4	US-09-904-920A-73	Sequence 73, Appl
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39	275	6.3	620	4	US-09-905-381A-73	Sequence 73, Appl
40	275	6.3	620	4	US-09-906-618-73	Sequence 73, Appl
41	272	6.2	1480	3	US-09-191-647-7	Sequence 7, Appli
42	272	6.2	1480	3	US-09-540-245A-7	Sequence 7, Appli
43	272	6.2	1480	3	US-09-540-153-7	Sequence 7, Appli
44	272	6.2	1480	5	PCT-US91-09055-2	Sequence 2, Appli
45	271	6.2	1139	4	US-09-513-505-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9438

Query Match 96.4%; Score 4197; DB 4; Length 844;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          31 EVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEI 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          36 EVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEI 95

Qy          91 QTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLK 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          96 QTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLK 155

Qy         151 TLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDL 210
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         156 TLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDL 215

Qy         211 SLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLE 270
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         216 SLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLE 275

Qy         271 KFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNF 330
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         276 KFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNF 335

Qy         331 GWQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGC 390
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Db        336 GWQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGC 395

Qy        391 CSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLI 450

Db        396 CSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLI 455

Qy        451 YLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQ 510

Db        456 YLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQ 515

Qy        511 LSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSS 570

Db        516 LSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSS 575

Qy        571 LAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMN 630

Db        576 LAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMN 635

Qy        631 KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRN 690

Db        636 KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRN 695

Qy        691 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 750

Db        696 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 755

Qy        751 YEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRR 810

Db        756 YEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRR 815

Qy        811 LRKALLDGKSWNPEGTVGTGCNWQEATSI 839

Db        816 LRKALLDGKSWNPEGTVGTGCNWQEATSI 844
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RESULT 2
US-08-514-014-4
; Sequence 4, Application US/08514014
; Patent No. 5707829
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  Kelleher, Kerry
;    APPLICANT:  Carlin, McKeough
;    TITLE OF INVENTION:  DNA SEQUENCES AND SECRETED PROTEINS
;    TITLE OF INVENTION:  ENCODED THEREBY
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc. -- Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/514,014
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI6000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  661 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-514-014-4

  Query Match           14.5%;  Score 629.5;  DB 1;  Length 661;
  Best Local Similarity  29.7%;  Pred. No. 5.3e-49;
  Matches  199;  Conservative  109;  Mismatches  274;  Indels   89;  Gaps   24;

Qy         25 SWEP-CVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVL 83

Db         23 SWDQMCIEKEANKTYNCENLGLSEIPDTLPNTTEFLEFSFNFLPTIHNRTFSRLMNLTFL 82

Qy         84 DLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLEN 143

Db         83 DLTRCQINWIHEDTFQSHHQLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEF 142

Qy        144 FPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPL 203

Db        143 IPVHNLENLESLYLGSNHISSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--A 199

Qy        204 LNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEF 263

Db        200 INLSLNFNGNNVKGIELGAFDSTVFQSL----NFGGTPNLSVIFNGLQNSTTQSLWLGTF 255

Qy        264 RNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIID-LFNCLTNVSSFSLVSVTIER 322

Db        256 EDIDD-EDISSAMLKGLCEMSVESLNLQ--EHRFSDISSTTFQCFTQLQELDLTATHLKG 312

Qy        323 VKDFSYNFGWQHLELVN------------CKF--GQFPTL-------KLKSLKRLTFTSN 361

Db        313 LPS-----GMKGLNLLKKLVLSVNHFDQLCQISAANFPSLTHLYIRGNVKKLHLGVGCLE 367

Qy        362 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSN-FLG 420

Db        368 KLGN---------LQTLDLSHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKE 418

Qy        421 LEQLEHLDFQ----HSNLKQMSEFS--VFLSLRNLIY--LDISHTHTRVAFNGIFNGLSS 472

Db        419 CPQLELLDLAFTRLHINAPQ-SPFQNLHFLQVLNLTYCFLDTSNQH-------LLAGLPV 470

Qy        473 LEVLKMAGNSFQENFL--PDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHN 530

Db        471 LRHLNLKGNHFQDGTITKTNLLQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHN 530

Qy        531 NFF--SLDTFPY-------KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDF 581

Db        531 SLTCDSIDSLSHLKGIYLNLAANSINIISPRLLPIL-----------SQQSTINLSHNPL 579

Qy        582 ACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSV 641

Db        580 DCTCSNIHFLTWYKENLHKLEGSEETTCANPPSLRGVKLSDVKLSCGI--TAIGIFFLIV 637

Qy        642 LVVSVVAVLVY 652

Db        638 FLL-LLAILLF 647
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```
RESULT 3
US-08-833-823-4
; Sequence 4, Application US/08833823
; Patent No. 5969093
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  Kelleher, Kerry
;    APPLICANT:  Carlin, McKeough
;    TITLE OF INVENTION:  DNA SEQUENCES AND SECRETED PROTEINS
;    TITLE OF INVENTION:  ENCODED THEREBY
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc. -- Legal Affairs
```

```
;       STREET:  87 CambridgePark Drive
;       CITY:  Cambridge
;       STATE:  Massachusetts
;       COUNTRY:  USA
;       ZIP:  02140
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/833,823
;       FILING DATE:  10-APR-1997
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/514,014
;       FILING DATE:  11-AUG-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Brown, Scott A.
;       REGISTRATION NUMBER:  32,724
;       REFERENCE/DOCKET NUMBER:  GI6000
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 498-8224
;       TELEFAX:  (617) 876-5851
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  661 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-833-823-4

  Query Match             14.5%;  Score 629.5;  DB 2;  Length 661;
  Best Local Similarity   29.7%;  Pred. No. 5.3e-49;
  Matches  199;  Conservative  109;  Mismatches  274;  Indels   89;  Gaps   24;

Qy         25 SWEP-CVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVL 83
              ||:  |:|   | || |  |   :||| || :|: |: ||| |  : : :|     |  |
Db         23 SWDQMCIEKEANKTYNCENLGLSEIPDTLPNTTEFLEFSFNFLPTIHNRTFSRLMNLTFL 82

Qy         84 DLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLEN 143
              ||:||:|  | :  :||   ||||:|||||:  :|  : :|  ||: |  ::| :::||
Db         83 DLTRCQINWIHEDTFQSHHQLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEF 142

Qy        144 FPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPL 203
              |: :|: |: | :  | | | | |: |    ||: ||  :| |  |    |:| | |
Db        143 IPVHNLENLESLYLGSNHISSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--A 199

Qy        204 LNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEF 263
              :|||: : |  :  |: |||       |    ||     :     ||       | || |
Db        200 INLSLNFNGNNVKGIELGAFDSTVFQSL----NFGGTPNLSVIFNGLQNSTTQSLWLGTF 255

Qy        264 RNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIID-LFNCLTNVSSFSLVSVTIER 322
              :  : |    : |:||| :::|   |   ::   ||    | | | :    | :  ::
Db        256 EDIDD-EDISSAMLKGLCEMSVESLNLQ--EHRFSDISSTTFQCFTQLQELDLTATHLKG 312

Qy        323 VKDFSYNFGWQHLELVN-----------CKF--GQFPTL-------KLKSLKRLTFTSN 361
              :       | : | |:             |:     ||:|         :| |
Db        313 LPS-----GMKGLNLLKKLVLSVNHFDQLCQISAANFPSLTHLYIRGNVKKLHLGVGCLE 367

Qy        362 KGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSN-FLG 420
              | ||          |: |||| | :    |||       : |: |:|| |  : : |  |
Db        368 KLGN---------LQTLDLSHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKE 418

Qy        421 LEQLEHLDFQ----HSNLKQMSEFS--VFLSLRNLIY--LDISHTHTRVAFNGIFNGLSS 472
              |||  ||       | |  | | |    || : || |  || |: |        :  ||
Db        419 CPQLELLDLAFTRLHINAPQ-SPFQNLHFLQVLNLTYCFLDTSNQH-------LLAGLPV 470

Qy        473 LEVLKMAGNSFQENFL--PDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHN 530
              |  | : || ||:  :   ::   : :|  | || | |  :    ||:||  :  :::|||
Db        471 LRHLNLKGNHFQDGTITKTNLLQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHN 530

Qy        531 NFF--SLDTFPY-------KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDF 581
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              :   |:|:  :          ||: :: . |  |:          |  : :||: |
Db        531 SLTCDSIDSLSHLKGIYLNLAANSINIISPRLLPIL----------SQQSTINLSHNPL 579

Qy        582 ACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSVLSV 641
              |||  :  || | |:    |   |   || |   :|: :  : ::| :  | ||:  | |
Db        580 DCTCSNIHFLTWYKENLHKLEGSEETTCANPPSLRGVKLSDVKLSCGI--TAIGIFFLIV 637

Qy        642 LVVSVVAVLVY 652
               :: ::|:|::
Db        638 FLL-LLAILLF 647


RESULT 4
US-09-982-308B-23
; Sequence 23, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
;  APPLICANT: Dalie, Barbara
;  APPLICANT:  Fan, Xuedong
;  APPLICANT:  Lundell, Daniel
;  APPLICANT:  Lunn, Charles A.
;  APPLICANT:  Tan, Jimmy C.
;  APPLICANT:  Zavodny, Paul J.
;  TITLE OF INVENTION: Mammalian TNF-alpha Convertases
;  FILE REFERENCE: JB0601QC
;  CURRENT APPLICATION NUMBER: US/09/982,308B
;  CURRENT FILING DATE:  2001-10-17
;  PRIOR APPLICATION NUMBER: 09/156,163
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 08/889,909
;  PRIOR FILING DATE: 1997-07-10
;  PRIOR APPLICATION NUMBER: 60/021,710
;  PRIOR FILING DATE: 1996-07-12
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;   LENGTH: 784
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-982-308B-23

  Query Match             13.8%;  Score 599.5;  DB 4;  Length 784;
  Best Local Similarity   27.0%;  Pred. No. 4.1e-46;
  Matches  233;  Conservative  128;  Mismatches  282;  Indels  219;  Gaps   38;

Qy         48 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 107
              ||  |  : |:|||| | : :: :        || | |:   | |||: :: ||  |  |
Db         46 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 105

Qy        108 ILTGNPIQSLALGAFSGLSSLQKL-----------VAVETNLASLENFPIGHLKT---- 151
              |: | : :|:   |  ||||  |              :: ::|  |:   :|:: |
Db        106 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 165

Qy        152 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK----------IQSI 190
                       |:|| :  : :||:: |:   :: |: || |  :           |:
Db        166 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 224

Qy        191 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 244
              | :||            |  |:  :|  :  |    : : | | ||     :||  |||
Db        225 ECLELR-----------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 271

Qy        245 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 297
              |  ||  ||      |   | ||   |    :|    |||    :   || |
Db        272 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 326

Qy        298 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 357
              |:  |::    |       :|:|  | |  |          || |   |
Db        327 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------ 357

Qy        358 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 412
                          | |||:|||| |      |    |    :    ||: | |  |
Db        358 ------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 397
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Qy        413 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 472
                                 ||    ::|::  |    |:|:||  :|||
Db        398 -------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 422

Qy        473 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 529
                  |||    :|:       : :|:||  ::  ::    |        :|::|::|:
Db        423 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 466

Qy        530 N--NFFSLD--------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 571
              |  | |||:                | |    |  | ||  | | | |  |::|  |  :|
Db        467 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 525

Qy        572 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 626
                |    |:| |:||  || |    ::| | :|          | :||  :|  |  : ::
Db        526 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 581

Qy        627 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 674
                  |      : |:      |:: :  || ::|:  ::: ::    ::  |        || |
Db        582 VSECHRIALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 641

Qy        675 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 734
              |||| || :|  || | :|: ||   |||:|||| ||||||  |  ||| :  || | :
Db        642 DAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 700

Qy        735 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQ-VELYRLLSRNT 793
              |:|::|::| || :| : :    |  :    | |:|: :||  : |:  :| :::  |
Db        701 FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKT 760

Qy        794 YLEWEDSVLGRHIFWRRLRKAL 815
              ||||      |  ||  || |:
Db        761 YLEWPMDEAQREGFWVNLRAAI 782
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RESULT 5
US-09-949-016-8799
; Sequence 8799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8799

Query Match 12.4%; Score 539; DB 4; Length 775;
Best Local Similarity 26.6%; Pred. No. 1.6e-40;
Matches 218; Conservative 120; Mismatches 264; Indels 218; Gaps 37;

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Qy         48 IPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTL 107
                 ||  |  : |:|||| | : :: :       || | |:   | |||: :: ||  |  |
Db         81 IPSGLTEAVKSLDLSNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHL 140

Qy        108 ILTGNPIQSLALGAFSGLSSLQKL-----------VAVETNLASLENFPIGHLKT---- 151
                |: | : :|:   |  |||| |            :: ::|  |:   :|:: |
Db        141 DLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKI 200

Qy        152 ----------LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK-----------IQSI 190
                       |:|| :  : :||:: |:   :: |: || |   :            |:
Db        201 QRKDFAGLTFLEELEIDASDLQSYE-PKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSV 259

```
Qy        191 YCTDLRVLHQMPLLNLSLDLSLNPMNF--IQPGAFKEIRLHKLTLRN---NFDSL-NVMK 244
              | :||              |  |:  :|  :  |    : : | | ||     :||  |||
Db        260 ECLELR------------DTDLDTFHFSELSTGETNSL-IKKFTFRNVKITDESLFQVMK 306

Qy        245 TC--IQGLAGLEVHRLVL---GEFRNEGNLEKFDKSALEGLCNLTIEEFRLA--YLDYYL 297
                | ||  ||      |   | ||  |    |  :|    |||    :   || |
Db        307 LLNQISGLLELEFDDCTLNGVGNFRASDNDRVIDPGKVE---TLTIRRLHIPRFYLFY-- 361

Qy        298 DDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLT 357
              |:  |::      |       :|:|  | |             || |   |
Db        362 -DLSTLYSLTERVK-----RITVENSKVF----------LVPCLLSQ------------ 392

Qy        358 FTSNKGGNAFSEVDLPSLEFLDLSRN-----GLSFKGCCSQSDFGTTSLKYLDLSFNGVI 412
                          | |||:|||| |       |     |    :    ||: | |  |
Db        393 ------------HLKSLEYLDLSENLMVEEYLKNSAC----EDAWPSLQTLILRQN--- 432

Qy        413 TMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSS 472
                             ||    ::|::  |    |:|:||  :|||
Db        433 -------------HL----ASLEKTGE--TLLTLKNLTNIDISK---------------- 457

Qy        473 LEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLS---PTAFNSLSSLQVLNMSH 529
                       |||    :|:       : :|:||  ::  ::    |        :|::|::|:
Db        458 --------NSFHS--MPETCQWPEKMKYLNLSSTRIHSVTGCIP------KTLEILDVSN 501

Qy        530 N--NFFSLD--------------TFP-YKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 571
              |  | |||:                | |    |  | ||  | | | |  |::|  |  :|
Db        502 NNLNLFSLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSF-HTL 560

Qy        572 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEV-----ERMECATPSDKQGMPVLSLNIT 626
                |    |:| |:||  || |    ::| | :|          | :||  :|  |  : ::
Db        561 KTLEAGGNNFICSCEFLSFTQ----EQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLS 616

Qy        627 ---CQMNKTIIGVSVLSVLVVSVVAVLVYKFY--FHLMLLAGCIKYGR------GENI-Y 674
                  |      : |:      |:: :  || ::|:  ::: ::    ::  |        || |
Db        617 VSECHRTALVSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICY 676

Qy        675 DAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVI 734
              |||| || :|  || | :|: ||   |||:|||| ||||||  |  ||| :  || | :
Db        677 DAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTV 735

Qy        735 VVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKV 774
              |:|::|::| || :| : :    |  :    | |:|: :
Db        736 FVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPI 775
```

RESULT 6
US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-09-063-950-5

Query Match 7.3%; Score 316; DB 3; Length 605;
Best Local Similarity 24.4%; Pred. No. 4.1e-20;
Matches 157; Conservative 94; Mismatches 242; Indels 150; Gaps 23;

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Qy         33 VPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQT 92
                |  ::  |   |  ::|| :|  |: | |  | |  :  :| :   |  |:|   :: :
Db         53 VNELSVFCSSRNLTRLPDGIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGS 112
```
```

```
Qy          93 IEDGAYQSLSHLSTLILTGNPIQSLALGAFS----------------------GLSSL 128
               :|  |    | :|  | |  | ::|||:| |:                          || :|
Db         113 LEPQALLGLENLCHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLEDGLFEGLGNL 172

Qy         129 QKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQ 188
                 |     :|| | :     |  |:|| :| | : ::  |  || |  |  |||| | ::
Db         173 WDLNLGWNSLAVLPDAAFRGLGGLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALR 231

Qy         189 SIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCI 247
               :|       |  |:| |   | |  | :  : |||| :: |  | | :|     :::
Db         232 AI---KANVFAQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTF 286

Qy         248 QGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCL 307
                || || | ||              :|:  |   | |:       ::|:::
Db         287 PGLLGLRVLRL--------------SHNAIASLRPRTFEDL------HFLEEL------- 319

Qy         308 TNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGN 365
                     |    | :: : |:  |   ||::     |   :|: :   ||  :  |  ||
Db         320 ------QLGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKVGAFLGLTNVAVMNLSGN 372

Qy         366 AFSEVDLPSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL 419
                :||    |  | : :  |  :| |       :  | : |: | |  ||:: :    |
Db         373 CLR--NLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFAGLSGLRRLFLKDNGLVGIEEQSL 430

Qy         420 -GLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKM 478
                || :|  ||  : |                ||     : :| ||  || | :
Db         431 WGLAELLELDLTSNQL---------------------THLP---HQLFQGLGKLEYLLL 465

Qy         479 AGNSFQENFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDT 537
               : |   |  || |    |:   :||:|  :|| |  :   ||  |: ||: :|   || |
Db         466 SHNRLAE--LPADALGPLQRAFWLDVSHNRLEALPGSLLASLGRLRYLNLRNN---SLRT 520

Qy         538 FPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQS-------- 589
               |  :                          |  |  | |  | : |:|  ::
Db         521 FTPQ--------------------------PPGLERLWLEGNPWDCSCPLKALRDFALQN 554

Qy         590 ------FLQWI---KDQRQLLVEVERMECATPSDKQGMPVLSL 623
                    |:| |    | :  :    : ||:| :  |: :  |
Db         555 PSAVPRFVQAICEGDDCQPPVYTYNNITCASPPEVAGLDLRDL 597
```

RESULT 7
US-09-949-016-10995
; Sequence 10995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10995
;   LENGTH: 623
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10995

  Query Match   7.0%; Score 305; DB 4; Length 623;
  Best Local Similarity   24.3%; Pred. No. 4.4e-19;
  Matches 171; Conservative   96; Mismatches 260; Indels 178; Gaps   28;

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Qy           4 ASRLA---GTLIPAMAFLSCVR--PESWE----------------PCV----EVVPNIT 37
               | |:|   | |  |:  || |   | | |                ||    :    ::
Db          16 ACRMALRKGGLALALLLLSWVALGPRSLEGADPGTPGEAEGPACPAACVCSYDDDADELS 75

Qy          38 YQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGA 97
                 |   |  ::|| :|  |: | |  | |  :  :| :   |  |:|   :: ::|  |
Db          76 VFCSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQA 135

Qy          98 YQSLSHLSTLILTGNPIQSLALGAFS----------------------GLSSLQKLVA 133
                 | :|  | |  | ::||||| |:                          || ||  |
Db         136 LLGLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNL 195

Qy         134 VETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCT 193
                  :|| | :     | :|:|| :| | : ::  |  || |  |  |||| | :::|
Db         196 GWNSLAVLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI--- 251

Qy         194 DLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAG 252
                 |  |:| |   | |  | :  : |||| :: |  | | :|     :::    || |
Db         252 KANVFVQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLG 309

Qy         253 LEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSS 312
                | | ||                :|:  |   | ::       ::|:::
Db         310 LRVLRL--------------SHNAIASLRPRTFKDL------HFLEEL------------ 337

Qy         313 FSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEV 370
                  |    | :: : |:  |   ||::     |   :|  :   ||  :  |  ||
Db         338 -QLGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR-- 393

Qy         371 DLPSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQ 423
               :||    |  | : :  |  :| |       :  | : |: | |  ||:: :    | || :
Db         394 NLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAE 453

Qy         424 LEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSF 483
                |  ||   : |                ||     : :| ||  || | :: |
Db         454 LLELDLTSNQL---------------------THLP---HRLFQGLGKLEYLLLSRNRL 488

Qy         484 QENFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKC 542
                |  || |    |:   :||:|  :|| |  :   |  |: |:: :|   || ||  :
Db         489 AE--LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ- 542

Qy         543 LNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD------ 596
                                  |  |  | |  | : | |     |: ::|
Db         543 -------------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNP 573

Qy         597 ---QRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 638
                  | :    |  :|  |:          ||||     ::|: :
Db         574 SAVPRFVQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 612
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RESULT 8
US-08-190-802A-49
; Sequence 49, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
;   APPLICANT: Mochly-Rosen, Daria
;   APPLICANT: Ron, Dorit
;   TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
;   TITLE OF INVENTION: Thereof
;   NUMBER OF SEQUENCES: 265
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Dehlinger & Associates
;   STREET: P.O. Box 60850
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94306-0850
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/190,802A
;   FILING DATE: 01-FEB-1994
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:

```
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  8600-0139
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-190-802A-49

  Query Match             7.0%;  Score 303;  DB 1;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 6.4e-19;
  Matches  157;  Conservative   91;  Mismatches  243;  Indels  152;  Gaps   24;

Qy         40 CMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQ 99
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy        100 SLSHLSTLILTGNPIQSLALGAFS----------------------GLSSLQKLVAVE 135
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        136 TNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDL 195
Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KA 235

Qy        196 RVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLE 254
Db        236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLR 293

Qy        255 VHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFS 314
Db        294 VLRL--------------SHNAIASLRPRTFKDL------HFLEEL-------------Q 320

Qy        315 LVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDL 372
Db        321 LGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NL 377

Qy        373 PSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLE 425
Db        378 PEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELL 437

Qy        426 HLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQE 485
Db        438 ELDLTSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE 472

Qy        486 NFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLN 544
Db        473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ--- 524

Qy        545 SLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD-------- 596
Db        525 ----------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSA 557

Qy        597 -QRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 638
Db        558 VPRFVQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594


RESULT 9
US-08-477-346-49
; Sequence 49, Application US/08477346
; Patent No. 6262023
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,346
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/487,072
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-477-346-49

  Query Match             7.0%;  Score 303;  DB 3;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 6.4e-19;
  Matches  157;  Conservative   91;  Mismatches  243;  Indels  152;  Gaps   24;

Qy         40 CMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQ 99
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy        100 SLSHLSTLILTGNPIQSLALGAFS----------------------GLSSLQKLVAVE 135
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        136 TNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDL 195
Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KA 235

Qy        196 RVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLE 254
Db        236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLR 293

Qy        255 VHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFS 314
Db        294 VLRL--------------SHNAIASLRPRTFKDL------HFLEEL-------------Q 320

Qy        315 LVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDL 372
Db        321 LGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NL 377

Qy        373 PSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLE 425
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Db        378 PEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELL 437

Qy        426 HLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQE 485

Db        438 ELDLTSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE 472

Qy        486 NFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLN 544

Db        473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ--- 524

Qy        545 SLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD-------- 596

Db        525 ----------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSA 557

Qy        597 -QRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 638

Db        558 VPRFVQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594


RESULT 10
US-08-473-089-49
; Sequence 49, Application US/08473089
; Patent No. 6342368
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/473,089
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-473-089-49

  Query Match             7.0%;  Score 303;  DB 3;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 6.4e-19;
  Matches  157;  Conservative   91;  Mismatches  243;  Indels  152;  Gaps   24;

Qy         40 CMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQ 99

Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy        100 SLSHLSTLILTGNPIQSLALGAFS----------------------GLSSLQKLVAVE 135

Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        136 TNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDL 195

Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KA 235

Qy        196 RVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLE 254

Db        236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLR 293

Qy        255 VHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFS 314

Db        294 VLRL-------------SHNAIASLRPRTFKDL------HFLEEL------------Q 320

Qy        315 LVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDL 372

Db        321 LGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NL 377

Qy        373 PSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLE 425

Db        378 PEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELL 437

Qy        426 HLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQE 485

Db        438 ELDLTSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE 472

Qy        486 NFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLN 544

Db        473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ--- 524

Qy        545 SLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD-------- 596

Db        525 ----------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSA 557

Qy        597 -QRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 638

Db        558 VPRFVQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594


RESULT 11
US-08-487-072A-49
; Sequence 49, Application US/08487072A
; Patent No. 6423684
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,072A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.20
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-487-072A-49

  Query Match             7.0%;  Score 303;  DB 4;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 6.4e-19;
  Matches  157;  Conservative   91;  Mismatches  243;  Indels  152;  Gaps   24;

Qy         40 CMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQ 99
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy        100 SLSHLSTLILTGNPIQSLALGAFS----------------------GLSSLQKLVAVE 135
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        136 TNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDL 195
Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KA 235

Qy        196 RVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLE 254
Db        236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLR 293

Qy        255 VHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFS 314
Db        294 VLRL--------------SHNAIASLRPRTFKDL------HFLEEL-------------Q 320

Qy        315 LVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDL 372
Db        321 LGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NL 377

Qy        373 PSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLE 425
Db        378 PEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELL 437

Qy        426 HLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQE 485
Db        438 ELDLTSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE 472

Qy        486 NFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLN 544
Db        473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ--- 524

Qy        545 SLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD-------- 596
Db        525 ----------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSA 557

Qy        597 -QRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 638
Db        558 VPRFVQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594


RESULT 12
US-09-538-092-1087
; Sequence 1087, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1087
;   LENGTH: 605
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number P35858
US-09-538-092-1087

  Query Match             7.0%;  Score 303;  DB 4;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 6.4e-19;
  Matches  157;  Conservative   91;  Mismatches  243;  Indels  152;  Gaps   24;

Qy         40 CMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQ 99
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy        100 SLSHLSTLILTGNPIQSLALGAFS----------------------GLSSLQKLVAVE 135
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        136 TNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDL 195
Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KA 235

Qy        196 RVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLE 254
Db        236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLR 293

Qy        255 VHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFS 314
Db        294 VLRL--------------SHNAIASLRPRTFKDL------HFLEEL-------------Q 320

Qy        315 LVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDL 372
Db        321 LGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NL 377

Qy        373 PSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLE 425
Db        378 PEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELL 437

Qy        426 HLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQE 485
Db        438 ELDLTSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE 472

Qy        486 NFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLN 544
Db        473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ--- 524

Qy        545 SLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD-------- 596
Db        525 ----------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSA 557

Qy        597 -QRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 638
Db        558 VPRFVQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594


RESULT 13
US-09-538-092-1325
; Sequence 1325, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
```

```
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1325
;   LENGTH: 662
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number Q14392
US-09-538-092-1325

  Query Match             6.9%;  Score 299.5;  DB 4;  Length 662;
  Best Local Similarity   25.9%;  Pred. No. 1.6e-18;
  Matches  187;  Conservative   94;  Mismatches  259;  Indels  181;  Gaps   35;

Qy         28 PCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSR 87
              ||  |   ::  |  |   ::|  ||  |: |||| | || : :     :  |: ||||
Db         25 PCKMVDKKVS--CQVLGLLQVPSVLPPDTETLDLSGNQLRSILASPLGFYTALRHLDLST 82

Qy         88 CEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLAS-----LE 142
              ||  :: ||:|:|:||  | |  | :      :  ||  | :: ::: :  |     ||
Db         83 NEISFLQPGAFQALTHLEHLSLAHNRLAMATALSAGGLGPLPRVTSLDLSGNSLYSGLLE 142

Qy        143 NFPIGHLKTLKELNVAHNLIQSFKLPEY-FSNLTNLEHLDLSSNKIQSIYCTDLRVLHQM 201
              :|  :|  |::| | :  :|  : | :: || ||| || :  |         | ::
Db        143 RL-LGEAPSLHTLSLAENSLT--RLTRHTFRDMPALEQLDLHSNVLMDIEDGAFEGLPRL 199

Qy        202 PLLNLS----------------LDLSLNPMNFI----QPGAFKEIRLHKLTLRNN---- 236
              ||||                ||||  | :       || |  | :|  | || |
Db        200 THLNLSRNSLTCISDFSLQQLRVLDLSCNSIEAFQTASQPQA--EFQLTWLDLRENKLLH 257

Qy        237 FDSLNVMKTCIQGLAGLEVHRLVLGEFRN-----------------EGNLEKFDKSAL 277
              |  |  :  |       : ||  |  ::                 ||      | |
Db        258 FPDLAALPRLIYLNLSNNLIRLPTGPPQDSKGIHAPSEGWSALPLSAPSGNASGRPLSQL 317

Qy        278 EGLCNLTIEEFRLAYLDYYLDDIIDLF------NCLTNVSSFSLVSVTIERVKDFSYNFG 331
              | :|:  |  |   | :|: :  |        |||   :  | |:    : | |:|
Db        318 LNL-DLSYNEIEL-IPDSFLEHLTSLCFLNLSRNCLRTFEARRLGSLPCLMLLDLSHN-A 374

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEV------DLPSLEFLDLSRNGL 385
              : |||      |  || |:             |||  ::      :| ||: |:|  | :
Db        375 LETLELGARALGSLRTLLLQ-----------GNALRDLPPYTFANLASLQRLNLQGNRV 422

Qy        386 S---------FKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQ 436
              |           || : |  | |||: | |  | :           | |    | |: | :
Db        423 SPCGGPDEPGPSGCVAFS--GITSLRSLSLVDNEI----------ELLRAGAFLHTPLTE 470

Qy        437 MSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGL-SSLEVLKMAGNSFQ--ENFLPDIFT 493
                        ||:|        |  || :|||| : ||     :  ||
Db        471 --------------LDLSSNPGLEVATGALGGLEASLEVLALQGNGLMVLQVDLPCFIC 515

Qy        494 ELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSL 553
                 |  |:|:: :|  |    |:    ||:||::  || |||    |   :  |:
Db        516 ----LKRLNLAENRLSHL--PAWTQAVSLEVLDL-RNNSFSL--LPGSAMGGLE------ 560

Qy        554 NHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQ-RQLLVEVERME---C 609
                          :||  | | |  :| | :     |:  |  |  |:|:  :   |
Db        561 --------------TSLRRLYLQGNPLSC-CGN----GWLAAQLHQGRVDVDATQDLIC 600

Qy        610 ATPSDKQGMPVLSLNIT----CQMN--KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAG 663
              | ::    :||:      |:    | |  : :|: ::|| :           |  ||
Db        601 RFSSQEE----VSLSHVRPEDCEKGGLKNINLIIILTFILVSAIL---------LTTLAA 647

Qy        664 C 664
              |
Db        648 C 648


RESULT 14
US-09-949-016-6619
; Sequence 6619, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6619
;   LENGTH: 662
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-6619

  Query Match             6.9%;  Score 299.5;  DB 4;  Length 662;
  Best Local Similarity   25.9%;  Pred. No. 1.6e-18;
  Matches  187;  Conservative   94;  Mismatches  259;  Indels  181;  Gaps   35;

Qy         28 PCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSR 87
              ||  |   ::  |  |   ::|  ||  |: |||| | || : :     :  |: ||||
Db         25 PCKMVDKKVS--CQVLGLLQVPSVLPPDTETLDLSGNQLRSILASPLGFYTALRHLDLST 82

Qy         88 CEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLAS-----LE 142
              ||  :: ||:|:|:||  | |  | :      :  ||  | :: ::: :  |     ||
Db         83 NEISFLQPGAFQALTHLEHLSLAHNRLAMATALSAGGLGPLPRVTSLDLSGNSLYSGLLE 142

Qy        143 NFPIGHLKTLKELNVAHNLIQSFKLPEY-FSNLTNLEHLDLSSNKIQSIYCTDLRVLHQM 201
              :|  :|  |::| | :  :|  : | :: || ||| || :  |         | ::
Db        143 RL-LGEAPSLHTLSLAENSLT--RLTRHTFRDMPALEQLDLHSNVLMDIEDGAFEGLPRL 199

Qy        202 PLLNLS----------------LDLSLNPMNFI----QPGAFKEIRLHKLTLRNN---- 236
              ||||                ||||  | :       || |  | :|  | || |
Db        200 THLNLSRNSLTCISDFSLQQLRVLDLSCNSIEAFQTASQPQA--EFQLTWLDLRENKLLH 257

Qy        237 FDSLNVMKTCIQGLAGLEVHRLVLGEFRN-----------------EGNLEKFDKSAL 277
              |  |  :  |       : ||  |  ::                 ||      | |
Db        258 FPDLAALPRLIYLNLSNNLIRLPTGPPQDSKGIHAPSEGWSALPLSAPSGNASGRPLSQL 317

Qy        278 EGLCNLTIEEFRLAYLDYYLDDIIDLF------NCLTNVSSFSLVSVTIERVKDFSYNFG 331
              | :|:  |  |   | :|: :  |        |||   :  | |:    : | |:|
Db        318 LNL-DLSYNEIEL-IPDSFLEHLTSLCFLNLSRNCLRTFEARRLGSLPCLMLLDLSHN-A 374

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEV------DLPSLEFLDLSRNGL 385
              : |||      |  || |:             |||  ::      :| ||: |:|  | :
Db        375 LETLELGARALGSLRTLLLQ-----------GNALRDLPPYTFANLASLQRLNLQGNRV 422

Qy        386 S---------FKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQ 436
              |           || : |  | |||: | |  | :           | |    | |: | :
Db        423 SPCGGPDEPGPSGCVAFS--GITSLRSLSLVDNEI----------ELLRAGAFLHTPLTE 470

Qy        437 MSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGL-SSLEVLKMAGNSFQ--ENFLPDIFT 493
                        ||:|        |  || :|||| : ||     :  ||
Db        471 --------------LDLSSNPGLEVATGALGGLEASLEVLALQGNGLMVLQVDLPCFIC 515

Qy        494 ELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSL 553
                 |  |:|:: :|  |    |:    ||:||::  || |||    |   :  |:
Db        516 ----LKRLNLAENRLSHL--PAWTQAVSLEVLDL-RNNSFSL--LPGSAMGGLE------ 560
```

```
Qy        554 NHIMTSKKQELQHFPSSLAPLNLTQNDFACTCEHQSFLQWIKDQ-RQLLVEVERME---C 609
                          :||  | |  |  :| | :      |:  |  |  |:|:  :   |
Db        561 --------------TSLRRLYLQGNPLSC-CGN----GWLAAQLHQGRVDVDATQDLIC 600

Qy        610 ATPSDKQGMPVLSLNIT----CQMN--KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAG 663
                | ::    :||:      |:    | |  : :|: ::|| :          |  ||
Db        601 RFSSQEE----VSLSHVRPEDCEKGGLKNINLIIILTFILVSAIL---------LTTLAA 647

Qy        664 C 664
              |
Db        648 C 648


RESULT 15
US-09-949-016-10710
; Sequence 10710, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10710
;   LENGTH: 665
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10710

  Query Match             6.9%;  Score 299.5;  DB 4;  Length 665;
  Best Local Similarity   25.9%;  Pred. No. 1.6e-18;
  Matches  187;  Conservative   94;  Mismatches  259;  Indels  181;  Gaps   35;

Qy         28 PCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSR 87
              ||  |   ::  |  |   ::|  ||  |: |||| | || : :     :  |: ||||
Db         28 PCKMVDKKVS--CQVLGLLQVPSVLPPDTETLDLSGNQLRSILASPLGFYTALRHLDLST 85

Qy         88 CEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLAS-----LE 142
               ||  :: ||:|:|:||  | |  | :      :  ||  | :: ::: :  |       ||
Db         86 NEISFLQPGAFQALTHLEHLSLAHNRLAMATALSAGGLGPLPRVTSLDLSGNSLYSGLLE 145

Qy        143 NFPIGHLKTLKELNVAHNLIQSFKLPEY-FSNLTNLEHLDLSSNKIQSIYCTDLRVLHQM 201
              :|   :|  |::| | :   :|  : | :: || ||| || :  |       | ::
Db        146 RL-LGEAPSLHTLSLAENSLT--RLTRHTFRDMPALEQLDLHSNVLMDIEDGAFEGLPRL 202

Qy        202 PLLNLS-----------------LDLSLNPMNFI----QPGAFKEIRLHKLTLRNN---- 236
              ||||                 |||| | :       || |  | :|  | || |
Db        203 THLNLSRNSLTCISDFSLQQLRVLDLSCNSIEAFQTASQPQA--EFQLTWLDLRENKLLH 260

Qy        237 FDSLNVMKTCIQGLAGLEVHRLVLGEFRN-----------------EGNLEKFDKSAL 277
              |  |  :   |       : ||  |  ::                ||      | |
Db        261 FPDLAALPRLIYLNLSNNLIRLPTGPPQDSKGIHAPSEGWSALPLSAPSGNASGRPLSQL 320

Qy        278 EGLCNLTIEEFRLAYLDYYLDDIIDLF------NCLTNVSSFSLVSVTIERVKDFSYNFG 331
              | :|:  |  |  | :|: :  |       |||    :  | |:    : | |:|
Db        321 LNL-DLSYNEIEL-IPDSFLEHLTSLCFLNLSRNCLRTFEARRLGSLPCLMLLDLSHN-A 377

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEV------DLPSLEFLDLSRNGL 385
              : |||      |  || |:              |||  ::      :| ||: |:|  | :
Db        378 LETLELGARALGSLRTLLLQ-----------GNALRDLPPYTFANLASLQRLNLQGNRV 425

Qy        386 S---------FKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQ 436
              |           || : |  | |||: | |  | :          | |    | |: | :

Db        426 SPCGGPDEPGPSGCVAFS--GITSLRSLSLVDNEI----------ELLRAGAFLHTPLTE 473

Qy        437 MSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGL-SSLEVLKMAGNSFQ--ENFLPDIFT 493
                              ||:|          |  || :||||| : ||     :  ||
Db        474 --------------LDLSSNPGLEVATGALGGLEASLEVLALQGNGLMVLQVDLPCFIC 518

Qy        494 ELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSL 553
                  |  |:|:: :|  |   |:    ||:||::  || |||   |   :  |:
Db        519 ----LKRLNLAENRLSHL--PAWTQAVSLEVLDL-RNNSFSL--LPGSAMGGLE------ 563

Qy        554 NHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQ-RQLLVEVERME---C 609
                          :||  | |  |  :| | :      |:  |  |  |:|:  :   |
Db        564 --------------TSLRRLYLQGNPLSC-CGN----GWLAAQLHQGRVDVDATQDLIC 603

Qy        610 ATPSDKQGMPVLSLNIT----CQMN--KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAG 663
                | ::    :||:      |:    | |  : :|: ::|| :          |  ||
Db        604 RFSSQEE----VSLSHVRPEDCEKGGLKNINLIIILTFILVSAIL---------LTTLAA 650

Qy        664 C 664
              |
Db        651 C 651


Search completed: March 12, 2005, 19:59:05
Job time : 26.0639 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:01 ; Search time 21.6477 Seconds
(without alignments)
3729.074 Million cell updates/sec

Title: US-09-396-985B-98
Perfect score: 4355
Sequence: 1 MMSASRLAGTLIPAMAFLSC.....SWNPEGTVGTGCNWQEATSI 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	663	15.2	661	2	I56258	RP105 - mouse
2	474	10.9	786	2	T08664	Toll protein-like
3	454	10.4	1097	2	A29943	Toll protein precu
4	433	9.9	1389	2	T13852	gene wheeler prote
5	421	9.7	1385	2	T13887	tlr protein - frui
6	396	9.1	1066	2	T15864	hypothetical prote
7	333.5	7.7	1134	1	A29944	chaoptin precursor
8	316	7.3	605	2	JC5239	insulin-like growt
9	305	7.0	853	2	T17461	disease resistance
10	303	7.0	605	2	A41915	insulin-like growt
11	299.5	6.9	662	2	S42799	garp precursor - h
12	299.5	6.9	1531	2	T42218	slit-1 protein hom
13	296.5	6.8	994	2	H96510	probable disease r
14	296	6.8	603	2	JC1282	insulin-like growt
15	295	6.8	907	2	JG0193	G protein-coupled
16	294	6.8	845	2	T07039	Hcr9-0 protein - t
17	292.5	6.7	603	2	T24315	hypothetical prote
18	292.5	6.7	907	2	JE0176	orphan G protein-c
19	290	6.7	603	2	JC6128	insulin-like growt
20	290	6.7	855	2	T07015	Cf-4A protein - to
21	289.5	6.6	1112	2	T10504	disease resistance
22	289	6.6	855	2	T17460	disease resistance
23	284.5	6.5	1134	2	T04587	hypothetical prote
24	281.5	6.5	622	2	JC7973	synleurin - human
25	280	6.4	890	2	T00800	disease resistance
26	279	6.4	1027	2	B85089	receptor protein k
27	278.5	6.4	1019	2	C96519	probable disease r
28	278	6.4	1091	2	A58532	glial cell membran
29	276.5	6.3	768	2	T17462	disease resistance
30	276	6.3	983	2	G84524	probable disease r
31	275	6.3	1523	2	T13953	MEGF5 protein - ra
32	272	6.2	1469	2	B36665	slit protein 2 pre
33	272	6.2	1480	2	A36665	slit protein 1 pre
34	270	6.2	1143	2	T10636	hypothetical prote
35	268	6.2	910	2	G84648	probable disease r
36	267	6.1	766	2	T01817	hypothetical prote
37	267	6.1	1784	2	C96615	hypothetical prote
38	266	6.1	863	2	A55173	cf-9 protein precu
39	263.5	6.1	967	2	T48210	hypothetical prote
40	262.5	6.0	1109	2	T18536	receptor-like prot
41	261.5	6.0	1051	2	T13174	gp150 protein - fr
42	260	6.0	1064	2	B86465	probable Protein k
43	259	5.9	1029	2	T00712	protein kinase hom
44	257.5	5.9	738	2	T19938	hypothetical prote
45	256	5.9	771	2	T02565	disease resistance

ALIGNMENTS

RESULT 1
I56258
RP105 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56258
R;Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995
A;Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a me
A;Reference number: I56258; MUID:95204928; PMID:7897216
A;Accession: I56258
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-661 <RES>
A;Cross-references: UNIPROT:Q62192; GB:D37797; NID:g761711; PIDN:BAA07043.1; PID:g761712

Query Match 15.2%; Score 663; DB 2; Length 661;
Best Local Similarity 28.7%; Pred. No. 1.4e-33;
Matches 196; Conservative 116; Mismatches 289; Indels 82; Gaps 16;

```
Qy          14 AMAFLSC-VRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSY 72
               |:   ||     | : |:|   | || |  |   :||  || ||: |: ||| |  : :
Db          12 ALFLASCRATTSSDQKCIEKEVNKTYNCENLGLNEIPGTLPNSTECLEFSFNVLPTIQNT 71

Qy          73 SFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLV 132
               :|     | |||:||:|  | :  :||   | ||:|| ||:  :|  | ||  :|: |
Db          72 TFSRLINLTFLDLTRCQIYWIHEDTFQSQHRLDTLVLTANPLIFMAETALSGPKALKHLF 131

Qy         133 AVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYC 192
              ::| ::|::  |: : |||: | :  | | | |||: |     |: ||  :| | :
Db         132 FIQTGISSIDFIPLHNQKTLESLYLGSNHISSIKLPKGFPT-EKLKVLDFQNNAIHYLSK 190

Qy         193 TDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAG 252
               |:  | |   ||||:|: | :  |:||||      |    ||     :    :||
Db         191 EDMSSLQQ--ATNLSLNLNGNDIAGIEPGAFDSAVFQSL----NFGGTQNLLVIFKGLKN 244

Qy         253 LEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSS 312
               :  | || | :  : |    :  |||| :::|   |    |: :   : |:| :
Db         245 STIQSLWLGTFEDMDD-EDISPAVFEGLCEMSVESINL-QKHYFFNISSNTFHCFS---- 298

Qy         313 FSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPT--LKLKSLKRLTFTSNKGGN--AFS 368
                          | | |:|      : |:  : | :||:|  ::||  |    |
Db         299 -----------------GLQELDLTATHLSELPSGLVGLSTLKKLVLSANKFENLCQIS 340

Qy         369 EVDLPSLEF-----------------------LDLSRNGLSFKGCCSQSDFGTTSLKY 403
               : |||                          |||| : :    ||:      : |:
Db         341 ASNFPSLTHLSIKGNTKRLELGTGCLENLENLRELDLSHDDIETSDCCNLQLRNLSHLQS 400

Qy         404 LDLSFNGVITMSSN-FLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVA 462
               |:||:|  ::: :  |    ||| ||   : ||     | | :|  |  |::||:   ::
Db         401 LNLSYNEPLSLKTEAFKECPQLELLDLAFTRLKVKDAQSPFQNLHLLKVLNLSHSLLDIS 460
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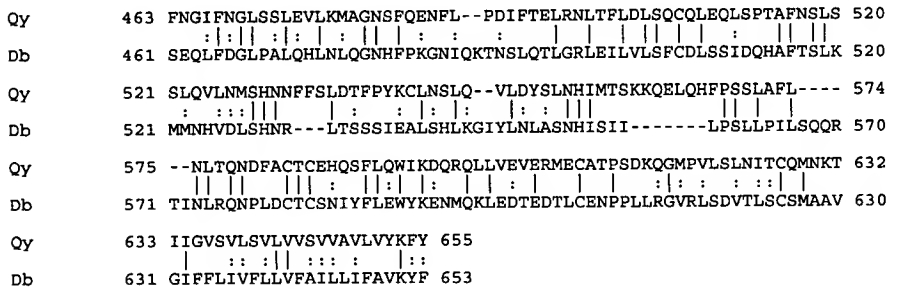
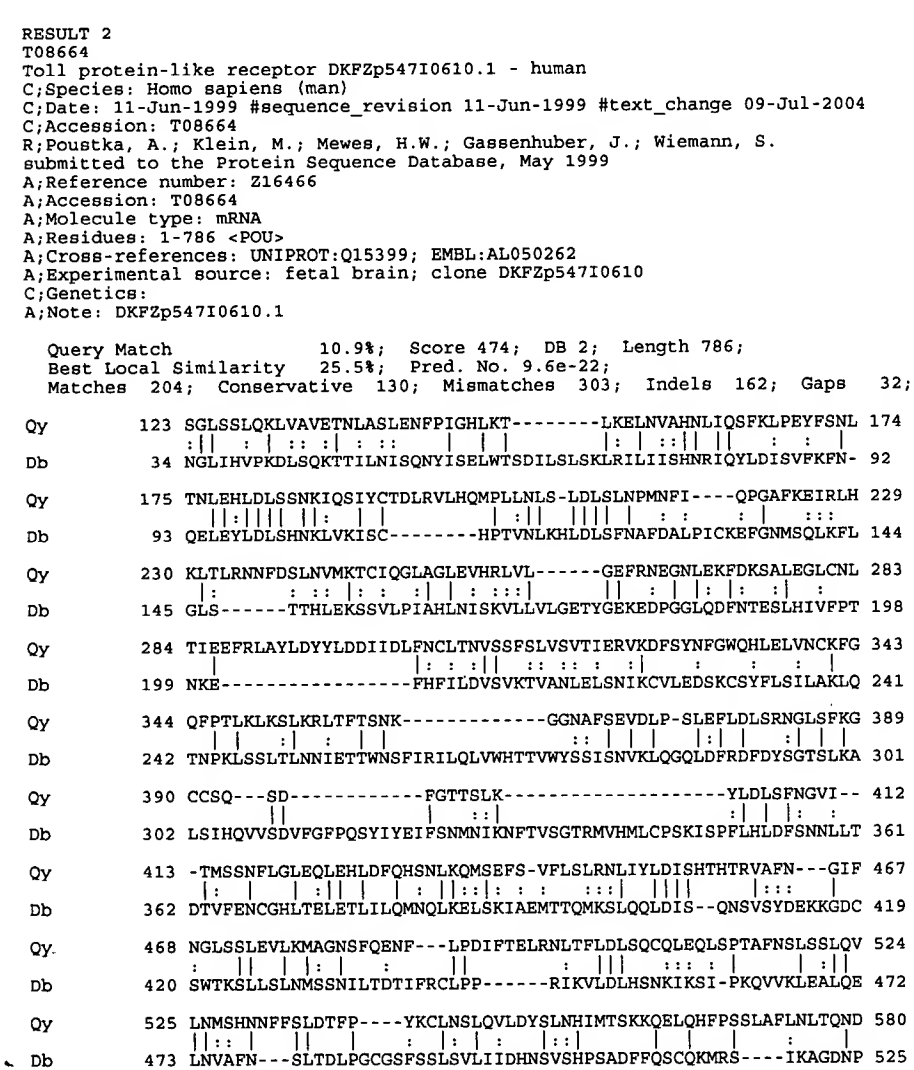
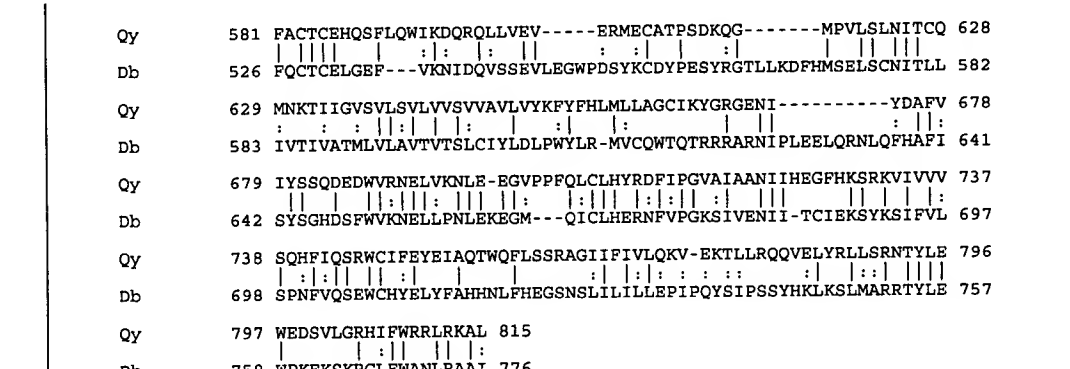


RESULT 2
T08664
Toll protein-like receptor DKFZp547I0610.1 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08664
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16466
A;Accession: T08664
A;Molecule type: mRNA
A;Residues: 1-786 <POU>
A;Cross-references: UNIPROT:Q15399; EMBL:AL050262
A;Experimental source: fetal brain; clone DKFZp547I0610
C;Genetics:
A;Note: DKFZp547I0610.1

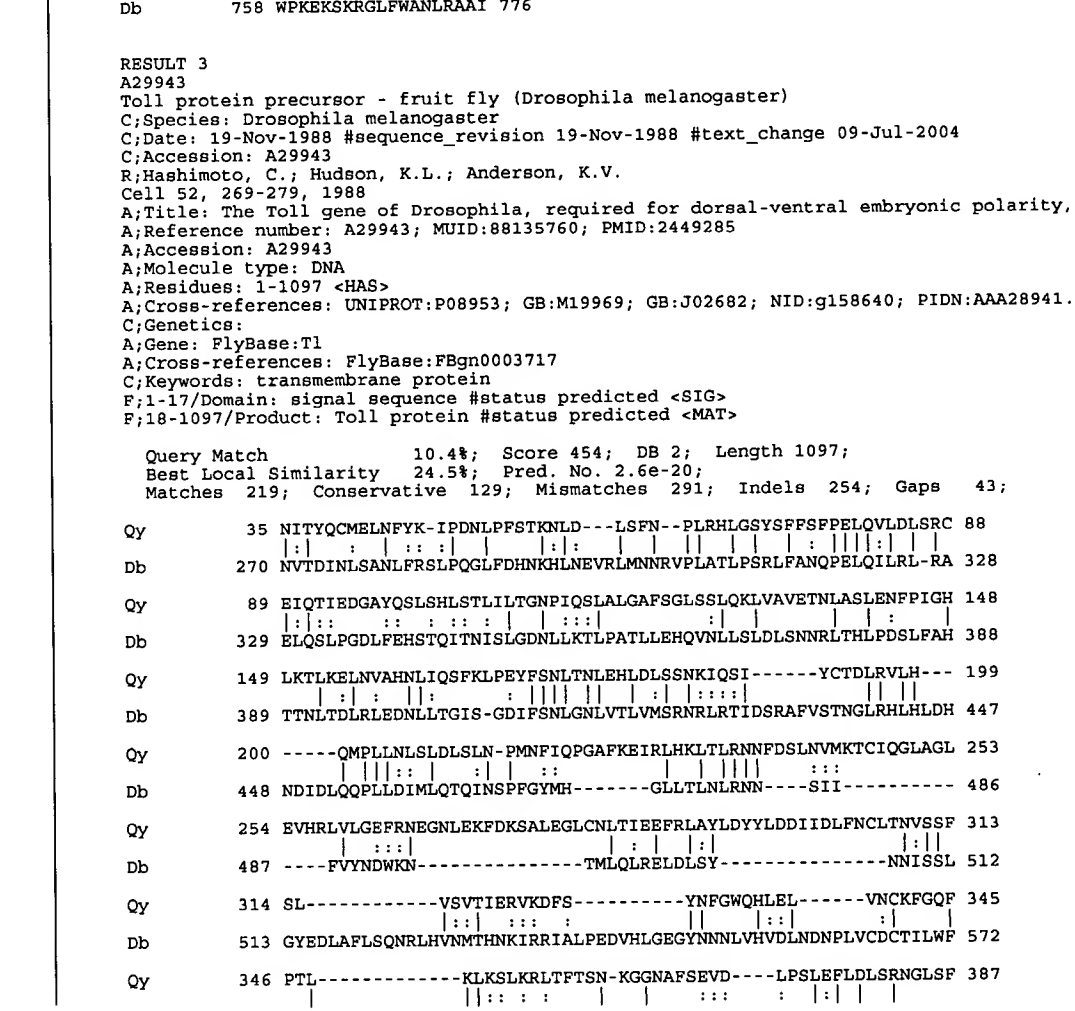
Query Match 10.9%; Score 474; DB 2; Length 786;
Best Local Similarity 25.5%; Pred. No. 9.6e-22;
Matches 204; Conservative 130; Mismatches 303; Indels 162; Gaps 32;





RESULT 3
A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A29943
R;Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A;Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, ap
A;Reference number: A29943; MUID:88135760; PMID:2449285
A;Accession: A29943
A;Molecule type: DNA
A;Residues: 1-1097 <HAS>
A;Cross-references: UNIPROT:P08953; GB:M19969; GB:J02682; NID:g158640; PIDN:AAA28941.1;
C;Genetics:
A;Gene: FlyBase:Tl
A;Cross-references: FlyBase:FBgn0003717
C;Keywords: transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-1097/Product: Toll protein #status predicted <MAT>

Query Match 10.4%; Score 454; DB 2; Length 1097;
Best Local Similarity 24.5%; Pred. No. 2.6e-20;
Matches 219; Conservative 129; Mismatches 291; Indels 254; Gaps 43;



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Db        573 IQLVRGVHKPQYSRQFKLRTDRLVCSQPNVLEGTPVRQIEPQTLICPLDFSDDPRERKCP 632

Qy        388 KGC-CSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSL 446
              :|| |    :     | | :: :     | |   : :| :|   | |:: |       | |
Db        633 RGCNCHVRTYD----KALVINCH-----SGNLTHVPRLPNL---HKNMQLME-----LHL 675

Qy        447 RNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQC 506
              |   | :   :|         |  |:  | :|||                  ||| :|: |
Db        676 ENNTLLRLPSANT--------PGYESVTSLHLAGN--------------NLTSIDVDQL 712

Qy        507 QLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQH 566
              |           |::|                  || | ||:     | |
Db        713 ------PT-----------NLTH-----------------LDISWNHL-----QMLN- 730

Qy        567 FPSSLAFLN---------LTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQG 617
              : | |||          |: | : | |  :  | : :|  : : :   | |
Db        731 -ATVLGFLNRTMKWRSVKLSGNPWMCDCTAKPLLLFTQDNFERIGDRNEMMCVNAEMPTR 789

Qy        618 MPVLSLNITCQMNKTI-IGVSV---LSVLVVSVVAVLVYKF--------YFHLMLLAGCI 665
              |  || |  |   | : | ::|   |: |:    | | |||        | | :||
Db        790 MVELSTNDICPAEKGVFIALAVVIALTGLLAGFTAALYYKFQTEIKIWLYAHNLLL---- 845

Qy        666 KYGRGENI-----YDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAA 720
              :   |::     :|||: || :|: :: : ||   || |    ||||:| ||:: |  |
Db        846 WFVTEEDLDKDKKFDAFISYSHKDQSFIEDYLVPQLEHGPQKFQLCVHERDWLVGGHIPE 905

Qy        721 NIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIV---LQKVEKT 777
              ||:      ||: |:|:||:||:| |   |:  |         |: || |:   :  |||
Db        906 NIM-RSVADSRRTIIVLSQNFIKSEWARLEFRAAHRSALNEGRSRIIVIIYSDIGDVEK- 963

Qy        778 LLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGTVGTG 830
              | :::: |  |  ||||:| |       || :|| ||   :   | | :| |
Db        964 -LDEELKAY--LKMNTYLKWGDP-----WFWDKLRFALPHRR---PVGNIGNG 1005
```

RESULT 4
T13852
gene wheeler protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13852
R;Eldon, E.; Kooyer, S.; D'evelyn, D.; Duman, M.; Lawinger, P.; Botas, J.; Bellen, H.
Development 120, 885-899, 1994
A;Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simila
A;Reference number: Z17796; MUID:95324375; PMID:7600965
A;Accession: T13852
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1389 <ELD>
A;Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:g415682; PID:g1019104; PIDN:AAA7920
C;Genetics:
A;Gene: wheeler
A;Cross-references: FlyBase:FBgn0004364

  Query Match   9.9%; Score 433; DB 2; Length 1389;
  Best Local Similarity   24.4%; Pred. No. 7.2e-19;
  Matches 217; Conservative 138; Mismatches 356; Indels 178; Gaps   34;

```
Qy         59 LDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLA 118
              |:|| | |  :|| :|      ||:||:    |  ||:||:  | :| || |  | : :|
Db        338 LNLSNNALTRIGSKTFKELYFLQILDMRNNSIGHIEEGAFLPLYNLHTLNLAENRLHTLD 397

Qy        119 LGAFSGLSSLQKLVAVETNLASL-ENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNL 177
              |:||  | ||  :  || |: |:    :  ||||::: |  |  ::||   :|: |
Db        398 NRIFNGLYVLTKL-TLNNNLVSIVESQAFRNCSDLKELDLSSN--QLTEVPEAVQDLSML 454

Qy        178 EHLDLSSNKIQSIYCTDLRVLHQMPLLNL--------------------SLDLSLNPMNF 217
              : |||  |:|      | |:|:  | |                    |:|: | :
Db        455 KTLDLGENQISEFKNNTFRNLNQLTGLRLIDNRIGNITVGMFQDLPRLSVLNLAKNRIQS 514

Qy        218 IQPGAF-KEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNE---------- 266
              |: ||| |   :  : |  ||       | | |:       | |    |
Db        515 IERGAFDKNTEIEAIRLDKNF------LTDINGIFATLASLLWLNLSENHLVWFDYAFIP 568

Qy        267 GNLEKFD--KSALEGLCNL--TIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIER 322
              ||:  |   : :| | |      || |:  ||   : | ::   ::  :|  |: :
Db        569 SNLKWLDIHGNYIEALGNYYKLQEEIRVTTLDASHNRITEI-GAMSVPNSIELLFINNNI 627

Qy        323 VKDFSYN--FGWQHLELVNCKFGQFPTLKLKSLKRLTFTSNK-------GGNAFS----- 368
              :     |       | |:       : | :|:    :: |       ||| |
Db        628 IGQIQANTFVDKTRLARVDLYANVLSKISLNALRVAPVSAEKPVPEFYLGGNPFECDCSM 687

Qy        369 ----------------EVDLPSLEFL-------------DLSRNGLSFK---------GC 390
                             ||| ::| |                || :    |         |
Db        688 EWLQRINNLTTRQHPHVVDLGNIECLMPHSRSAPLRPLASLSASDFVCKYESHCPPTCHC 747

Qy        391 CSQSDFGTTSLKYLDLSFNGVITMSSNFL--GLEQLEHLDFQHSNLKQMSEFSVFLSLRN 448
              |          :   : |      | ::| :  | : |  |      |          ::|   |
Db        748 CEYEQCECEVICPGNCSCFHDATWATNIVDCGRQDLAAL----PNRIPQDVSDLYLDGNN 803

Qy        449 LIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQL 508
              :  |:: |    |       ::    |:|  |:                 :| ||  | |   :|
Db        804 MPELEVGHLTGRRNLRALYLNASNLMTLQNGS-----------LAQLVNLRVLHLENNKL 852

Qy        509 EQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFP 568
              |  | | ||  |: | : :|    :    :: | ||:||    | : :    : :|
Db        853 TALEGTEFRSLGLLRELYLHNNMLTHISNATFEPLVSLEVLRLDNNRLSSLPHLQYRH-- 910

Qy        569 SSLAFLNLTQNDFACTCEH-QSFLQWIKDQRQLLVEVERMECATPSDKQGMPVL------ 621
              ||  | | :| ::| |:  :   |:: |   :: :   : |      |: : ::
Db        911 -SLQGLTLGRNAWSCRCQQLRELAQFVSDNAMVVRDAHDIYCLDAGIKRELELIGNLANG 969

Qy        622 ----------SLNITCQMNKT-IIG------VSVLSVLVVSVVAVLVYKFYFHLMLLAGC 664
                       : ||:   :    ||       | ||  ||| :: | |::     : | |
Db        970 PDCSDLLDASASNISSSQDLAGAIGCPCWPAVLVLIFLVVVLIIVFVFRESVRMWLFA-- 1027

Qy        665 IKYG------RGEN---IYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPG 715
              ||       | |:   :||| :::| :| ::|   :   || | |||:||:  || :|
Db       1028 -HYGVRVCEPRFEDAGKLYDAIILHSEKDYEFVCRNIAAELEHGRPPFRLCIQQRD-LPP 1085

Qy        716 VAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQK-- 773
              |    :: ||   |||:|:|:::: : : |   |:  |    |  |  |:     ||
Db       1086 QASHLQLV-EGARASRKIILVLTRNLLATEWNRIEFRNA----FHESLRGL----AQKLV 1136

Qy        774 -VEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHI------FWRRLRKAL 815
              :|:| : : |     ||   ||:   ||     :       || :|| |:
Db       1137 IIEETSVSAEAEDVAELS--PYLK---SVPSNRLLTCDRYFWEKLRYAI 1180
```

RESULT 5
T13887
tlr protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13887
R;Chiang, C.; Beachy, P.A.
Mech. Dev. 47, 225-239, 1994
A;Title: Expression of a novel Toll-like gene spans the parasegment boundary and contrib
A;Reference number: Z17805; MUID:95151581; PMID:7848870
A;Accession: T13887
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1385 <CHI>
A;Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PIDN:AAB33383
C;Genetics:
A;Cross-references: FlyBase:FBgn0004364
A;Note: tlr

  Query Match   9.7%; Score 421; DB 2; Length 1385;
  Best Local Similarity   24.0%; Pred. No. 4e-18;
  Matches 213; Conservative 139; Mismatches 359; Indels 178; Gaps   33;

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Qy         59 LDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLA 118
              |:|| | |  :|| :|      ||:||:    |  ||:||:  | :| || |  | : :|
Db        338 LNLSNNALTRIGSKTFKELYFLQILDMRNNSIGHIEEGAFLPLYNLHTLNLAENRLHTLD 397
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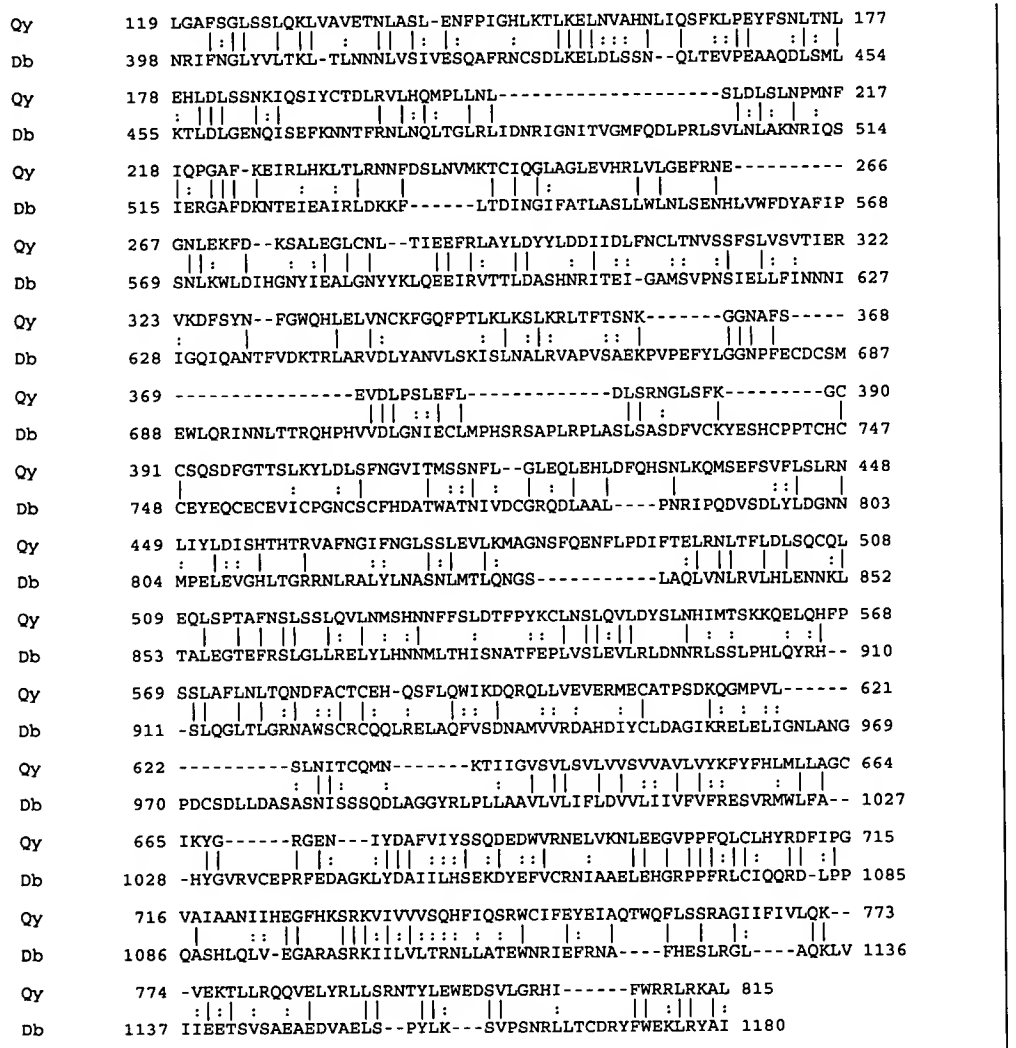

RESULT 6
T15864
hypothetical protein C56E6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15864
R;Fulton, L.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C56E6.
A;Reference number: S69019
A;Accession: T15864
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1066 <FUL>
A;Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:g1055114; PID:g1055120; PIDN:AAA810
C;Genetics:
A;Gene: CESP:C56E6.6
A;Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3; 9

Query Match 9.1%; Score 396; DB 2; Length 1066;
Best Local Similarity 26.9%; Pred. No. 1e-16;
Matches 156; Conservative 100; Mismatches 227; Indels 98; Gaps 24;

RESULT 7
A29944
chaoptin precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: photoreceptor cell-specific membrane protein
C;Species: Drosophila melanogaster
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29944; A21123
R;Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
Cell 52, 291-301, 1988
A;Title: Chaoptin, a cell surface glycoprotein required for Drosophila photoreceptor cel
A;Reference number: A29944; MUID:88135762; PMID:3124963
A;Accession: A29944
A;Molecule type: DNA
A;Residues: 1-1134 <REI>
A;Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M1901
R;Zipursky, S.L.; Venkatesh, T.R.; Teplow, D.B.; Benzer, S.
Cell 36, 15-26, 1984
A;Title: Neuronal development in the Drosophila retina: monoclonal antibodies as molecul
A;Reference number: A21123; MUID:84106810; PMID:6420071
A;Accession: A21123
A;Molecule type: protein
A;Residues: 31-43,'HX',46-49,'H' <ZIP>
C;Genetics:
A;Gene: FlyBase:chp
A;Cross-references: FlyBase:FBgn0000313

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A;Introns: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
C;Superfamily: chaoptin; leucine-rich alpha-2-glycoprotein repeat homology
C;Keywords: cell adhesion; glycoprotein; membrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-1134/Product: chaoptin #status predicted <MAT>
F;80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR
F;103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;303-325/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F;551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
F;577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
F;601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>
F;625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR23>
F;649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>
F;673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR25>
F;708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>
F;733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR27>
F;757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR28>
F;781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>
F;805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR30>
F;828-851/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR31>
F;854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
F;879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
F;903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
F;928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F;949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
F;973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
F;996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
F;1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
F;1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

  Query Match             7.7%;  Score 333.5;  DB 1;  Length 1134;
  Best Local Similarity   23.0%;  Pred. No. 8.4e-13;
  Matches  177;  Conservative  114;  Mismatches  249;  Indels  231;  Gaps   30;

Qy          50 DNLPFSTKNLDLSFNPLRHLGSYSFPFSPPELQV-------------------------L 83
               |:|  | : |||| | |  |     | :|  |:|                         |
Db         346 DSLVNSLQILDLSGNNLTKLHHKLFNNFDVLRVISMRDNKIKIQKPTETFNAVHYTLLKL 405

Qy          84 DLS-----RCEIQTIEDGA----YQSLS-------------------HLSTLILTGNPIQ 115
               |||         :||: :       :|||                   |  | :|   :
Db         406 DLSGDRNDPTNLQTLRNMTRMRNMRSLSISRLGSSSVGPEDFKDFGVELEDLQITRASLS 465

Qy         116 SLALGAFSGLSSLQKLVAVETNLASLEN---FPIGHLKTLKELNVAHNLIQSFKLPEYFS 172
                :   ||  :  |::|   |  ::|:||     |||  :|  | ::|     |    |
Db         466 GIQSHAFKHVRGLKRLDFSENGISSIENDAFHEIGH--SLISLKMSHGYSGSALPAEPLR 523

Qy         173 NLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFK---EIRLH 229
               :||:|: || |:| | |:  |     |  : |     |:|  | :  :  | |:     :|
Db         524 HLTSLQELDFSNNHISSMSDTSFHFLKNLRL----LELHDNRIEQVLKGTFQGDIHSKLE 579

Qy         230 KLTLRNN---------FDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEG- 279
               :::|| |          |  |  ::        |: :::   | |   ||:: :  :| |
Db         580 EISLRFNHLTSISQHTFFDLEALRK-----LHLDDNKIDKIERRAFMNLDELEYLSLRGN 634

Qy         280 -LCNLTIEEF----RLAYLDYYLDDI----IDLFNCLTNVSSFSLVSVTIERVKDFSYNF 330
                : ||  | |    :|  ||   : :      | |: :  :|: : |:|:  :::   ||
Db         635 KINNLADESFQNLPKLEILDMAFNQLPNFNFDYFDQVGTLSNLN-VNVSHNQIRQLMYNS 693

Qy         331 GWQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSF--K 388
               |                                 | |    :   ::: |||| | :|
Db         694 SW----------------------------SGRNEHGGMYHSNIKILDLSHNNISIIHP 724

Qy         389 GCCSQSDFGTT--------------------SLKYLDLSFNGVITMSSN-FLGLEQLEH 426
               |    ::   |                    |::||||:| :  :  : |   :||:
Db         725 GYFRPAEISLTHLHLGYNSLMNTTRDVFGNMPHLQWLDLSYNWIHELDFDAFKNTKQLQL 784

Qy         427 LDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR-VAFNGIFNG---------------- 469
               : | |: |  : :  :|  :: |  :| || | |  :  |  :||
Db         785 VFFGHNYLSDIPQ-DIFKPVQGLRIVDFSHNHLRGLPDNLFYNGGMEKLDVSHNMMLKIP 843

Qy         470 ---LSSLEVLKMAGNSFQENFLP-----DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSS 521
                  ||||  | :       ||:      |:  : |:| :||:|   | ::    | ::
Db         844 SSSLSSLAALTLCELHLSNNFISTIHSMDLSNKFRSLRYLDISYNYLLRIDDAVFATMPK 903

Qy         522 LQVLNMSHN--------NFF-------------SLDTFPYKCLNSLQVLDYSLNHIMTS 559
               | ||::|||        :|                || | |   | |:       | : |
Db         904 LAVLDLSHNRDLKVMDKSFMGLENSLIKLGLENVSLSTVPEIRLKYLREFRLGYNE-LPS 962

Qy         560 KKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQ--- 616
                ||| |  |:|  |:|: ||                    |  |  |  | |  ::
Db         963 IPQELAHNMSNLRMLDLSNND-------------------LTNVPLMTQALPHLRRLML 1002

Qy         617 -GMPVLSLNITCQMNKTIIGVSV-LSVLVVSVVAVLVYKFYFHLMLLAGCI 665
                | |: |||     | :  ||:  | :| :|   :  :::        ||:
Db        1003 SGNPITSLN-----NNSFDGVNEDLEMLDISNFRLHYFEY--------GCL 1040


RESULT 8
JC5239
insulin-like growth factor acid-labile chain - baboon
C;Species: Papio sp. (baboon)
C;Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C;Accession: JC5239
R;Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-lik
A;Reference number: JC5239; MUID:97040714; PMID:8886027
A;Contents: liver
A;Accession: JC5239
A;Molecule type: mRNA
A;Residues: 1-605 <DEL>
C;Comment: This factor is structurally related to proinsulin and have insuline-like meta

  Query Match             7.3%;  Score 316;  DB 2;  Length 605;
  Best Local Similarity   24.4%;  Pred. No. 4.5e-12;
  Matches  157;  Conservative   94;  Mismatches  242;  Indels  150;  Gaps   23;

Qy          33 VPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQT 92
               |  ::  |   |  ::|| :|  |: | | | |  :  :|  :   |  |:|  :: :
Db          53 VNELSVFCSSRNLTRLPDGIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGS 112

Qy          93 IEDGAYQSLSHLSTLILTGNPIQSLALGAFS----------------------GLSSL 128
               :|  |   | :|  | |  | ::|||:|  |:                     || :|
Db         113 LEPQALLGLENLCHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLEDGLFEGLGNL 172

Qy         129 QKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQ 188
                |      :|| | :      |  |:|| :| | : ::  |  || |  | |||| | ::
Db         173 WDLNLGWNSLAVLPDAAFRGLGGLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALR 231

Qy         189 SIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCI 247
               :|      |  |:| |  | |  | :  : |||  ::  |  | | :|     :::
Db         232 AI---KANVFAQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTF 286

Qy         248 QGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCL 307
               || || | ||              :|:  |   | |:       ::|:::
Db         287 PGLLGLRVLRL-------------SHNAIASLRPRTFEDL------HFLEEL------- 319

Qy         308 TNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGN 365
                      |    | :: : |:  |   ||::      |   :|: :   ||  :  |  ||
Db         320 ------QLGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKVGAFLGLTNVAVMNLSGN 372
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Qy        366 AFSEVDLPSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL 419
Db        373 CLR--NLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFAGLSGLRRLFLKDNGLVGIEEQSL 430

Qy        420 -GLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKM 478
Db        431 WGLAELLELDLTSNQL----------------------THLP---HQLFQGLGKLEYLLL 465

Qy        479 AGNSFQENFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDT 537
Db        466 SHNRLAE--LPADALGPLQRAFWLDVSHNRLEALPGSLLASLGRLRYLNLRNN---SLRT 520

Qy        538 FPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQS-------- 589
Db        521 FTPQ-------------------------PPGLERLWLEGNPWDCSCPLKALRDFALQN 554

Qy        590 ------FLQWI---KDQRQLLVEVERMECATPSDKQGMPVLSL 623
Db        555 PSAVPRFVQAICEGDDCQPPVYTYNNITCASPPEVAGLDLRDL 597
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RESULT 9
T17461
disease resistance protein D - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17461
R;Parniske, M.; Jones, J.D.
Proc. Natl. Acad. Sci. U.S.A. 96, 5850-5855, 1999
A;Title: Recombination between diverged clusters of the tomato Cf-9 plant disease resist
A;Reference number: Z18801; MUID:99254130; PMID:10318973
A;Accession: T17461
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-853 <PAR>
A;Cross-references: UNIPROT:Q9ZS82; EMBL:AF119040; NID:g4235640; PID:g4235641; PIDN:AAD1
C;Genetics:
A;Gene: NL0D

Query Match 7.0%; Score 305; DB 2; Length 853;
Best Local Similarity 24.5%; Pred. No. 3.4e-11;
Matches 192; Conservative 106; Mismatches 291; Indels 194; Gaps 35;

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Qy         35 NITYQCMELNFY------KIPDNLPF----STKNLDLSFN-----PLRHLGSYSFFSFPE 79
Db         79 NTTGQVIELDLRCSQLQGKLHSNSSLFQLSNLKRLDLSYNDFTGSPI----SPKFGEFSN 134

Qy         80 LQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG------AFSGLSSLQKLVA 133
Db        135 LTHLDLFDSNFTGIIPSEISHLSKLYVLRTSTDYPYGLSLGPHNFELLLKNLTQLRELNL 194

Qy        134 VETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCT 193
Db        195 YDVNLSS--TIPSNFSSHLTNLRLAYTELRGI-LPERFFHLSNLESLDLSFNPQLTVRFP 251

Qy        194 DLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGL 253
Db        252 TTKWNSSASLVNLYL-AGVNIADRI-PESFSHL-------------------------T 283

Qy        254 EVHRLVLGEFRNEGNLEKFDKSALEGLCNLT-IEEFRLAYLDY-YLDDIIDLFNCLTNVS 311
Db        284 ALHKLHMGYTNLSGPIPK-------PLWNLTHIESL---FLDYNHLEGPISHFTIFEKLK 333

Qy        312 SFSLVSVTIE-RVKDFSYNFGWQHLELV----NCKFGQFPT--LKLKSLKRLTFTSNK-G 363
Db        334 SLSLGNNNFDGRLEFLSFNRSWMKLERLDFSSNFLTGPIPSNVSGLQNLQQLILSSNHLN 393

Qy        364 GNAFSEV-DLPSLEFLDLSRNGLSFK-------------------GCCSQSDFGTTSLK 402
Db        394 GTIPSWIFSLPSLTVLNLSDNTLSGKIQEFKSKTLYFVSLEQNKLEGPIPRSLLNQQFLQ 453

Qy        403 YLDLSFNGVI-TMSSNFLGLEQLEHLDFQHSNLK--------QMSEFSVFLSLRNLIYLD 453
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Db        454 ALLLSHNNISGHISSAICNLKTFILLNLKSNNLEGTIPQCLGEMSELQV---------LD 504

Qy        454 ISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSP 513
Db        505 LSNNSLSGTMNTTFSIGNPLHIIKLDWNKLQGKVPPSLI-NCKKLELLDLSNNELNDTFP 563

Qy        514 TAFNSLSSLQVLNMSHN----------------------NFFSLDTFPYKCLNSLQVL-- 549
Db        564 KWLGDLPNLQVLNFRSNKLYGPIRTNNLFAKIRVVDLSSNGFSGD-LPVSFFENFEAMKI 622

Qy        550 ----------------DYSLNHIMTSKK---QELQHFPSSLAFLNLTQNDFACTCEH-QS 589
Db        623 NGENNGTRKYVADLYSDYYKNYLIVTTKGLDQELSRVLTTQIIIDLSKNKFE---GHIPN 679

Qy        590 FLQWIKDQRQLLVEVERMECATPSDKQGMPVL------SLNITCQMNKTIIGVSVLSVLV 643
Db        680 IIGDLIGLRTLNLSHNVLEGHIPASFQNLSVLESLDLSSNKISGAIPQQLASLTFLEVLN 739

Qy        644 VSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPF 703
Db        740 LS---------HNHLV---GCIPKGKQ---FDSFENSSYLGNDGLR---------GLPPS 775

Qy        704 QLC 706
Db        776 RDC 778
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RESULT 10
A41915
insulin-like growth factor-binding complex acid-labile chain precursor - human
N;Alternate names: Acid-Labile Subunit (ALS)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A41915
R;Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
Mol. Endocrinol. 6, 870-876, 1992
A;Title: Structure and functional expression of the acid-labile subunit of the insulin-l
A;Reference number: A41915; MUID:92357025; PMID:1379671
A;Accession: A41915
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-605 <LEO>
A;Cross-references: UNIPROT:P35858; GB:M86826; NID:g184807; PIDN:AAA36047.1; PID:g184808
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:110171)
F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

Query Match 7.0%; Score 303; DB 2; Length 605;
Best Local Similarity 24.4%; Pred. No. 2.9e-11;
Matches 157; Conservative 91; Mismatches 243; Indels 152; Gaps 24;

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Qy         40 CMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQ 99
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119
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Qy        100 SLSHLSTLILTGNPIQSLALGAFS-----------------------GLSSLQKLVAVE 135
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        136 TNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDL 195
Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRL-AYLQPALFSGLAELRELDLSRNALRAI---KA 235

Qy        196 RVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLE 254
Db        236 NVFVQLPRLQ-KLYLDRNLIAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLR 293

Qy        255 VHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFS 314
Db        294 VLRL--------------SHNAIASLRPRTFKDL------HFLEEL------------Q 320

Qy        315 LVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS--NKGGNAFSEVDL 372
Db        321 LGHNRIRQLAERSFE-GLGQLEVLTLDHNQLQEVKAGAFLGLTNVAVMNLSGNCLR--NL 377

Qy        373 PSLEFLDLSR-NGLSFKGCC-----SQSDFGTTSLKYLDLSFNGVITMSSNFL-GLEQLE 425
Db        378 PEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSGLRRLFLKDNGLVGIEEQSLWGLAELL 437

Qy        426 HLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQE 485
Db        438 ELDLTSNQL----------------------THLP---HRLFQGLGKLEYLLLSRNRLAE 472

Qy        486 NFLP-DIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLN 544
Db        473 --LPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNN---SLRTFTPQ--- 524

Qy        545 SLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKD-------- 596
Db        525 ----------------------PPGLERLWLEGNPWDCGCP----LKALRDFALQNPSA 557

Qy        597 -QRQLLVEVERMECATPSDKQGMPVLSLNITCQMNKTIIGVSV 638
Db        558 VPRFVQAICEGDDCQPPAYTYN------NITCASPPEVVGLDL 594
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RESULT 11
S42799
garp precursor - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S42799; I37407
R;Birnbaum, D.
submitted to the EMBL Data Library, July 1993
A;Reference number: S42799
A;Accession: S42799
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-662 <BIR>
A;Cross-references: UNIPROT:Q14392
R;Ollendorff, V.; Noguchi, T.; deLapeyriere, O.; Birnbaum, D.
Cell Growth Differ. 5, 213-219, 1994
A;Title: The GARP gene encodes a new member of the family of leucine-rich repeat-contain
A;Reference number: I37407; MUID:94235567; PMID:8180135
A;Accession: I37407
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-662 <RES>
A;Cross-references: EMBL:Z24680; NID:g439295; PIDN:CAA80847.1; PID:g439296
C;Genetics:
A;Gene: GDB:GARP; D11S833E
A;Cross-references: GDB:433911
A;Map position: 11q13.5-11q14
F;50-73/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;74-97/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;98-121/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;150-173/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;174-197/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;198-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;244-265/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;266-289/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;316-339/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;340-363/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;364-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;411-433/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;444-466/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;467-490/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;492-514/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;515-536/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F;537-560/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>

Query Match 6.9%; Score 299.5; DB 2; Length 662;
Best Local Similarity 25.9%; Pred. No. 5.3e-11;
Matches 187; Conservative 94; Mismatches 259; Indels 181; Gaps 35;

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Qy         28 PCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSR 87
Db         25 PCKMVDKKVS--CQVLGLLQVPSVLPPDTETLDLSGNQLRSILASPLGFYTALRHLDLST 82

Qy         88 CEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLAS-----LE 142
Db         83 NEISFLQPGAFQALTHLEHLSLAHNRLAMATALSAGGLGPLPRVTSLDLSGNSLYSGLLE 142

Qy        143 NFPIGHLKTLKELNVAHNLIQSFKLPEY-FSNLTNLEHLDLSSNKIQSIYCTDLRVLHQM 201
Db        143 RL-LGEAPSLHTLSLAENSLT--RLTRHTFRDMPALEQLDLHSNVLMDIEDGAFEGLPRL 199

Qy        202 PLLNLS-----------------LDLSLNPMNFI----QPGAFKEIRLHKLTLRNN---- 236
Db        200 THLNLSRNSLTCISDFSLQQLRVLDLSCNSIEAFQTASQPQA--EFQLTWLDLRENKLLH 257

Qy        237 FDSLNVMKTCIQGLAGLEVHRLVLGEFRN-------------------EGNLEKFDKSAL 277
Db        258 FPDLAALPRLIYLNLSNNLIRLPTGPPQDSKGIHAPSEGWSALPLSAPSGNASGRPLSQL 317

Qy        278 EGLCNLTIEEFRLAYLDYYLDDIIDLF------NCLTNVSSFSLVSVTIERVKDFSYNFG 331
Db        318 LNL-DLSYNEIEL-IPDSFLEHLTSLCFLNLSRNCLRTFEARRLGSLPCLMLLDLSHN-A 374

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEV------DLPSLEFLDLSRNGL 385
Db        375 LETLELGARALGSLRTLLLQ-----------GNALRDLPPYTFANLASLQRLNLQGNRV 422

Qy        386 S---------FKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQ 436
Db        423 SPCGGPDEPGPSGCVAFS--GITSLRSLSLVDNEI----------ELLRAGAFLHTPLTE 470

Qy        437 MSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGL-SSLEVLKMAGNSFQ--ENFLPDIFT 493
Db        471 --------------LDLSSNPGLEVATGALGGLEASLEVLALQGNGLMVLQVDLPCFIC 515

Qy        494 ELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSL 553
Db        516 ----LKRLNLAENRLSHL--PAWTQAVSLEVLDL-RNNSFSL--LPGSAMGGLE------ 560

Qy        554 NHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQ-RQLLVEVERME---C 609
Db        561 --------------TSLRRLYLQGNPLSC-CGN----GWLAAQLHQGRVDVDATQDLIC 600

Qy        610 ATPSDKQGMPVLSLNIT----CQMN--KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAG 663
Db        601 RFSSQEE----VSLSHVRPEDCEKGGLKNINLIIILTFILVSAIL---------LTTLAA 647

Qy        664 C 664
Db        648 C 648
```

RESULT 12
T42218
slit-1 protein homolog - rat
N;Alternate names: MEGF4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42218
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T42218
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1531 <NAK>
A;Cross-references: UNIPROT:O88279; EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF4
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r

Query Match 6.9%; Score 299.5; DB 2; Length 1531;
Best Local Similarity 22.1%; Pred. No. 1.6e-10;
Matches 167; Conservative 95; Mismatches 260; Indels 233; Gaps 27;

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Qy          4 ASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLDLSF 63
              |  |:    |||   ||              |      |  || ||| :   : |
Db        274 ACTLSSGSCPAMC--SC-------------SNGIVDCRGKGLTAIPANLPETMTEIRLEL 318

Qy         64 NPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFS 123
              | :: :   :|  : :|: :|||  :|  |   |:| |  |::|:| || |  |  | |
Db        319 NGIKSIPPGAFSPYRKLRRIDLSNNQIAEIAPDAFQGLRSLNSLVLYGNKITDLPRGVFG 378

Qy        124 GLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLS 183
              || :|| |:                    ||   | |   : |: | :| ||  | |
Db        379 GLYTLQLLL---------------------LNA--NKINCIR-PDAFQDLQNLSLLSLY 413

Qy        184 SNKIQSI---YCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240
              |||||:    | || :          :| |: ||  ||     | :          :|
Db        414 DNKIQSLAKGTFTSLRAIQ-------TLHLAQNP--FICDCNLKWLA--------DFLRT 456

Qy        241 NVMKTCIQGLAGLEVHRLV---LGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYL 297
              | ::|   |        ||    :|: ::    :||  || |       : |     ||:|
Db        457 NPIET--TGARCASPRRLANKRIGQIKS----KKFRCSAKE-------QYFIPGTEDYHL 503

Qy        298 D-----DIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKF------GQFP 346
              :     |:      |     |       : : :: :          | | | :       | |
Db        504 NSECTSDVACPHKCRCEASVVECSGLKLSKIPE-RIPQSTTELRLNNNEISILEATGLFK 562

Qy        347 TLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDL 406
              ||  ||::  ::||       ||::  : |                  | ||:  | |
Db        563 --KLSHLKKINLSNNK----VSEIEDGTFE-------------------GATSVSELHL 596

Qy        407 SFNGVITMSSN-FLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNG 465
              : | : :: |  | ||: |  |  ::: :  :    | |  |||:  | :    |
Db        597 TANQLESVRSGMFRGLDGLRTLMLRNNRISCIHNDS-FTGLRNVRLLSLYDNHITTISPG 655

Qy        466 IFNGLSSLEVLKMAGNSFQENF---------------------------------------- 487
              |: | :|  | :  | | |
Db        656 AFDTLQALSTLNLLANPFNCNCQLAWLGDWLRKRKIVTGNPRCQNPDFLRQIPLQDVAFP 715

Qy        488 ----------------------------------------LPDIFTEL--------- 495
                                                     :|   |||
Db        716 DFRCEEGQEEVGCLPRPQCPQECACLDTVVRCSNKHLQALPKGIPKNVTELYLDGNQFTL 775

Qy        496 --------RNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQ 547
                     : |  :|||  ::  || ::| ::| |  |  | :|:|    :    :: | |||:
Db        776 VPGQLSTFKYLQLVDLSNNKISSLSNSSFTNMSQLTTLILSYNALQCIPPLAFQGLRSLR 835

Qy        548 VLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERM 607
              :|     | : | ::        :|||: | :  |  | |  :    |:|    :   |
Db        836 LLSLHGNDVSTLQEGIFADV-TSLSHLAIGANPLYCDCHLRWLSSWVKTGYK---EPGIA 891
```

```
Qy        608 ECA-----------TPSDK---QGMPVLSLNITC 627
                ||           ||: |   || | |::   |
Db        892 RCAGPPEMEGKLLLTTPAKKFECQGPPSLAVQAKC 926
```

RESULT 13
H96510
probable disease resistance protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H96510
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96510
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-994 <STO>
A;Cross-references: UNIPROT:Q9C637; GB:AE005173; NID:g11321768; PIDN:AAG34245.1; GSPDB:GN
C;Genetics:
A;Gene: F2G19.6
A;Map position: 1

Query Match 6.8%; Score 296.5; DB 2; Length 994;
Best Local Similarity 23.0%; Pred. No. 1.4e-10;
Matches 161; Conservative 102; Mismatches 271; Indels 167; Gaps 31;

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Qy          2 MSASRLAGTLIPAMAFLSCVRPESWEPC---------VEVVPNITYQCMELNFYKIPDNL 52
              ||:  ::  :    :::  :|  : : |          | ::||:    :: |     ||
Db        213 MSSVDISSAIPIEFSYMWSLRSLTLKGCNLLGRFPNSVLLIPNLESISLDHNL-----NL 267

Qy         53 PFSTKNLDLSFNPLRHLGSY----------SFFSFPELQVLDLSRCEIQTIEDGAYQSLS 102
                |  |  |  | |  |  |            |  :   |  | | :          : :|||
Db        268 EGSLPNF-LRNNSLLKLSIYNTSFSGTIPNSISNLKHLTSLKLQQSAFSGRIPSSLRSLS 326

Qy        103 HLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFP--IGHLKTLKELNVAHN 160
              ||| |:|: |          : | |  |          : ||    ||| : :|  |: ::: |
Db        327 HLSNLVLSENNFVGEIPSSVSNLKQLTLFDVSDNNLNG--NFPSSLLNLNQLRYIDICSN 384

Qy        161 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMP--LLNLS----LDLSLNP 214
                | ||   | |:|||          |                :|  | |:|    | ||| |
Db        385 HFTGF-LPPTISQLSNLEFFSACDNSFTG----------SIPSSLFNISSLTTLGLSYNQ 433

Qy        215 MNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDK 274
              :|                  |: |:                        :|   |    :
Db        434 LN--------------------DTTNI--------------------KNISLLHNLQR 451

Qy        275 SALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSV---TIERVKDFSYNFG 331
                |:          |: : :|       :|:|   |  : | :|  :   |      |  ::
Db        452 LLLDN------NNFKASQVD------LDVFLSLKRLVSLALSGIPLSTTNITSDSEFSSH 499

Qy        332 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVD-----LPSLEFLDLSRNGL- 385
              ::|||  |   :||   ::: : |:        |   :|      || |  :||| | |
Db        500 LEYLELSGCNIIEFPEF-IRNQRNLSSIDLSNNNIKGQVPNWLWRLPELSTVDLSNNSLI 558

Qy        386 SFKGCCSQSDFGTTSLKYLDLSFNGVITMSSN------FLGLEQLEHLDFQHSNLKQMSE 439
              | |          ||| |  |   :: :|||       |:    :::    ::|
Db        559 GFNG----------SLKALSGSKIVMLDLSSNAFQGPLFMPPRGIQYFLGSYNNFTGYIP 608

Qy        440 FSVFLSLRNLIYLDISHTHTRVAFNGIFNGL---------SSLEVLKMAGNSFQENFLPD 490
              |:   | | : ||:|        |   :||          ||| || :  ||  :  ||:
Db        609 PSI-CGLANPLILDLS--------NNNLHGLIPRCLEAQMSSLSVLNLRNNSL-DGSLPN 658

Qy        491 IFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY--KCLNSLQV 548
```

```
Db        659 IFMNAKVLSSLDVSHNTLEGKLPASLAGCSALEILNVESNNI--NDTFPFWLNSLPKLQV 716

Qy        549 LDYSLNHIMTSKKQELQH-------FPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLL 601

Db        717 LVLRSNNF----RGTLHNVDGVWFGFP-LLRITDVSHNDFVGTLPSDYFMNWTAISKS-- 769

Qy        602 VEVERMECATPSD---KQGMPVLSLNITCQMNKTIIGVSVL 639

Db        770 -ETELQYIGDPEDYGYYTSLVLMNKGVSMEMQRILTKYTVI 809


RESULT 14
JC1282
insulin-like growth factor-binding protein acid labile chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1282
R;Dai, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A;Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A;Reference number: JC1282; MUID:93038676; PMID:1384485
A;Accession: JC1282
A;Molecule type: mRNA
A;Residues: 1-603 <DAI>
A;Cross-references: UNIPROT:P35859; GB:S46785; NID:g258002; PIDN:AAB23770.2; PID:g570593
A;Experimental source: liver
A;Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

  Query Match             6.8%;  Score 296;  DB 2;  Length 603;
  Best Local Similarity   24.1%;  Pred. No. 7.8e-11;
  Matches  155;  Conservative   84;  Mismatches  243;  Indels  162;  Gaps   24;

Qy         40 CMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQ 99

Db         60 CSSKNLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALL 119

Qy        100 SLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVA- 158

Db        120 GLQNLYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGW 179

Qy        159 ----------------HNLI-----QSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLR 196

Db        180 NSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSV---KAN 236

Qy        197 VLHQMPLLNLSLDLSLNPMNFIQPGAFKEIR-LHKLTLRNNFDSLNVMKTCIQGLAGLEV 255

Db        237 VFVHLPRLQ-KLYLDRNLITAVAPGAFLGMKALRWLDLSHN-RVAGLMEDTFPGLLGLHV 294

Qy        256 HRLV----------------LGEFR-NEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYL 297

Db        295 LRLAHNAIASLRPRTFKDLHFLEELQLGHNRIRQLGERTFEGLGQLEV----LTLNDNQI 350

Qy        298 DDI-IDLFNCLTNVSSFSLVSVTI----ERV---KDFSYNFGWQHLELVNCKFGQFPTLK 349

Db        351 TEVRVGAFSGLFNVAVMNLSGNCLRSLPERVFQGLDKLHSLHLEHSCLGHVRLHTF--AG 408

Qy        350 LKSLKRLTFTSNKGGNAFSEVD------LPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKY 403

Db        409 LSGLRRLFLRD----NSISSIEEQSLAGLSELLELDLTTNRLTH--LPRQLFQGLGHLEY 462

Qy        404 LDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAF 463

Db        463 LLLSYNQLTTLSAEVLG----------------------PLQRAFWLDISHNHLETLA 498

Qy        464 NGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQ 523

Db        499 EGLFSSLGRVRYLSLRNNSLQ-TFSP--------------QPGLERL------------ 530

Qy        524 VLNMSHNNFFSLDTFPYKCLNSLQVL-DYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFA 582

Db        531 ----------WLDANPWDCSCPLKALRDFALQN------------PGVVPRFVQT----- 563

Qy        583 CTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSLNIT 626

Db        564 -VCE--------GDDCQPVYTYNNITCAGPANVSGLDLRDVSET 598


RESULT 15
JG0193
G protein-coupled receptor FEX - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C;Accession: JG0193
R;Hermey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.
Biochem. Biophys. Res. Commun. 254, 273-279, 1999
A;Title: Identification of a novel seven-transmembrane receptor with homology to glycopr
A;Reference number: JG0193; MUID:99121227; PMID:9920770
A;Accession: JG0193
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-907 <HER>

  Query Match             6.8%;  Score 295;  DB 2;  Length 907;
  Best Local Similarity   23.0%;  Pred. No. 1.5e-10;
  Matches  167;  Conservative  110;  Mismatches  243;  Indels  206;  Gaps   32;

Qy         11 LIPAMAFLSCVRPESWEPCVEVVPN----------------ITYQCMELNFYKIPDNLPFS 55

Db          9 LLSLLALLQLVAAGS-SPGPDAIPRGCPSHCHCELDGRMLLRVDCSDLGLSELPSNLSVF 67

Qy         56 TKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSH----LSTLILTG 111

Db         68 TSYLDLSMNNISQLPA----------------------------SLLHRLCFLEELRLAG 99

Qy        112 NPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYF 171

Db        100 NALTHIPKGAFTGLHSLKVLMLQNNQLRKVPEEALQNLRSLQSLRLDANHI-SYVPPSCF 158

Qy        172 SNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEI-RLHK 230

Db        159 SGLHSLRHLWLDDNALTDVPVQAFRSLSALQ----AMTLALNKIHHIADYAFGNLSSLVV 214

Qy        231 LTLRNN-FDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFR 289

Db        215 LHLHNNRIHSLG--KKCFDGLHSLETLDL------NYNNLDEF-PTAIKTLSN------- 258

Qy        290 LAYLDYYLDDIIDL----FNCLTNVSSFSLVSVTI-ERVKDFSYNFGWQHLELVNCKFGQ 344

Db        259 LKELGFHSNNIRSIPERAF-----VGNPSLITIHFYDNPIQFVGVSAFQHLP-------E 306

Qy        345 FPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSF--KGCCSQSDFGTTSLK 402

Db        307 LRTLTLNGASHITEFPHLTGTA-------TLESLTLTGAKISSLPQAVCDQ----LPNLQ 355

Qy        403 YLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVA 462

Db        356 VLDLSYNLLEDLPS-LSGCQKLQKIDLRHN---------------------------- 384

Qy        463 FNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSL 522

Db        385 -----------EIYEIKGSTFQQLF---------NLRSLNLAWNKIAIIHPNAFSTLPSL 424

Qy        523 QVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQ------HFPSSLAFLNL 576

Db        425 IKLDLSSN---LLSSFPVTGL-------HGLTHLKLTGNRALQSLIPSANFP-ELKIIEM 473

Qy        577 TQNDFACT---CE--HQSFLQWIKDQRQLLVEVERMECA--TPSDKQGMPVLSLNITCQM 629

Db        474 PSAYQCCAFGGCENVYKISNQWNKDDGNSVDDLHKKDAGLFQVQDERDLEDFLLDFEEDL 533

Qy        630 NK----------------------TIIGVSVLSVLVVS---VVAVLVYK---FYFHLM 659

Db        534 ----------------------------------------------------------- 534
```

```
Db        534 NALHSVQCSPSPGPFKPCEHLFGSWLIRIGVWTTAVLTLSCNALVALTVFRTPLYISSIK 593

Qy        660 LLAGCI 665
              || | |
Db        594 LLIGVI 599
```

Search completed: March 12, 2005, 19:57:10
Job time : 25.6477 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:15:31 ; Search time 86.9834 Seconds
(without alignments)
3712.721 Million cell updates/sec

Title: US-09-396-985B-99
Perfect score: 4345
Sequence: 1 MMPPWLLARTLIMALFFSCL.....GKASNPEQTAEEEQETATWT 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2847	65.5	839	6	ABU04773	Abu04773 Human exp
2	2847	65.5	839	6	ABU04774	Abu04774 Human exp
3	2847	65.5	839	6	ABU04775	Abu04775 Human exp
4	2847	65.5	839	7	ADC78785	Adc78785 Human PRO
5	2847	65.5	839	7	ADD48826	Add48826 Human Pro
6	2829.5	65.1	837	2	AAW86361	Aaw86361 Human DNA
7	2829.5	65.1	837	5	AAE16102	Aae16102 Human DNA
8	2829.5	65.1	837	6	ABU04776	Abu04776 Human exp
9	2822.5	65.0	837	5	AAE16116	Aae16116 Human DNA
10	2788.5	64.2	795	8	ADO57791	Ado57791 Rhesus mo
11	2785.5	64.1	801	8	ADO57797	Ado57797 Squirrel
12	2785.5	64.1	808	8	ADO57803	Ado57803 Chimpanze
13	2781.5	64.0	808	8	ADO57782	Ado57782 Chimpanze
14	2777.5	63.9	795	8	ADO57800	Ado57800 Hamadryas
15	2763.5	63.6	808	8	ADO57785	Ado57785 Gorilla t
16	2747.5	63.2	801	8	ADO57788	Ado57788 Gibbon to
17	2730.5	62.8	799	2	AAW86352	Aaw86352 Human DNA
18	2730.5	62.8	799	5	AAE16093	Aae16093 Human DNA
19	2730.5	62.8	799	5	ABB83162	Abb83162 Human Tol
20	2730.5	62.8	799	6	ABR42963	Abr42963 Human Tol
21	2730.5	62.8	799	7	ADB39121	Adb39121 Human tol
22	2730.5	62.8	799	8	ADP56656	Adp56656 Human Tol
23	2730.5	62.8	799	8	ADP48597	Adp48597 Human Tol
24	2548.5	58.7	745	8	ADO57794	Ado57794 White-fac
25	2461	56.6	738	8	ADP29455	Adp29455 Human sec
26	942	21.7	179	7	ADC42707	Adc42707 Murine To
27	886	20.4	208	3	AAY88059	Aay88059 Human Tol
28	748	17.2	178	8	ADN12270	Adn12270 IL-1R/TLR
29	619.5	14.3	661	2	AAW28510	Aaw28510 Product o
30	619.5	14.3	661	2	AAW87556	Aaw87556 B cell su
31	619.5	14.3	661	7	ADC38652	Adc38652 Human sec
32	618.5	14.2	661	7	ADF69098	Adf69098 Human MP5
33	610.5	14.1	650	3	AAY82527	Aay82527 Human RP1
34	596.5	13.7	661	2	AAW47274	Aaw47274 Human B-c
35	580	13.3	1032	5	AAO21588	Aao21588 Murine To
36	580	13.3	1032	7	ADE85953	Ade85953 Mouse Tol
37	580	13.3	1032	7	ABW01559	Abw01559 Murine To
38	559	12.9	1059	5	AAO21587	Aao21587 Murine To
39	559	12.9	1059	7	ADE85951	Ade85951 Human Tol
40	559	12.9	1059	8	ADQ88188	Adq88188 Human 122
41	557	12.8	1041	2	AAY41768	Aay41768 Human PRO
42	557	12.8	1041	2	AAY05867	Aay05867 Human Tol
43	557	12.8	1041	3	AAB44324	Aab44324 Human PRO
44	557	12.8	1041	6	ABO25270	Abo25270 Novel hum
45	557	12.8	1041	6	ABU72276	Abu72276 Novel hum

ALIGNMENTS

RESULT 1
ABU04773
ID ABU04773 standard; protein; 839 AA.
XX
AC ABU04773;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1439.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1439; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a

```
CC   mammal an immunogenic response directed against any of the purified
CC   polypeptide. The purified polypeptide, or the antibody that binds to this
CC   polypeptide, is useful for treating cancer. The polypeptide is also
CC   useful for identifying compounds that binds to a naturally processed
CC   class I or class II MHC-binding polypeptide. The polypeptides and
CC   polynucleotides are particularly useful for treating or preventing
CC   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC   lymphoma or leukaemia. These are also useful for screening agents for
CC   treating the above mentioned diseases. This sequence represents an
CC   expressed protein tag (EPT) isolated from human tissue for translational
CC   profiling. Note: This sequence does not appear in the printed
CC   specification but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 839 AA;

  Query Match             65.5%;  Score 2847;  DB 6;  Length 839;
  Best Local Similarity   67.6%;  Pred. No. 7.2e-237;
  Matches  559;  Conservative  101;  Mismatches  163;  Indels    4;  Gaps    4;

Qy          1 MMPPWLLARTLIMAL-FFSCLTPGSLNPCIEVVPNITYQCMDQKLSKVPDDIPSSTKNID 59
              ||    || ||| |: | ||: | |  ||:||||||||||||:    |:||::| ||||:|
Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         60 LSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWHGLHHLSNLILTGNPIQSFSPG 119
              ||||||: | |||| :| ||| ||||||||:|||| |:  | ||| |||||||||| : |
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        120 SFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAHNFIHSCKLPAYFSNLTNLVHV 179
              :||||:||: |||||| |||||:|||| | |||:|||||| | | ||| |||||||| |:
Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        180 DLSYNYIQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHELTLRGNFNSS 239
              ||| | ||:|   ||: | : | :|||||:||||::|||  ||: |:||:|||| ||:|
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        240 NIMKTCLQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDI 299
              |:||||:| |||| ||||:||||::| ||| |: | :||||::||:|||| | : : |||
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        300 VK-FHCLANVSAMSLAGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTM 358
              :  |:|| |||: ||  |:|: ::|   :| || | :: |:  ||||| |  || || |
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        359 NKGSISFKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMG 418
              |||  :| :| |||| :|||||| ||| |||| || || ||::|||||| | ||:||:|
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        419 LEELQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAG 478
              ||:|:|||||| ||:::||| |||| |:|||||:|:|:: |:||| ||:||  |||||
Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        479 NSFKDNTLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSHY 538
              |||::| | ::|    |||||||:|||||:|   |::|  ||:|||||||   ||:  |
Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        539 NQLYSLSTLDCSFNRIETS-KGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQKQF 597
                | ||  || | | | || |  ||||| |||| ||| |  || |||| ||||:|:|:|
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        598 LVNVEQMTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVVSVIVVSTVAFLIYHFYFHLI 657
              || ||:| |||| :    ||   | || | |||| |||:||:||| || |:| |||||:
Db        601 LVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLM 659

Qy        658 LIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFHLCLHYRDFIPGVAIA 717
              |:||| || |||:|||||||||||:|||||||||||||||| | ||||||||||||||||
Db        660 LLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIA 719

Qy        718 ANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLL 777
              |||| |||||||||||||:|||||||||||||||||||||:|||||||:||||:||
Db        720 ANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLL 779

Qy        778 RQQVELYRLLSRNTYLEWEDNPLGRHIFWRRLKNALLDGKASNPEQT 824
```

```
              ||||||||||||||||||||: ||||||||||: ||||||: ||| |
Db        780 RQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGT 826
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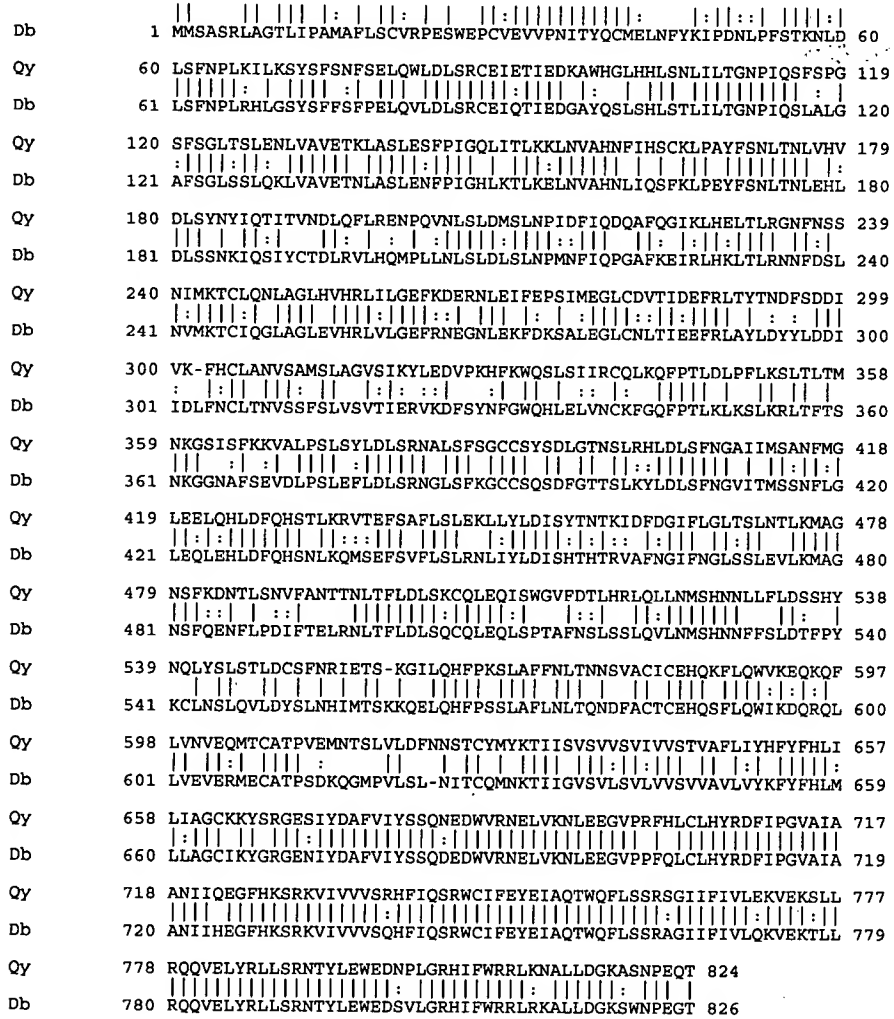
RESULT 2
ABU04774
ID   ABU04774 standard; protein; 839 AA.
XX
AC   ABU04774;
XX
DT   29-JAN-2003 (first entry)
XX
DE   Human expressed protein tag (EPT) #1440.
XX
KW   Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW   protease; protease inhibitor; transporter; cytoskeletal protein;
KW   receptor; transcription factor; cancer; MHC;
KW   major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW   adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200278524-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-US009671.
XX
PR   28-MAR-2001; 2001US-0279495P.
PR   21-MAY-2001; 2001US-0292544P.
PR   08-AUG-2001; 2001US-0310801P.
PR   01-OCT-2001; 2001US-0326370P.
PR   04-DEC-2001; 2001US-0336780P.
PR   20-FEB-2002; 2002US-0358985P.
XX
PA   (ZYCO-) ZYCOS INC.
XX
PI   Chicz RM, Tomlinson AJ, Urban RG;
XX
DR   WPI; 2003-040607/03.
XX
PT   New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT   cytoskeletal proteins, receptors or transcription factors), useful for
PT   treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT   leukemia.
XX
PS   Example 2; SEQ ID NO 1440; 134pp; English.
XX
CC   The invention describes a purified polypeptide, which comprises a
CC   fragment of a kinase, phosphatase, protease, protease inhibitor,
CC   transporter, cytoskeletal protein, receptor or transcription factor. The
CC   polypeptide is useful as an immunogenic composition for eliciting in a
CC   mammal an immunogenic response directed against any of the purified
CC   polypeptide. The purified polypeptide, or the antibody that binds to this
CC   polypeptide, is useful for treating cancer. The polypeptide is also
CC   useful for identifying compounds that binds to a naturally processed
CC   class I or class II MHC-binding polypeptide. The polypeptides and
CC   polynucleotides are particularly useful for treating or preventing
CC   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC   lymphoma or leukaemia. These are also useful for screening agents for
CC   treating the above mentioned diseases. This sequence represents an
CC   expressed protein tag (EPT) isolated from human tissue for translational
CC   profiling. Note: This sequence does not appear in the printed
CC   specification but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 839 AA;

  Query Match   65.5%; Score 2847; DB 6; Length 839;
  Best Local Similarity   67.6%; Pred. No. 7.2e-237;
  Matches 559; Conservative 101; Mismatches 163; Indels   4; Gaps   4;

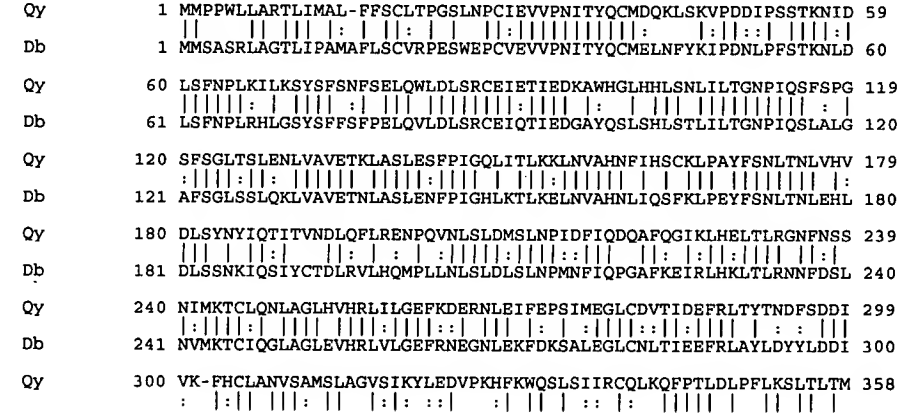
Qy   1 MMPPWLLARTLIMAL-FFSCLTPGSLNPCIEVVPNITYQCMDQKLSKVPDDIPSSTKNID 59



RESULT 3
ABU04775
ID ABU04775 standard; protein; 839 AA.
XX
AC ABU04775;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1441.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.

XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1441; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 839 AA;

Query Match 65.5%; Score 2847; DB 6; Length 839;
Best Local Similarity 67.6%; Pred. No. 7.2e-237;
Matches 559; Conservative 101; Mismatches 163; Indels 4; Gaps 4;



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Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        359 NKGSISFKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMG 418

Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        419 LEELQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAG 478

Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        479 NSFKDNTLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSHY 538

Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        539 NQLYSLSTLDCSFNRIETS-KGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQKQF 597

Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        598 LVNVEQMTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVVSVIVVSTVAFLIYHFYFHLI 657

Db        601 LVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLM 659

Qy        658 LIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFHLCLHYRDFIPGVAIA 717

Db        660 LLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIA 719

Qy        718 ANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLL 777

Db        720 ANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLL 779

Qy        778 RQQVELYRLLSRNTYLEWEDNPLGRHIFWRRLKNALLDGKASNPEQT 824

Db        780 RQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGT 826
```

RESULT 4
ADC78785
ID ADC78785 standard; protein; 839 AA.
XX
AC ADC78785;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human PRO protein #7.
XX
KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease.
XX
OS Homo sapiens.
XX
PN WO2003034984-A2.
XX
PD 01-MAY-2003.
XX
PF 15-OCT-2002; 2002WO-US033070.
XX
PR 19-OCT-2001; 2001US-0340083P.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Gurney AL;
XX
DR WPI; 2003-481990/45.
DR N-PSDB; ADC78784.
XX
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
PT medicament for diagnosing or treating cancer or inflammatory bowel
PT disorder e.g., ulcerative colitis or Crohn's disease.
XX
PS Claim 12; SEQ ID NO 14; 327pp; English.
XX
CC The invention comprises the amino acid and coding sequences of human PRO
CC proteins. The DNA and protein sequences of the invention are useful for
CC the diagnosis and treatment of cancer and inflammatory bowel disease
CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
CC sequence represents a human PRO protein of the invention.
XX
SQ Sequence 839 AA;

Query Match 65.5%; Score 2847; DB 7; Length 839;
Best Local Similarity 67.6%; Pred. No. 7.2e-237;
Matches 559; Conservative 101; Mismatches 163; Indels 4; Gaps 4;

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Qy          1 MMPPWLLARTLIMAL-FFSCLTPGSLNPCIEVVPNITYQCMDQKLSKVPDDIPSSTKNID 59

Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         60 LSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWHGLHHLSNLILTGNPIQSFSPG 119

Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        120 SFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAHNFIHSCKLPAYFSNLTNLVHV 179

Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        180 DLSYNYIQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHELTLRGNFNSS 239

Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        240 NIMKTCLQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDI 299

Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        300 VK-FHCLANVSAMSLAGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTM 358

Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        359 NKGSISFKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMG 418

Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        419 LEELQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAG 478

Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        479 NSFKDNTLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSHY 538

Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        539 NQLYSLSTLDCSFNRIETS-KGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQKQF 597

Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        598 LVNVEQMTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVVSVIVVSTVAFLIYHFYFHLI 657

Db        601 LVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLM 659

Qy        658 LIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFHLCLHYRDFIPGVAIA 717

Db        660 LLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIA 719

Qy        718 ANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLL 777

Db        720 ANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLL 779

Qy        778 RQQVELYRLLSRNTYLEWEDNPLGRHIFWRRLKNALLDGKASNPEQT 824

Db        780 RQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGT 826
```

RESULT 5
ADD48826
ID ADD48826 standard; protein; 839 AA.
XX
AC ADD48826;
XX

```
DT   02-DEC-2004  (revised)
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein AAF05316, SEQ ID NO 14536.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; AAF05316.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Example 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (described in Table 3
CC   of the specification) which is differentially expressed during pain.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 839 AA;

  Query Match             65.5%;  Score 2847;  DB 7;  Length 839;
  Best Local Similarity   67.6%;  Pred. No. 7.2e-237;
  Matches  559;  Conservative  101;  Mismatches  163;  Indels    4;  Gaps    4;

Qy          1 MMPPWLLARTLIMAL-FFSCLTPGSLNPCIEVVPNITYQCMDQKLSKVPDDIPSSTKNID 59
              ||    || ||| |: | ||:.| |  ||:||||||||||:    |:||::| ||||:|
Db          1 MMSASRLAGTLIPAMAFLSCVRPESWEPCVEVVPNITYQCMELNFYKIPDNLPFSTKNLD 60

Qy         60 LSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWHGLHHLSNLILTGNPIQSFSPG 119
              ||||||: | |||| :| ||| |||||||||:|||| |:  | ||| |||||||||| : |
Db         61 LSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALG 120

Qy        120 SFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAHNFIHSCKLPAYFSNLTNLVHV 179
              :||||:||: |||||| |||||:|||| | |||:|||||| | | ||| |||||||| |:
Db        121 AFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHL 180

Qy        180 DLSYNYIQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHELTLRGNFNSS 239
              ||| | ||:|   ||: | : | :|||||:||||::|||  ||: |:||:|||| ||:|
Db        181 DLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSL 240

Qy        240 NIMKTCLQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDI 299
              |:||||:| |||| |||||:||||::| ||| |: | :||||::||:|||| | : : |||
Db        241 NVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDI 300

Qy        300 VK-FHCLANVSAMSLAGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTM 358
              :  |:|| ||||: ||  |:|: ::|   :| || | :: |:  ||||| |  || || |
Db        301 IDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTS 360

Qy        359 NKGSISFKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMG 418
              |||  :| :| |||| :|||||| ||| |||| || || ||::|||||| | ||:||:|
Db        361 NKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLG 420

Qy        419 LEELQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAG 478
              ||:|:|||||| ||:::||| ||||  |:|||||:|:|:: |:||| ||:||  |||||
Db        421 LEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAG 480

Qy        479 NSFKDNTLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSHY 538
              |||::| | ::|    ||||||||:|||||:|   |::|  ||:|||||||   ||:  |
Db        481 NSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPY 540

Qy        539 NQLYSLSTLDCSFNRIETS-KGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQKQF 597
                | ||  || | | | || |  ||||| |||| ||| |  || |||| ||||:|:|:|
Db        541 KCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQL 600

Qy        598 LVNVEQMTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVVSVIVVSTVAFLIYHFYFHLI 657
              || ||:| |||| :     ||   | || | |||| |||:||:||| || |:| |||||:
Db        601 LVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLM 659

Qy        658 LIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFHLCLHYRDFIPGVAIA 717
              |:||| || |||:|||||||||||:|||||||||||||||| | |||||||||||||||
Db        660 LLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIA 719

Qy        718 ANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLL 777
              |||| |||||||||||||:|||||||||||||||||||||:|||||||:||||:||
Db        720 ANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLL 779

Qy        778 RQQVELYRLLSRNTYLEWEDNPLGRHIFWRRLKNALLDGKASNPEQT 824
              |||||||||||||||||||: |||||||||: |||||: ||| |
Db        780 RQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGT 826


RESULT 6
AAW86361
ID   AAW86361 standard; protein; 837 AA.
XX
AC   AAW86361;
XX
DT   15-MAR-1999  (first entry)
XX
DE   Human DNAX toll-like receptor DTLR4.
XX
KW   DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KW   interleukin 1 receptor; phosphate metabolism; innate immunity response;
KW   modulate inflammatory function; morphological effect;
KW   immunological disorder.
XX
OS   Homo sapiens.
XX
PN   WO9850547-A2.
XX
PD   12-NOV-1998.
```

```
XX
PF   07-MAY-1998;   98WO-US008979.
XX
PR   07-MAY-1997;   97US-0044293P.
PR   22-JAN-1998;   98US-0072212P.
PR   05-MAR-1998;   98US-0076947P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Hardiman GT,  Rock FL,  Bazan JF,  Kastelein RA;
XX
DR   WPI; 1999-059670/05.
DR   N-PSDB; AAV80675.
XX
PT   Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
PT   metabolism, modulate inflammatory function or innate immunity responses.
XX
PS   Claim 3; Page 147-149; 171pp; English.
XX
CC   The present invention specifically describes human DNAX toll-like
CC   receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
CC   in the present invention. Also described are: (1) a fusion protein
CC   comprising a DTLR protein or peptide; (2) a binding compound, preferably
CC   an antibody or antibody fragment which specifically binds to a DTLR
CC   protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
CC   ; (4) an expression vector comprising the nucleic acid of (3); and (5) a
CC   host cell comprising the vector of (4). The host cell of (5) can be used
CC   to produce the DTLR proteins. The DTLR proteins can be used to alter
CC   phosphate metabolism, to modulate inflammatory function, innate immunity
CC   responses or morphological effects. The DTLR proteins can be used in the
CC   treatment of conditions exhibiting abnormal expression of the receptors
CC   of their ligands. These abnormalities are typically manifested by
CC   immunological disorders
XX
SQ   Sequence 837 AA;

  Query Match             65.1%;  Score 2829.5;  DB 2;  Length 837;
  Best Local Similarity   67.7%;  Pred. No. 2.4e-235;
  Matches  556;  Conservative  101;  Mismatches  159;  Indels    5;  Gaps    5;

Qy          7 LARTLIMAL-FFSCLTPGSLNPCIEVVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPL 65
              || ||| |: | ||: | |  ||:| |||||||||:    |:||::| ||||:|||||||
Db          6 LAGTLIPAMAFLSCVRPESWEPCVE-VPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPL 64

Qy         66 KILKSYSFSNFSELQWLDLSRCEIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLT 125
              : | |||| :| ||| |||||||||:|||| |:  | ||| |||||||||| : |:||||:
Db         65 RHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLS 124

Qy        126 SLENLVAVETKLASLESFPIGQLITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNY 185
              ||: |||||| |||||:|||| | |||:|||||| | | ||| |||||||| |:||| |
Db        125 SLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK 184

Qy        186 IQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTC 245
              ||:|   ||: | : | :|||||:||||::|||  ||: |:||:|||| ||:| |:|||
Db        185 IQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTC 244

Qy        246 LQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVK-FHC 304
              :| |||| ||||:||||::| ||| |: | :||||::||:|||| | : : |||:  |:|
Db        245 IQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNC 304

Qy        305 LANVSAMSLAGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSIS 364
              | |||: ||  |:|: ::|   :| || | :: |:  ||||| |  || || | |||  :
Db        305 LTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNA 364

Qy        365 FKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQH 424
              | :| |||| :|||||| ||| |||| || || ||::|||||| | ||:||:|||:|:|
Db        365 FSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEH 424

Qy        425 LDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDN 484
              |||||| ||:::||| ||||  |:|||||:|:|:: |:||| ||:||  |||||||::|
Db        425 LDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQEN 484

Qy        485 TLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSL 544
              | ::|    ||||||||:|||||:|   |::|  ||:|||||||   ||:  |  | ||
Db        485 FLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSL 544

Qy        545 STLDCSFNRIETS-KGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQ 603
              || | | | || |  ||||| |||| ||| |  || |||| ||||:|:|:| || ||:
Db        545 QVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVER 604

Qy        604 MTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVVSVIVVSTVAFLIYHFYFHLILIAGCK 663
              | |||| :     ||   | || | |||| |||:||:||| || |:| |||||:|:|||
Db        605 MECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCI 663

Qy        664 KYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFHLCLHYRDFIPGVAIAANIIQE 723
              || |||:|||||||||:|||||||||||||||| | |||||||||||||||| |
Db        664 KYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHE 723

Qy        724 GFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVEL 783
              |||||||||||||:|||||||||||||||||||||||:|||||||:||||:||||||||
Db        724 GFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVEL 783

Qy        784 YRLLSRNTYLEWEDNPLGRHIFWRRLKNALLDGKASNPEQT 824
              |||||||||||||: |||||||||: ||||||: ||| |
Db        784 YRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGT 824


RESULT 7
AAE16102
ID   AAE16102 standard; protein; 837 AA.
XX
AC   AAE16102;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human DNAX Toll like receptor (DTLR) 4 #2.
XX
KW   Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW   interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS   Homo sapiens.
XX
PN   WO200190151-A2.
XX
PD   29-NOV-2001.
XX
PF   23-MAY-2001; 2001WO-US016766.
XX
PR   25-MAY-2000; 2000US-0207558P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Hardiman GT,  Rock FL,  Bazan JF,  Kastelein RA,  Ho SWK,  Liu Y;
XX
DR   WPI; 2002-083085/11.
DR   N-PSDB; AAD26292.
XX
PT   New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT   conditions exhibiting abnormal expression of the receptors of their
PT   ligands, particularly abnormalities manifested by immunological
PT   disorders.
XX
PS   Claim 3; Page 41; 297pp; English.
XX
CC   The invention relates to mammalian receptor proteins, e.g., primate,
CC   human DNAX Toll like receptor (DTLR) protein and their corresponding
CC   nucleic acids. The DTLR is useful for treating conditions exhibiting
CC   abnormal expression of the receptors of their ligands. Such abnormality
CC   is manifested by immunological disorders. In particular, the DTLR is
CC   useful for treating various disease or disorders associated with abnormal
CC   expression or abnormal triggering of response to a ligand. The DTLR is
CC   also useful as an immunogen for the production of antisera or antibodies
CC   specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC   receptor family members, for the DTLR or its various fragments. The
CC   purified DTLR can be used to screen monoclonal antibodies or antigen-
CC   binding fragments. The antibodies are useful for screening expression
```

CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTLR or cells that express it. The present sequence is
CC human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33.
CC Note: The present sequence SEQ ID NO 26 is stated to be similar to the
CC sequence shown in page 240-243 (AAE16116). However these sequences differ
CC at several locations
XX
SQ Sequence 837 AA;

Query Match 65.1%; Score 2829.5; DB 5; Length 837;
Best Local Similarity 67.7%; Pred. No. 2.4e-235;
Matches 556; Conservative 101; Mismatches 159; Indels 5; Gaps 5;

```
Qy          7 LARTLIMAL-FFSCLTPGSLNPCIEVVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPL 65
              || ||| |: | ||: | |  ||:| |||||||||:    |:||::| ||||:|||||||
Db          6 LAGTLIPAMAFLSCVRPESWEPCVE-VPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPL 64

Qy         66 KILKSYSFSNFSELQWLDLSRCEIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLT 125
              : | |||| :| ||| |||||||:|||| |:  | ||| |||||||||| : |:||||:
Db         65 RHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLS 124

Qy        126 SLENLVAVETKLASLESFPIGQLITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNY 185
              ||: |||||| |||||:|||| | |||:|||||| | | ||| |||||||| |:||| |
Db        125 SLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK 184

Qy        186 IQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTC 245
              ||:|   ||: | : | :|||||:||||::|||  ||: |:||:|||| ||:| |:||||
Db        185 IQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTC 244

Qy        246 LQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVK-FHC 304
              :| |||| ||||:||||::| ||| |: | :||||::||:|||| | : : |||:  |:|
Db        245 IQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNC 304

Qy        305 LANVSAMSLAGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSIS 364
              | |||: ||  |:|: ::|   :| || | :: |:  ||||| |  || || | |||  :
Db        305 LTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNA 364

Qy        365 FKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQH 424
              | :| |||| :|||||| ||| |||| || || ||::|||||| | ||:||:|||:|:|
Db        365 FSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEH 424

Qy        425 LDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDN 484
              |||||| ||:::||| |||| |:|||||:|:|:: |:||| ||:||  |||||||::|
Db        425 LDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQEN 484

Qy        485 TLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSL 544
              | ::|    ||||||||:|||||:|   |::|  ||:|||||||   ||:  |  | ||
Db        485 FLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSL 544

Qy        545 STLDCSFNRIETS-KGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQ 603
              || | | | || |  ||||| |||| ||| |  || |||| ||||:|:|:| || ||:
Db        545 QVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVER 604

Qy        604 MTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVVSVIVVSTVAFLIYHFYFHLILIAGCK 663
              | |||| :    ||   | || | |||| |||:||:||| || |:| |||||:|:|||
Db        605 MECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCI 663

Qy        664 KYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFHLCLHYRDFIPGVAIAANIIQE 723
              || |||:||||||||||:|||||||||||||||| | |||||||||||||||||| |
Db        664 KYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHE 723

Qy        724 GFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVEL 783
              ||||||||||||:|||||||||||||||||||||||:|||||||:||||:||||||||
Db        724 GFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVEL 783

Qy        784 YRLLSRNTYLEWEDNPLGRHIFWRRLKNALLDGKASNPEQT 824
              |||||||||||||: |||||||||: |||||: ||| |
Db        784 YRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGT 824
```

RESULT 8
ABU04776

ID ABU04776 standard; protein; 837 AA.
XX
AC ABU04776;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1442.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1442; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 837 AA;

Query Match 65.1%; Score 2829.5; DB 6; Length 837;
Best Local Similarity 67.7%; Pred. No. 2.4e-235;
Matches 556; Conservative 101; Mismatches 159; Indels 5; Gaps 5;

```
Qy          7 LARTLIMAL-FFSCLTPGSLNPCIEVVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPL 65
              || ||| |: | ||: | |  ||:| |||||||||:    |:||::| ||||:|||||||
Db          6 LAGTLIPAMAFLSCVRPESWEPCVE-VPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPL 64

Qy         66 KILKSYSFSNFSELQWLDLSRCEIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLT 125
              : | |||| :| ||| |||||||:|||| |:  | ||| |||||||||| : |:||||:
Db         65 RHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLS 124
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Qy        126 SLENLVAVETKLASLESFPIGQLITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNY 185
              ||: |||||| |||||:|||| | |||:|||||| | | ||| |||||||| |:||| |
Db        125 SLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK 184

Qy        186 IQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTC 245
              ||:|    ||: | : | :|||||:||||::|||   ||: |:||:|||| ||:| |:||||
Db        185 IQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTC 244

Qy        246 LQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVK-FHC 304
              :| |||| ||||:||||::| ||| |: | :||||::||:|||| | : : |||:  |:|
Db        245 IQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNC 304

Qy        305 LANVSAMSLAGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSIS 364
              | |||: ||  |:|: ::|   :| || | :: |:  ||||| |  || || | |||  :
Db        305 LTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNA 364

Qy        365 FKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQH 424
              | :| |||| :|||||| ||| |||| || || ||::|||||| | ||:||:|||:|:|
Db        365 FSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEH 424

Qy        425 LDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDN 484
              |||||| ||:::||| |||  |:||||:|:|:: |:||| ||:||  ||||||||::|
Db        425 LDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQEN 484

Qy        485 TLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSL 544
              | ::|    |||||||:|||||:|   |::|  ||:|||||||   ||:  |  | ||
Db        485 FLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSL 544

Qy        545 STLDCSFNRIETS-KGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQ 603
                || | | || |  ||||| |||| ||| |  || |||| ||||:|:|:| || ||:
Db        545 QVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVER 604

Qy        604 MTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVVSVIVVSTVAFLIYHFYFHLILIAGCK 663
              | |||| :     ||   | || | |||| |||:||:||| || |:| |||||:|:|||
Db        605 MECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCI 663

Qy        664 KYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFHLCLHYRDFIPGVAIAANIIQE 723
              || |||:||||||||||:|||||||||||||||| | |||||||||||||||||||||| |
Db        664 KYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHE 723

Qy        724 GFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVEL 783
              |||||||||||||:|||||||||||||||||||||||:|||||||:||||:||||||||
Db        724 GFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVEL 783

Qy        784 YRLLSRNTYLEWEDNPLGRHIFWRRLKNALLDGKASNPEQT 824
              |||||||||||||: |||||||||: ||||||: ||| |
Db        784 YRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGT 824
```

RESULT 9
AAE16116
ID AAE16116 standard; protein; 837 AA.
XX
AC AAE16116;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX Toll like receptor (DTLR) 4 #2, alternative version.
XX
KW Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 211
FT /label= Unknown
FT /note= "Encoded by AAY"
XX
PN WO200190151-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US016766.
XX
PR 25-MAY-2000; 2000US-0207558P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX
DR WPI; 2002-083085/11.
DR N-PSDB; AAD26306.
XX
PT New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
XX
PS Claim 3; Page 240-243; 297pp; English.
XX
CC The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTLR or its various fragments. The
CC purified DTLR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTLR or cells that express it. The present sequence is
CC human DTLR4 protein, alternative version. The DTLR4 gene is located on
CC chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
CC be similar to the sequence shown in page 41 (AAE16102). However these
CC sequences differ at several locations
XX
SQ Sequence 837 AA;

Query Match 65.0%; Score 2822.5; DB 5; Length 837;
Best Local Similarity 67.6%; Pred. No. 9.5e-235;
Matches 555; Conservative 101; Mismatches 160; Indels 5; Gaps 5;

```
Qy          7 LARTLIMAL-FFSCLTPGSLNPCIEVVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPL 65
              || ||| |: | ||: | |  ||:| |||||||||:    |:||::| ||||:|||||||
Db          6 LAGTLIPAMAFLSCVRPESWEPCVE-VPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPL 64

Qy         66 KILKSYSFSNFSELQWLDLSRCEIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLT 125
              : | |||| :| ||| |||||||||:|||| |:  | ||| |||||||||| : |:||||:
Db         65 RHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLS 124

Qy        126 SLENLVAVETKLASLESFPIGQLITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNY 185
              ||: |||||| |||||:|||| | |||:|||||| | | ||| |||||||| |:||| |
Db        125 SLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK 184

Qy        186 IQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTC 245
              ||:|    ||: | : | :|||||:|| |::|||  ||: |:||:|||| ||:| |:||||
Db        185 IQSIYCTDLRVLHQMPLLNLSLDLSLXPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTC 244

Qy        246 LQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVK-FHC 304
              :| |||| ||||:||||::| ||| |: | :||||::||:|||| | : : |||:  |:|
Db        245 IQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNC 304

Qy        305 LANVSAMSLAGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSIS 364
              | |||: ||  |:|: ::|   :| || | :: |:  ||||| |  || || | |||  :
Db        305 LTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNA 364

Qy        365 FKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQH 424
              | :| |||| :|||||| ||| |||| || || ||::|||||| | ||:||:|||:|:|
Db        365 FSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEH 424
```

```
Qy        425 LDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDN 484
              |||||| ||:::||| |||| |:|||||:|:|:: |:||| ||:|| ||||||||::|
Db        425 LDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQEN 484

Qy        485 TLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSL 544
               | ::|    |||||||:|||||:|   |::|  ||:|||||||   ||:  |  | ||
Db        485 FLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSL 544

Qy        545 STLDCSFNRIETS-KGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQ 603
              || | | || |  ||||| |||| ||| |  || |||| ||||:|:|:| || ||:
Db        545 QVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVER 604

Qy        604 MTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVVSVIVVSTVAFLIYHFYFHLILIAGCK 663
              | |||| :     ||   | || | |||| |||:||:||| || |:| |||||:|:|||
Db        605 MECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCI 663

Qy        664 KYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEGVPRFHLCLHYRDFIPGVAIAANIIQE 723
              || |||:||||||||||:|||||||||||||||| | |||||||||||||||||| |
Db        664 KYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHE 723

Qy        724 GFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVEL 783
              |||||||||||||:|||||||||||||||||||||||:|||||:|||:|||||||
Db        724 GFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVEL 783

Qy        784 YRLLSRNTYLEWEDNPLGRHIFWRRLKNALLDGKASNPEQT 824
              |||||||||||||: |||||||||: ||||||: ||| |
Db        784 YRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGKSWNPEGT 824
```

RESULT 10
ADO57791
ID ADO57791 standard; protein; 795 AA.
XX
AC ADO57791;
XX
DT 12-AUG-2004 (first entry)
XX
DE Rhesus monkey toll-like receptor 4 SEQ ID NO:12.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; rhesus monkey.
XX
OS Macaca mulatta.
XX
FH Key   Location/Qualifiers
FT Misc-difference 635
FT   /label= Lys, Asn
XX
PN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
DR WPI; 2004-400726/37.
DR N-PSDB; ADO57789, ADO57790.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Disclosure; SEQ ID NO 12; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents rhesus monkey TLR4.
XX
SQ Sequence 795 AA;

Query Match 64.2%; Score 2788.5; DB 8; Length 795;
Best Local Similarity 68.3%; Pred. No. 7.7e-232;
Matches 543; Conservative 98; Mismatches 151; Indels 3; Gaps 3;

```
Qy         31 VVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIE 90
              ||||||||||:    |:||::| ||||:|||||||: | |||| :| ||| ||||||||:
Db          1 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 60

Qy         91 TIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLIT 150
              |||| |:  | ||| |||||||||| : |:||||:||: |||||| |||||:|||| | |
Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        151 LKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMS 210
              ||:|||||| | | ||| |||||||| |:||| | || |   ||| | : |  |||||:|
Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQNIYCKDLQVLHQMPLSNLSLDLS 180

Qy        211 LNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEI 270
              ||||:|||  ||: |:||:|||| ||:  |:||||:| |||| ||||:||||::|||||
Db        181 LNPINFIQPGAFKEIRLHKLTLRSNFDDLNVMKTCIQGLAGLEVHRLVLGEFRNERNLEE 240

Qy        271 FEPSIMEGLCDVTIDEFRLTYTNDFSDDIVK-FHCLANVSAMSLAGVSIKYLEDVPKHFK 329
              |: | :||||::||:|||||| : : |:|:  |:||||||: ||  |||| :||   :|:
Db        241 FDKSSLEGLCNLTIEEFRLTYLDYYLDNIIDLFNCLANVSSFSLVSVSIKRVEDFSYNFR 300

Qy        330 WQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLSYLDLSRNALSFSGCC 389
              || | :: |: :|||||:|  || || | |||  :| :| |||| :|||||| ||| |||
Db        301 WQHLELVNCKFEQFPTLELESLKRLTFTANKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        390 SYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLY 449
              | || || ||::|||||| | ||:||:|||:|:|||||| ||:::|| |||| |:|
Db        361 SQSDFGTTSLKYLDLSFNDVITMSSNFLGLEKLEHLDFQHSNLKQMSQFSVFLSLRNLIY 420

Qy        450 LDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLSKCQLEQI 509
              ||||:|:|:: |:||| || ||  ||||||||::| | ::| :  ||||||||:|||||:
Db        421 LDISHTHTRVAFNGIFDGLLSLKVLKMAGNSFQENFLPDIFTDLKNLTFLDLSQCQLEQL 480

Qy        510 SWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIETSKG-ILQHFPKSL 568
              |   ||||::||:|||||||   ||:  |  | ||  || | | | ||    ||||| ||
Db        481 SPTAFDTLNKLQVLNMSHNNFFSLDTFPYKCLPSLQVLDYSLNHIMTSNNQELQHFPSSL 540

Qy        569 AFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQMTCATPVEMNTSLVLDFNNSTCYMY 628
              || ||| |  || |||| ||||:|:|:| ||  |:| |||| :     ||   | || |
Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEAERMECATPSDKQGMPVLSL-NITCQMN 599

Qy        629 KTIISVSVVSVIVVSTVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRN 688
              |||| ||| ||:||| || |:| |||||:|:|||  | |||:|||||||||||:|||||
Db        600 KTIIGVSVFSVLVVSVVAVLVYKFYFHLMLLAGCIXYGRGENIYDAFVIYSSQDEDWVRN 659

Qy        689 ELVKNLEEGVPRFHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFE 748
              |||||||||| | |||||||||||||||||| |||||||||||||:|||||||||
Db        660 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 719

Qy        749 YEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNPLGRHIFWRR 808
              |||||||||||||:|||||||:||||:|||||||||||||||||||||: ||:|||||||
Db        720 YEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGQHIFWRR 779

Qy        809 LKNALLDGKASNPEQ 823
              |: |||||:: |||:
Db        780 LRKALLDGRSWNPEE 794
```

RESULT 11

```
ADO57797
ID   ADO57797 standard; protein; 801 AA.
XX
AC   ADO57797;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Squirrel monkey toll-like receptor 4 SEQ ID NO:18.
XX
KW   toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW   immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW   sepsis; severe sepsis; septic shock; asthma; squirrel monkey.
XX
OS   Saimiri sciureus.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 14
FT                   /label= Leu, Phe
XX
PN   WO2004042365-A2.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-US036247.
XX
PR   01-NOV-2002; 2002US-0423113P.
XX
PA   (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI   Messier W;
XX
DR   WPI; 2004-400726/37.
DR   N-PSDB; ADO57795, ADO57796.
XX
PT   Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT   in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT   sequence of the Old World monkey with that of a human.
XX
PS   Disclosure; SEQ ID NO 18; 111pp; English.
XX
CC   The invention relates to a novel method for identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an old world monkey
CC   comprising comparing the TLR4 polynucleotide sequence of the Old World
CC   monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC   method of the invention has antibacterial, immunosuppressive, and
CC   antiasthmatic activity. The method is useful in identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC   change may be associated with reduced sensitivity to Gram-negative
CC   bacterial infection. The methods, agents and composition are useful in
CC   treating sepsis, severe sepsis or septic shock and asthma. The present
CC   sequence represents squirrel monkey TLR4.
XX
SQ   Sequence 801 AA;

  Query Match             64.1%;  Score 2785.5;  DB 8;  Length 801;
  Best Local Similarity   68.3%;  Pred. No. 1.4e-231;
  Matches  544;  Conservative   90;  Mismatches  159;  Indels    3;  Gaps    3;

Qy         31 VVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIE 90
              ||||:|||||:    |:||:|| ||||:||||||: | |:|| || ||| ||||||:|:
Db          1 VVPNVTYQCMELNXYKIPDNIPFSTKNLDLSFNPLRHLGSHSFFNFPELQVLDLSRCDIQ 60

Qy         91 TIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLIT 150
              |||| |:  | ||| |||||||||: : |:||||:||: |||||| | |||:|||| | |
Db         61 TIEDGAYQSLSHLSTLILTGNPIQNLALGAFSGLSSLQKLVAVETHLLSLENFPIGHLKT 120

Qy        151 LKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMS 210
              || |||||| | | ||| |||||||| |:||| | || |   ||| | : | :|||||:|
Db        121 LKDLNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNNIQNIYCKDLQVLHQMPLLNLSLDLS 180

Qy        211 LNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEI 270
              ||||:|||  ||: |:||:|||| ||:| | ||||:| |||| ||||:||||::|||:|
Db        181 LNPINFIQPGAFKEIRLHKLTLRNNFDSLNAMKTCIQGLAGLEVHRLVLGEFRNERNIED 240

Qy        271 FEPSIMEGLCDVTIDEFRLTYTNDFSDDIVK-FHCLANVSAMSLAGVSIKYLEDVPKHFK 329
              |: | :||||::||:|||| | :|| |||:  |:||||||: ||  | || :||   :|:
Db        241 FDKSALEGLCNLTINEFRLAYLDDFLDDIIDLFNCLANVSSFSLVNVHIKRVEDFSYNFR 300

Qy        330 WQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLSYLDLSRNALSFSGCC 389
              || | :: |  :||| | |  || || | |||   | :| |||| :|||||| ||| |||
Db        301 WQHLELVNCVFQQFPPLKLKSLKRLTFTANKGRNHFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        390 SYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLY 449
              | || || ||::|||||| | | :||:|||:|:|||||| ||:::||| |||| |:|
Db        361 SQSDFGTTSLKYLDLSFNDVITMGSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 420

Qy        450 LDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLSKCQLEQI 509
              ||||:|:|:: |:||| || ||  |||||||||: | | ::| :  || |||||:|||||:
Db        421 LDISHTHTRVAFNGIFNGLFSLKVLKMAGNSFQQNFLEDIFTDLNNLIFLDLSECQLEQL 480

Qy        510 SWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIETSKG-ILQHFPKSL 568
              |   ||:| ||::|||||||    ||:  |  ||||  || | | | |||   ||||| ||
Db        481 SPTAFDSLPRLRILNMSHNNFFALDTFPYKHLYSLQVLDYSLNHIGTSKNQELQHFPSSL 540

Qy        569 AFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQMTCATPVEMNTSLVLDFNNSTCYMY 628
              || ||| |  || |||| ||||:|:|:: || |||| ||||:       ||   | || |
Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRRLLVEVEQMECATPLNRKGIPVLSL-NITCQMS 599

Qy        629 KTIISVSVVSVIVVSTVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRN 688
              |||| |||:||:||| || |:| |||||:|:||| || ||||: ||||||||||:||||||
Db        600 KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENTYDAFVIYSSQDEDWVRN 659

Qy        689 ELVKNLEEGVPRFHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFE 748
              |||||||||| | |||||||||||||||| ||||||||||||:||||||||||
Db        660 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 719

Qy        749 YEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNPLGRHIFWRR 808
              |||||||||||||:|||||||:|||||||||||||||||||||||||||: |||||||||
Db        720 YEIAQTWQFLSSRAGIIFIVLQKVEKSLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRR 779

Qy        809 LKNALLDGKASNPEQT 824
              |: |||||:  ||| |
Db        780 LRKALLDGRPWNPEGT 795


RESULT 12
ADO57803
ID   ADO57803 standard; protein; 808 AA.
XX
AC   ADO57803;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Chimpanzee toll-like receptor 4 SEQ ID NO:24.
XX
KW   toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW   immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW   sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS   Pan troglodytes.
XX
PN   WO2004042365-A2.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-US036247.
XX
PR   01-NOV-2002; 2002US-0423113P.
XX
PA   (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI   Messier W;
XX
DR   WPI; 2004-400726/37.
DR   N-PSDB; ADO57801, ADO57802.
XX
```

PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Disclosure; SEQ ID NO 24; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents chimpanzee TLR4.
XX
SQ Sequence 808 AA;

Query Match 64.1%; Score 2785.5; DB 8; Length 808;
Best Local Similarity 68.2%; Pred. No. 1.4e-231;
Matches 543; Conservative 99; Mismatches 151; Indels 3; Gaps 3;

```
Qy         31 VVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIE 90
              ||||||||||:    |:||::| ||||:|||||||: | |||| :| ||| ||||||||:
Db          1 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 60

Qy         91 TIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLIT 150
              |||| |:  | ||| |||||||||| : |:||||:||: |||||| |||||:|||| | |
Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        151 LKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMS 210
              ||:|||||| | | ||| |||||||| |:||| | ||:|   ||: | : | :|||||:|
Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 180

Qy        211 LNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEI 270
              |||::|||  ||: |:||:|||| ||:| |:||||:| |||| ||||:||||::| |||
Db        181 LNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEENLEK 240

Qy        271 FEPSIMEGLCDVTIDEFRLTYTNDFSDDIVK-FHCLANVSAMSLAGVSIKYLEDVPKHFK 329
              |: | :||||::||:|||| | : : |||:  |:|| |||: ||  |:|| ::|   :|
Db        241 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIKSVKDFSYNFG 300

Qy        330 WQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLSYLDLSRNALSFSGCC 389
              || | :::|:  ||||| |  || || | |||  :| :| |||| :|||||| ||| |||
Db        301 WQHLELVKCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        390 SYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLY 449
              | || || ||::|||||| | ||:||:|||:|:|||||| ||:::||| ||||  |:|
Db        361 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 420

Qy        450 LDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLSKCQLEQI 509
              ||||:|:|:: |:||| ||:||  |||||||::| | ::|    ||||||||:|||||:
Db        421 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 480

Qy        510 SWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIETS-KGILQHFPKSL 568
              |   |::|  ||:|||||||   ||:  |  | ||  || | | | || |  |||| ||
Db        481 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 540

Qy        569 AFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQMTCATPVEMNTSLVLDFNNSTCYMY 628
              || ||| |  || |||| ||||:|:|:| || ||:| |||| :    ||  | || |
Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQMN 599

Qy        629 KTIISVSVVSVIVVSTVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRN 688
              |||| |||:||:||| || |:| |||||:|:||| || |||:||||||||||:||||||
Db        600 KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRN 659

Qy        689 ELVKNLEEGVPRFHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFE 748
              |||||||||| | ||||||||||||||||| |||||||||||:||||||||||
Db        660 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 719

Qy        749 YEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNPLGRHIFWRR 808
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              ||||||||||||:|||||||:||||:|||:||||||||||||||||: |||||||||
Db        720 YEIAQTWQFLSSRAGIIFIVLQKVEKTLLRRQVELYRLLSRNTYLEWEDSVLGRHIFWRR 779

Qy        809 LKNALLDGKASNPEQT 824
              |: ||||||: ||| |
Db        780 LRKALLDGKSWNPEGT 795
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RESULT 13
ADO57782
ID ADO57782 standard; protein; 808 AA.
XX
AC ADO57782;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimpanzee toll-like receptor 4 SEQ ID NO:3.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS Pan troglodytes.
XX
PN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
DR WPI; 2004-400726/37.
DR N-PSDB; ADO57780, ADO57781.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Example 1; SEQ ID NO 3; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents chimpanzee TLR4.
XX
SQ Sequence 808 AA;

Query Match 64.0%; Score 2781.5; DB 8; Length 808;
Best Local Similarity 68.2%; Pred. No. 3.2e-231;
Matches 543; Conservative 98; Mismatches 152; Indels 3; Gaps 3;

```
Qy         31 VVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIE 90
              ||||||||||:    |:||::| ||||:|||||||: | |||| :| ||| ||||||||:
Db          1 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 60

Qy         91 TIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLIT 150
              |||| |:  | ||| |||||||||| : |:||||:||: |||||| |||||:|||| | |
Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        151 LKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMS 210
              ||:|||||| | | ||| |||||||| |:||| | ||:|   ||: | : | :|||||:|
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Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 180

Qy        211 LNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEI 270

Db        181 LNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEK 240

Qy        271 FEPSIMEGLCDVTIDEFRLTYTNDFSDDIVK-FHCLANVSAMSLAGVSIKYLEDVPKHFK 329

Db        241 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIKSVKDFSYNFG 300

Qy        330 WQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLSYLDLSRNALSFSGCC 389

Db        301 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        390 SYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLY 449

Db        361 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 420

Qy        450 LDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLSKCQLEQI 509

Db        421 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 480

Qy        510 SWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIETS-KGILQHFPKSL 568

Db        481 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSL 540

Qy        569 AFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQMTCATPVEMNTSLVLDFNNSTCYMY 628

Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQMN 599

Qy        629 KTIISVSVVSVIVVSTVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRN 688

Db        600 KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRN 659

Qy        689 ELVKNLEEGVPRFHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFE 748

Db        660 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 719

Qy        749 YEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNPLGRHIFWRR 808

Db        720 YEIAQTWQFLSSRAGIIFIVLQKVEKTLLRRQVELYRLLSRNTYLEWEDSVLGRHIFWRR 779

Qy        809 LKNALLDGKASNPEQT 824

Db        780 LRKALLDGKSWNPEGT 795
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RESULT 14
ADO57800
ID   ADO57800 standard; protein; 795 AA.
XX
AC   ADO57800;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Hamadryas baboon toll-like receptor 4 SEQ ID NO:21.
XX
KW   toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW   immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW   sepsis; severe sepsis; septic shock; asthma; hamadryas baboon.
XX
OS   Papio hamadryas.
XX
PN   WO2004042365-A2.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-US036247.
XX
PR   01-NOV-2002; 2002US-0423113P.
XX
PA   (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI   Messier W;
XX
DR   WPI; 2004-400726/37.
DR   N-PSDB; ADO57798, ADO57799.
XX
PT   Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT   in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT   sequence of the Old World monkey with that of a human.
XX
PS   Disclosure; SEQ ID NO 21; 111pp; English.
XX
CC   The invention relates to a novel method for identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an old world monkey
CC   comprising comparing the TLR4 polynucleotide sequence of the Old World
CC   monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC   method of the invention has antibacterial, immunosuppressive, and
CC   antiasthmatic activity. The method is useful in identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC   change may be associated with reduced sensitivity to Gram-negative
CC   bacterial infection. The methods, agents and composition are useful in
CC   treating sepsis, severe sepsis or septic shock and asthma. The present
CC   sequence represents hamadryas baboon TLR4.
XX
SQ   Sequence 795 AA;
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  Query Match             63.9%;  Score 2777.5;  DB 8;  Length 795;
  Best Local Similarity   68.2%;  Pred. No. 6.9e-231;
  Matches  542;  Conservative   95;  Mismatches  155;  Indels    3;  Gaps    3;

Qy         31 VVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIE 90

Db          1 VVPNITYQCMELNFYKIPDNIPFSTKNLDLSFNPLRHLGSYSFLRFPELQVLDLSRCEIQ 60

Qy         91 TIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLIT 150

Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        151 LKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMS 210

Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQNIYCKDLQVLHQMPLPNLSLDLS 180

Qy        211 LNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEI 270

Db        181 LNPINFIQPGAFKEIRLHKLTLRSNFDDLNVMKTCIQGLAGLEVHRLVLGEFRNERNLEE 240

Qy        271 FEPSIMEGLCDVTIDEFRLTYTNDFSDDIVK-FHCLANVSAMSLAGVSIKYLEDVPKHFK 329

Db        241 FDKSALEGLCNLTIEEFRLTYLDYYLDNIIDLFNCLANASSFSLVSVNIKRVEDFSYNFR 300

Qy        330 WQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLSYLDLSRNALSFSGCC 389

Db        301 WQHLELVNCKFEQFPTLELESLKRLTFTANKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        390 SYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLY 449

Db        361 SQSDFGTTSLKYLDLSFNDVITMGSNFLGLEQLEHLDFQHSNLKQMSQFSVFLSLRNLIY 420

Qy        450 LDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLSKCQLEQI 509

Db        421 LDISHTHTTVAFNGIFDGLLSLKVLKMAGNSFQENFLPDIFTDLKNLTFLDLSQCQLEQL 480

Qy        510 SWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIETSKG-ILQHFPKSL 568

Db        481 SPTAFDTLNKLQVLNMSHNNFFSLDVFPYKCLPSLQVLDYSLNHIMTSKNQEPQHFPSSL 540

Qy        569 AFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQMTCATPVEMNTSLVLDFNNSTCYMY 628

Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEAERMECATPSDKQGMPVLSV-NITCQMN 599

Qy        629 KTIISVSVVSVIVVSTVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRN 688

Db        600 KTIIGVSVFSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRN 659
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Qy        689 ELVKNLEEGVPRFHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFE 748
              |||||||||||  | ||||||||||||||||||  ||||||||||||:||||||||||
Db        660 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 719

Qy        749 YEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNPLGRHIFWRR 808
              |||||||||||||:|||||||:||||:|||||||||||||||||||||||: ||:||||||
Db        720 YEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGQHIFWRR 779

Qy        809 LKNALLDGKASNPEQ 823
              |: |||||:: |||:
Db        780 LRKALLDGRSWNPEE 794


RESULT 15
ADO57785
ID   ADO57785 standard; protein; 808 AA.
XX
AC   ADO57785;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Gorilla toll-like receptor 4 SEQ ID NO:6.
XX
KW   toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW   immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW   sepsis; severe sepsis; septic shock; asthma; gorilla.
XX
OS   Gorilla gorilla.
XX
PN   WO2004042365-A2.
XX
PD   21-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-US036247.
XX
PR   01-NOV-2002; 2002US-0423113P.
XX
PA   (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI   Messier W;
XX
DR   WPI; 2004-400726/37.
DR   N-PSDB; ADO57783, ADO57784.
XX
PT   Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT   in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT   sequence of the Old World monkey with that of a human.
XX
PS   Example 1; SEQ ID NO 6; 111pp; English.
XX
CC   The invention relates to a novel method for identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an old world monkey
CC   comprising comparing the TLR4 polynucleotide sequence of the Old World
CC   monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC   method of the invention has antibacterial, immunosuppressive, and
CC   antiasthmatic activity. The method is useful in identifying a nucleotide
CC   change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC   change may be associated with reduced sensitivity to Gram-negative
CC   bacterial infection. The methods, agents and composition are useful in
CC   treating sepsis, severe sepsis or septic shock and asthma. The present
CC   sequence represents gorilla TLR4.
XX
SQ   Sequence 808 AA;

  Query Match             63.6%;  Score 2763.5;  DB 8;  Length 808;
  Best Local Similarity   67.8%;  Pred. No. 1.2e-229;
  Matches  540;  Conservative   99;  Mismatches  154;  Indels    3;  Gaps    3;

Qy         31 VVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIE 90
              ||||||||||:    |:||::| ||||:|||||||: | |||| :| ||| ||||||||:
Db          1 VVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQ 60

Qy         91 TIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLIT 150
                ||||  |:  | ||| |||||||||| : |:||||:||: |||||| |||||:|||| | |
Db         61 TIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKT 120

Qy        151 LKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMS 210
              ||:|||||| | | ||| |||||||| ::||| | ||:|    ||: | : | :|||||:|
Db        121 LKELNVAHNLIQSFKLPEYFSNLTNLEYLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLS 180

Qy        211 LNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEI 270
              |||: |||  ||: |:||:|||| ||:| |:||||:| |||| | ||:||||::| |||
Db        181 LNPMTFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVRRLVLGEFRNEGNLEK 240

Qy        271 FEPSIMEGLCDVTIDEFRLTYTNDFSDDIVK-FHCLANVSAMSLAGVSIKYLEDVPKHFK 329
              |: | :||||::||:|||| | : : |||:  |:|| |||: ||  |:|: ::|   :|
Db        241 FDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFG 300

Qy        330 WQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLSYLDLSRNALSFSGCC 389
              || | :: |:  ||||| |  || || | |||  :| :| |||| :|||||| ||| |||
Db        301 WQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCC 360

Qy        390 SYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLY 449
              | || || ||::|||||||  | ||:||:|||:|:|||||||  ||:::||| ||||  |:|
Db        361 SQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIY 420

Qy        450 LDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLSKCQLEQI 509
              ||||:|:|:: |:||| ||:||  ||||||||::| | ::|    ||||||||:|||||:
Db        421 LDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQL 480

Qy        510 SWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIETS-KGILQHFPKSL 568
              |   |::|  ||:|||||||   ||:  |  | ||  || | | | || |  |||| ||
Db        481 SPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLRVLDYSLNHIMTSKKQELQHFPSSL 540

Qy        569 AFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQMTCATPVEMNTSLVLDFNNSTCYMY 628
              || ||| |  || |||| ||||:|:|:| || ||:| |||| :     ||   | || |
Db        541 AFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQMN 599

Qy        629 KTIISVSVVSVIVVSTVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRN 688
              |||| |||:||:||| || |:| |||||:|:||| || |||::||||||||:||||||
Db        600 KTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENVYDAFVIYSSQDEDWVRN 659

Qy        689 ELVKNLEEGVPRFHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFE 748
              |||||||||||  | ||||||||||||||||||  ||||||||||||:||||||||||
Db        660 ELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFE 719

Qy        749 YEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNPLGRHIFWRR 808
              |||||||||||||:|||||||:||||:|||||||||||||||||||||||: |||||||||
Db        720 YEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRR 779

Qy        809 LKNALLDGKASNPEQT 824
              |: ||||||: ||| |
Db        780 LRKALLDGKSWNPEGT 795


Search completed: March 12, 2005, 19:55:11
Job time : 90.9834 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:46 ; Search time 22.9539 Seconds
(without alignments)
2715.523 Million cell updates/sec

Title: US-09-396-985B-99
Perfect score: 4345
Sequence: 1 MMPPWLLARTLIMALFFSCL.....GKASNPEQTAEEEQETATWT 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2786.5	64.1	844	4	US-09-949-016-9438	Sequence 9438, Ap
2	619.5	14.3	661	1	US-08-514-014-4	Sequence 4, Appli
3	619.5	14.3	661	2	US-08-833-823-4	Sequence 4, Appli
4	494	11.4	784	4	US-09-982-308B-23	Sequence 23, Appl
5	432.5	10.0	775	4	US-09-949-016-8799	Sequence 8799, Ap
6	317.5	7.3	603	1	US-08-190-802A-50	Sequence 50, Appl
7	317.5	7.3	603	3	US-08-477-346-50	Sequence 50, Appl
8	317.5	7.3	603	3	US-08-473-089-50	Sequence 50, Appl
9	317.5	7.3	603	4	US-08-487-072A-50	Sequence 50, Appl
10	316.5	7.3	605	3	US-09-063-950-5	Sequence 5, Appli
11	291.5	6.7	605	1	US-08-190-802A-49	Sequence 49, Appl
12	291.5	6.7	605	3	US-08-477-346-49	Sequence 49, Appl
13	291.5	6.7	605	3	US-08-473-089-49	Sequence 49, Appl
14	291.5	6.7	605	4	US-08-487-072A-49	Sequence 49, Appl
15	291.5	6.7	605	4	US-09-538-092-1087	Sequence 1087, Ap
16	291.5	6.7	623	4	US-09-949-016-10995	Sequence 10995, A
17	287.5	6.6	1119	4	US-09-907-794A-294	Sequence 294, App
18	287.5	6.6	1119	4	US-09-905-125A-294	Sequence 294, App
19	287.5	6.6	1119	4	US-09-902-775A-294	Sequence 294, App
20	287.5	6.6	1119	4	US-09-906-700-294	Sequence 294, App
21	287.5	6.6	1119	4	US-09-903-603A-294	Sequence 294, App
22	287.5	6.6	1119	4	US-09-904-920A-294	Sequence 294, App
23	287.5	6.6	1119	4	US-09-909-064-294	Sequence 294, App
24	287.5	6.6	1119	4	US-09-905-381A-294	Sequence 294, App
25	287.5	6.6	1119	4	US-09-906-618-294	Sequence 294, App
26	286.5	6.6	1112	3	US-09-353-585-2	Sequence 2, Appli
27	285.5	6.6	1112	3	US-09-353-585-3	Sequence 3, Appli
28	285.5	6.6	1525	3	US-09-191-647-2	Sequence 2, Appli
29	285.5	6.6	1525	3	US-09-540-245A-2	Sequence 2, Appli
30	285.5	6.6	1525	3	US-09-540-153-2	Sequence 2, Appli
31	282	6.5	1529	4	US-09-312-283C-396	Sequence 396, App
32	273	6.3	1480	3	US-09-191-647-7	Sequence 7, Appli
33	273	6.3	1480	3	US-09-540-245A-7	Sequence 7, Appli
34	273	6.3	1480	3	US-09-540-153-7	Sequence 7, Appli
35	273	6.3	1480	5	PCT-US91-09055-2	Sequence 2, Appli
36	271	6.2	1480	3	US-09-182-024A-5	Sequence 5, Appli
37	269.5	6.2	1059	4	US-09-907-794A-290	Sequence 290, App
38	269.5	6.2	1059	4	US-09-905-125A-290	Sequence 290, App
39	269.5	6.2	1059	4	US-09-902-775A-290	Sequence 290, App
40	269.5	6.2	1059	4	US-09-906-700-290	Sequence 290, App
41	269.5	6.2	1059	4	US-09-903-603A-290	Sequence 290, App
42	269.5	6.2	1059	4	US-09-904-920A-290	Sequence 290, App
43	269.5	6.2	1059	4	US-09-909-064-290	Sequence 290, App
44	269.5	6.2	1059	4	US-09-905-381A-290	Sequence 290, App
45	269.5	6.2	1059	4	US-09-906-618-290	Sequence 290, App

ALIGNMENTS

RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9438

Query Match 64.1%; Score 2786.5; DB 4; Length 844;
Best Local Similarity 68.3%; Pred. No. 1.8e-238;
Matches 544; Conservative 98; Mismatches 152; Indels 3; Gaps 3;

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Qy         30 EVVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEI 89
              |||||||||||:    |:||::| ||||:|||||||: | |||| :| ||| ||||||||
Db         36 EVVPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEI 95

Qy         90 ETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLI 149
              :|||| |:  | ||| |||||||||| : |:||||:||: |||||| |||||:|||| |
Db         96 QTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLK 155

Qy        150 TLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDM 209
              |||:|||||| | | ||| |||||||| |:||| | ||:|   ||: | : | :|||||:
Db        156 TLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDL 215

Qy        210 SLNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLE 269
              ||||::|||  ||: |:||:|||| ||:| |:|||||:| |||| ||||:||||::| |||
Db        216 SLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLE 275

Qy        270 IFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVK-FHCLANVSAMSLAGVSIKYLEDVPKHF 328
              |: | :||||::||:|||| | : : |||:  |:|| |||: ||  |:|: ::|   :|
Db        276 KFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNF 335

Qy        329 KWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLSYLDLSRNALSFSGC 388
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Db        336 GWQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGC 395

Qy        389 CSYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLL 448

Db        396 CSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLI 455

Qy        449 YLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLSKCQLEQ 508

Db        456 YLDISHTHTRVAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQ 515

Qy        509 ISWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIETS-KGILQHFPKS 567

Db        516 LSPTAFNSLSSLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSS 575

Qy        568 LAFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQMTCATPVEMNTSLVLDFNNSTCYM 627

Db        576 LAFLNLTQNDFACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQM 634

Qy        628 YKTIISVSVVSVIVVSTVAFLIYHPYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVR 687

Db        635 NKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVR 694

Qy        688 NELVKNLEEGVPRFHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIF 747

Db        695 NELVKNLEEGVPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIF 754

Qy        748 EYEIAQTWQFLSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNPLGRHIFWR 807

Db        755 EYEIAQTWQFLSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWR 814

Qy        808 RLKNALLDGKASNPEQT 824

Db        815 RLRKALLDGKSWNPEGT 831
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RESULT 2
US-08-514-014-4
; Sequence 4, Application US/08514014
; Patent No. 5707829
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/514,014
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI6000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-514-014-4

Query Match 14.3%; Score 619.5; DB 1; Length 661;
Best Local Similarity 28.6%; Pred. No. 4.4e-46;
Matches 187; Conservative 126; Mismatches 296; Indels 45; Gaps 18;

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Qy         28 CIEVVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRC 87

Db         28 CIEKEANKTYNCENLGLSEIPDTLPNTTEFLEFSFNFLPTIHNRTFSRLMNLTFLDLTRC 87

Qy         88 EIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQ 147

Db         88 QINWIHEDTFQSHHQLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEFIPVHN 147

Qy        148 LITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSL 207

Db        148 LENLESLYLGSNHISSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--AINLSL 204

Qy        208 DMSLNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERN 267

Db        205 NFNGNNVKGIELGAFDSTVFQSLNFGGTPNLSVIFNG-LQNST---TQSLWLGTFEDIDD 260

Qy        268 LEIFEPSIMEGLCDVTIDEFRLTYTNDFSD-DIVKFHCLANVSAMSLAGVSIKYLEDVPK 326

Db        261 EDI-SSAMLKGLCEMSVESLNL-QEHRFSDISSTTFQCFTQLQELDLTAT---HLKGLPS 315

Qy        327 HFKWQSLSIIR------------CQLK--QFPTLDLPFLKSLTLTMNKGSISFKKVALPS 372

Db        316 GMK--GLNLLKKLVLSVNHFDQLCQISAANFPSLTHLYIRGNVKKLHLGVGCLEK--LGN 371

Qy        373 LSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAI-IMSANFMGLEELQHLDFQHST 431

Db        372 LQTLDLSHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKECPQLELLDLAFTR 431

Qy        432 LKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDNTL--SNV 489

Db        432 LHINAPQSPFQNLHFLQVLNLTYCFLDTSNQHLLAGLPVLRHLNLKGNHFQDGTITKTNL 491

Qy        490 FANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLL--FLDS-SHYNQLYSLST 546

Db        492 LQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHNSLTCDSIDSLSHLKGIY---- 547

Qy        547 LDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQMTC 606

Db        548 LNLAANSINIISPRLLPILSQQSTINLSHNPLDCTCSNIHFLTWYKENLHKLEGSEETTC 607

Qy        607 ATPVEMN----TSLVLDFNNSTCYMYKTIISVSVVSVIVVSTVAFLIYHFYFHL 656

Db        608 ANPPSLRGVKLSDVKLSCGITAIGIFFLIVFLLLLAILLFFAVKYLLRWKYQHI 661
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RESULT 3
US-08-833-823-4
; Sequence 4, Application US/08833823
; Patent No. 5969093
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA

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;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/833,823
;      FILING DATE:  10-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/514,014
;      FILING DATE:  11-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI6000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  661 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-833-823-4

  Query Match             14.3%;  Score 619.5;  DB 2;  Length 661;
  Best Local Similarity   28.6%;  Pred. No. 4.4e-46;
  Matches  187;  Conservative  126;  Mismatches  296;  Indels   45;  Gaps   18;

Qy         28 CIEVVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRC 87
Db         28 CIEKEANKTYNCENLGLSEIPDTLPNTTEFLEFSPNFLPTIHNRTFSRLMNLTFLDLTRC 87

Qy         88 EIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQ 147
Db         88 QINWIHEDTFQSHHQLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEFIPVHN 147

Qy        148 LITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSL 207
Db        148 LENLESLYLGSNHISSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--AINLSL 204

Qy        208 DMSLNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERN 267
Db        205 NFNGNNVKGIELGAFDSTVFQSLNFGGTPNLSVIFNG-LQNST---TQSLWLGTFEDIDD 260

Qy        268 LEIFEPSIMEGLCDVTIDEFRLTYTNDFSD-DIVKFHCLANVSAMSLAGVSIKYLEDVPK 326
Db        261 EDI-SSAMLKGLCEMSVESLNL-QEHRFSDISSTTFQCFTQLQELDLTAT---HLKGLPS 315

Qy        327 HFKWQSLSIIR-----------CQLK--QFPTLDLPFLKSLTLTMNKGSISFKKVALPS 372
Db        316 GMK--GLNLLKKLVLSVNHFDQLCQISAANFPSLTHLYIRGNVKKLHLGVGCLEK--LGN 371

Qy        373 LSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAI-IMSANFMGLEELQHLDFQHST 431
Db        372 LQTLDLSHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKECPQLELLDLAFTR 431

Qy        432 LKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDNTL--SNV 489
Db        432 LHINAPQSPFQNLHFLQVLNLTYCFLDTSNQHLLAGLPVLRHLNLKGNHFQDGTITKTNL 491

Qy        490 FANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLL--FLDS-SHYNQLYSLST 546
Db        492 LQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHNSLTCDSIDSLSHLKGIY---- 547

Qy        547 LDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQMTC 606
Db        548 LNLAANSINIISPRLLPILSQQSTINLSHNPLDCTCSNIHFLTWYKENLHKLEGSEETTC 607

Qy        607 ATPVEMN----TSLVLDFNNSTCYMYKTIISVSVVSVIVVSTVAFLIYHFYFHL 656
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Db         608 ANPPSLRGVKLSDVKLSCGITAIGIFFLIVFLLLLAILLFFAVKYLLRWKYQHI 661

RESULT 4
US-09-982-308B-23
; Sequence 23, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
;  APPLICANT: Dalie, Barbara
;  APPLICANT:  Fan, Xuedong
;  APPLICANT:  Lundell, Daniel
;  APPLICANT:  Lunn, Charles A.
;  APPLICANT:  Tan, Jimmy C.
;  APPLICANT:  Zavodny, Paul J.
;  TITLE OF INVENTION: Mammalian TNF-alpha Convertases
;  FILE REFERENCE: JB0601QC
;  CURRENT APPLICATION NUMBER: US/09/982,308B
;  CURRENT FILING DATE:  2001-10-17
;  PRIOR APPLICATION NUMBER: 09/156,163
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 08/889,909
;  PRIOR FILING DATE: 1997-07-10
;  PRIOR APPLICATION NUMBER: 60/021,710
;  PRIOR FILING DATE: 1996-07-12
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;   LENGTH: 784
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-982-308B-23

  Query Match             11.4%;  Score 494;  DB 4;  Length 784;
  Best Local Similarity   25.9%;  Pred. No. 8.2e-35;
  Matches  218;  Conservative  131;  Mismatches  319;  Indels  174;  Gaps   34;

Qy         44 LSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWHGLHHL 103
Db         43 LNSIPSGLTEAVKSLDLSNNRITYISN-----------SDLQRCV------------NL 78

Qy        104 SNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAHNFIHS 163
Db         79 QALVLTSNGINTIEEDSFSSLGSLEHLDLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKT 138

Qy        164 CKLPAYFSNLTNLVHVDL----SYNYIQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQD 219
Db        139 LGETSLFSHLTKLQILRVGNMDTFTKIQRKDFAGLTFLEE-------LEIDASDLQSYEP 191

Qy        220 QAFQGI----------KLHELTLRGNFNSSNIMKTCLQ----NLAGLHVHRLILGEFKD- 264
Db        192 KSLKSIQNVSHLILHMKQHILLLEIFVDVTSSVE-CLELRDTDLDTFHFSELSTGETNSL 250

Qy        265 -----ERNLEIFEPSIME---------GLCDVTIDEFRLTYTNDF--SDDIVKFHCLANV 308
Db        251 IKKFTFRNVKITDESLFQVMKLLNQISGLLELEFDDCTLNGVGNFRASDN---------- 300

Qy        309 SAMSLAGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTL-DLPFLKSLTLTMNKGSISFKK 367
Db        301 -------------DRVIDPGKVETLTIRRLHIPRFYLFYDLSTLYSLTERVKRITVENSK 347

Qy        368 V----------ALPSLSYLDLSRNA-----LSFSGC-CSYSDLGTNSLR--HL-DLSFNGA 409
Db        348 VFLVPCLLSQHLKSLEYLDLSENLMVEEYLKNSACEDAWPSLQTLILRQNHLASLEKTGE 407

Qy        410 IIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLT 469
Db        408 TLLT-----LKNLTNIDISKNSFHSMPETCQW--PEKMKYLNLSST-------------- 446

Qy        470 SLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNN 529
Db        447 ------------RIHSVTGCIPKT--LEILDVSNNNLNLFSL----NLPQLKELYISRNK 488
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Qy        530 LLFLDSSHYNQLYSLSTLDCSFNRIET-SKGILQHFPKSLAFFNLTNNSVACICEHQKFL 588
              |: |  :  : |  |  |  | | | | ||  |  | :|      |:  | ||   ||
Db        489 LMTLPDA--SLLPMLLVLKISRNAITTFSKEQLDSF-HTLKTLEAGGNNFICSCE---FL 542

Qy        589 QWVKEQKQFLVNV-----EQMTCATPVEMNTSLVLD--FNNSTCYMYKTIISVSVVSVIV 641
              : :|| | | |          | :|  :    | |   : | |:     :  :      ::
Db        543 SFTQEQ-QALAKVLIDWPANYLCDSPSHVRGQQVQDVRLSVSECHRIALVSGMCCALFLL 601

Qy        642 VSTVAFLIYHF----YFHLI--LIAGCKKYSRGES---IYDAFVIYSSQNEDWVRNELVK 692
              :    | : |    | ::   :   :|  :  |     ||||| || ::  || | :|:
Db        602 ILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICYDAFVSYSERDAYWVENLMVQ 661

Qy        693 NLEEGVPRFHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIA 752
              ||   | | |||| ||||||  |  ||| :   || | : |:| :|::| || :| : :
Db        662 ELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTVFVLSENFVKSEWCKYELDFS 720

Qy        753 QTWQFLSSRSGIIFIVLEKVEKSLLRQQ-VELYRLLSRNTYLEWEDNPLGRHIFWRRLKN 811
              |  :    | |:|| :||  : |:  :| ::::  |||||  :    |  ||  |:
Db        721 HFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKTYLEWPMDEAQREGFWVNLRA 780

Qy        812 AL 813
              |:
Db        781 AI 782
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RESULT 5
US-09-949-016-8799
; Sequence 8799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8799

Query Match 10.0%; Score 432.5; DB 4; Length 775;
Best Local Similarity 25.4%; Pred. No. 2.3e-29;
Matches 207; Conservative 116; Mismatches 290; Indels 201; Gaps 33;

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Qy         44 LSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWHGLHHL 103
              |: :|  :  : |::||| | :  : :            || ||            :|
Db         78 LNSIPSGLTEAVKSLDLSNNRITYISN----------SDLQRCV------------NL 113

Qy        104 SNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAHNFIHS 163
                |:|| | | :    ||| | |||:|       |::| |      | :|  ||:  |   :
Db        114 QALVLTSNGINTIEEDSFSSLGSLEHLDLSYNYLSNLSSSWFKPLSSLTFLNLLGNPYKT 173

Qy        164 CKLPAYFSNLTNLVHVDL----SYNYIQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQD 219
                : ||:|| |  : :    ::  ||      || |      |::  : :   :
Db        174 LGETSLFSHLTKLQILRVGNMDTFTKIQRKDFAGLTFLEE-------LEIDASDLQSYEP 226

Qy        220 QAFQGI----------KLHELTLRGNFNSSNIMKTCLQ----NLAGLHVHRLILGEFKD- 264
              :: : |          | | | |    : :: :: ||:    :|   |   |  ||
Db        227 KSLKSIQNVSHLILHMKQHILLLEIFVDVTSSVE-CLELRDTDLDTFHFSELSTGETNSL 285

Qy        265 -----ERNLEIFEPSIME---------GLCDVTIDEFRLTYTNDF--SDDIVKFHCLANV 308
                   ||::| : |: :          || ::  |:  |    :|  ||:
Db        286 IKKFTFRNVKITDESLFQVMKLLNQISGLLELEFDDCTLNGVGNFRASDN---------- 335

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Qy        309 SAMSLAGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTL-DLPFLKSLTLTMNKGSISFKK 367
                          : |     | ::|:| |  : :|     ||  | |||  : : ::   |
Db        336 ------------DRVIDPGKVETLTIRRLHIPRFYLFYDLSTLYSLTERVKRITVENSK 382

Qy        368 V---------ALPSLSYLDLSRNA-----LSFSGC-CSYSDLGTNSLR--HL-DLSFNGA 409
              |         | || |||||  |          |  | |  ::  | |  ||  |   |
Db        383 VFLVPCLLSQHLKSLEYLDLSENLMVEEYLKNSACEDAWPSLQTLILRQNHLASLEKTGE 442

Qy        410 IIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLT 469
              :::      |: | ::|   ::   : |   :   ||: ||::| |
Db        443 TLLT-----LKNLTNIDISKNSFHSMPETCQW--PEKMKYLNLSST------------- 481

Qy        470 SLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNN 529
                          : ::::     |  |  ||:|   |   |       | :|: | :| |
Db        482 -----------RIHSVTGCIPKT--LEILDVSNNNLNLFSL----NLPQLKELYISRNK 523

Qy        530 LLFLDSSHYNQLYSLSTLDCSFNRIET-SKGILQHFPKSLAFFNLTNNSVACICEHQKFL 588
              |: |  :  : |  |  |  | | | | ||  |  | :|      |:  | ||   ||
Db        524 LMTLPDA--SLLPMLLVLKISRNAITTFSKEQLDSF-HTLKTLEAGGNNFICSCE---FL 577

Qy        589 QWVKEQKQFLVNV-----EQMTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVVSVIVVS 643
              : :|| | | |          | :|  :    | |   ::| :   :    :
Db        578 SFTQEQ-QALAKVLIDWPANYLCDSPSHVRGQQVQDVRLSVSECHRTALVSGMCCAL--- 633

Qy        644 TVAFLIYHFYFHLILIAG--CKKY----------------------SRGESIYDAFVIY 678
              | |||: |  | ::                             ||    |||| |
Db        634 ----------FLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSR-NICYDAFVSY 682

Qy        679 SSQNEDWVRNELVKNLEEGVPRFHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRH 738
              | ::  || | :|: ||   | | |||| ||||||  |  ||| :   || | : |:| :
Db        683 SERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNII-DSIEKSHKTVFVLSEN 741

Qy        739 FIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKV 772
              |::| || :| : :    |  :    | |:|| :
Db        742 FVKSEWCKYELDFSHFRLFDENNDAAILILLEPI 775
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RESULT 6
US-08-190-802A-50
; Sequence 50, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
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;      LENGTH:  603 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor bind.
;      INDIVIDUAL ISOLATE:  pro. complex-rat, Fig. 33
US-08-190-802A-50

  Query Match             7.3%;  Score 317.5;  DB 1;  Length 603;
  Best Local Similarity   24.1%;  Pred. No. 2.6e-19;
  Matches  159;  Conservative   86;  Mismatches  223;  Indels  193;  Gaps   24;

Qy         39 CMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWH 98
              |  : |: :|||||  ||: : |  | |  : | :| | | | :|:|    : ::| :|
Db         60 CSSKNLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALL 119

Qy         99 GLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAH 158
              || :|  | |  | ::: : | |:   || :|      |  ||      |  |  ||:
Db        120 GLQNLYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGW 179

Qy        159 NF--------------IHSCKL---------PAYFSNLTNLVHVDLSYNYIQTITVNDLQ 195
              |               :|   |         || |  |  |  :||| | ::::  |
Db        180 NSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSVKANVFV 239

Qy        196 FLRENPQV-NLSLDMSLNPIDFIQDQAFQGIK-LHELTLRGNFNSSNIMKTCLQNLAGLH 253
              |   |::  | || :|  |  :   || |:| |  | |  |   : :|:     | |||
Db        240 HL---PRLQKLYLDRNL--ITAVAPGAFLGMKALRWLDLSHN-RVAGLMEDTFPGLLGLH 293

Qy        254 VHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSL 313
              | |                                              ||: :  ||
Db        294 VLR-------------------------------------------------LAHNAIASL 305

Qy        314 AGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNK----GSISFKKVA 369
                      |: ||                 || ||: | |  |:     |  :|:
Db        306 R----------PRTFK----------------DLHFLEELQLGHNRIRQLGERTFE--G 336

Qy        370 LPSLSYLDLSRNAL------SFSGCCSYS--DLGTNSLRHLDLSFNGAIIMSANFMGLEE 421
              |  |  | |: | :      :|||  : :  :|  | || |              | ||::
Db        337 LGQLEVLTLNDNQITEVRVGAFSGLFNVAVMNLSGNCLRSLP---------ERVFQGLDK 387

Qy        422 LQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSF 481
              |  |  :|| |  |   :                          | ||: |  | :
Db        388 LHSLHLEHSCLGHVRLHT------------------------FAGLSGLRRLFL----- 417

Qy        482 KDNTLSNV----FANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSH 537
              :||::|::     |  : |  |||:  :|  :   :|  |  |: | :|:| |  | :
Db        418 RDNSISSIEEQSLAGLSELLELDLTTNRLTHLPRQLFQGLGHLEYLLLSYNQLTTLSAEV 477

Qy        538 YNQLYSLSTLDCSFNRIET-SKGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQ-- 594
                 |  || | | :|| ::|:     : : : :| |||           ||    |
Db        478 LGPLQRAFWLDISHNHLETLAEGLFSSLGR-VRYLSLRNNS----------LQTFSPQPG 526

Qy        595 -KQFLVNVEQMTCATPVE-------MNTSLVLDFNNSTC--------YMYKTIISVSVVS 638
               ::  ::      |: |::        |  :|  |  : |        | |  |      :
Db        527 LERLWLDANPWDCSCPLKALRDFALQNPGVVPRFVQTVCEGDDCQPVYTYNNITCAGPAN 586

Qy        639 V 639
              |
Db        587 V 587


RESULT 7
US-08-477-346-50
; Sequence 50, Application US/08477346
; Patent No. 6262023
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,346
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/487,072
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  603 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor bind.
;      INDIVIDUAL ISOLATE:  pro. complex-rat, Fig. 33
US-08-477-346-50

  Query Match             7.3%;  Score 317.5;  DB 3;  Length 603;
  Best Local Similarity   24.1%;  Pred. No. 2.6e-19;
  Matches  159;  Conservative   86;  Mismatches  223;  Indels  193;  Gaps   24;

Qy         39 CMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWH 98
              |  : |: :|||||  ||: : |  | |  : | :| | | | :|:|    : ::| :|
Db         60 CSSKNLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALL 119

Qy         99 GLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAH 158
              || :|  | |  | ::: : | |:   || :|      |  ||      |  |  ||:
Db        120 GLQNLYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGW 179

Qy        159 NF--------------IHSCKL---------PAYFSNLTNLVHVDLSYNYIQTITVNDLQ 195
              |               :|   |         || |  |  |  :||| | ::::  |
Db        180 NSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSVKANVFV 239

Qy        196 FLRENPQV-NLSLDMSLNPIDFIQDQAFQGIK-LHELTLRGNFNSSNIMKTCLQNLAGLH 253
              |   |::  | || :|  |  :   || |:| |  | |  |   : :|:     | |||
Db        240 HL---PRLQKLYLDRNL--ITAVAPGAFLGMKALRWLDLSHN-RVAGLMEDTFPGLLGLH 293

Qy        254 VHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSL 313
              | |                                              ||: :  ||
Db        294 VLR-------------------------------------------------LAHNAIASL 305

Qy        314 AGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNK----GSISFKKVA 369
                      |: ||                 || ||: | |  |:     |  :|:
Db        306 R----------PRTFK----------------DLHFLEELQLGHNRIRQLGERTFE--G 336

Qy        370 LPSLSYLDLSRNAL------SFSGCCSYS--DLGTNSLRHLDLSFNGAIIMSANFMGLEE 421
              |  |  | |: | :      :|||  : :  :|  | || |              | ||::
Db        337 LGQLEVLTLNDNQITEVRVGAFSGLFNVAVMNLSGNCLRSLP---------ERVFQGLDK 387

Qy        422 LQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSF 481
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Db        388 LHSLHLEHSCLGHVRLHT------------------------FAGLSGLRRLFL----- 417

Qy        482 KDNTLSNV----FANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSH 537

Db        418 RDNSISSIEEQSLAGLSELLELDLTTNRLTHLPRQLFQGLGHLEYLLLSYNQLTTLSAEV 477

Qy        538 YNQLYSLSTLDCSFNRIET-SKGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQ-- 594

Db        478 LGPLQRAFWLDISHNHLETLAEGLFSSLGR-VRYLSLRNNS----------LQTFSPQPG 526

Qy        595 -KQFLVNVEQMTCATPVE-------MNTSLVLDFNNSTC--------YMYKTIISVSVVS 638

Db        527 LERLWLDANPWDCSCPLKALRDFALQNPGVVPRFVQTVCEGDDCQPVYTYNNITCAGPAN 586

Qy        639 V 639

Db        587 V 587
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RESULT 8
US-08-473-089-50
; Sequence 50, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,089
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
; INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
US-08-473-089-50

Query Match 7.3%; Score 317.5; DB 3; Length 603;
Best Local Similarity 24.1%; Pred. No. 2.6e-19;
Matches 159; Conservative 86; Mismatches 223; Indels 193; Gaps 24;

```
Qy         39 CMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWH 98

Db         60 CSSKNLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALL 119

Qy         99 GLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAH 158

Db        120 GLQNLYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGW 179

Qy        159 NF--------------IHSCKL---------PAYFSNLTNLVHVDLSYNYIQTITVNDLQ 195

Db        180 NSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSVKANVFV 239

Qy        196 FLRENPQV-NLSLDMSLNPIDFIQDQAFQGIK-LHELTLRGNFNSSNIMKTCLQNLAGLH 253

Db        240 HL---PRLQKLYLDRNL--ITAVAPGAFLGMKALRWLDLSHN-RVAGLMEDTFPGLLGLH 293

Qy        254 VHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSL 313

Db        294 VLR-----------------------------------------------LAHNAIASL 305

Qy        314 AGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNK----GSISFKKVA 369

Db        306 R----------PRTFK----------------DLHFLEELQLGHNRIRQLGERTFE--G 336

Qy        370 LPSLSYLDLSRNAL------SFSGCCSYS--DLGTNSLRHLDLSFNGAIIMSANFMGLEE 421

Db        337 LGQLEVLTLNDNQITEVRVGAFSGLFNVAVMNLSGNCLRSLP---------ERVFQGLDK 387

Qy        422 LQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSF 481

Db        388 LHSLHLEHSCLGHVRLHT------------------------FAGLSGLRRLFL----- 417

Qy        482 KDNTLSNV----FANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSH 537

Db        418 RDNSISSIEEQSLAGLSELLELDLTTNRLTHLPRQLFQGLGHLEYLLLSYNQLTTLSAEV 477

Qy        538 YNQLYSLSTLDCSFNRIET-SKGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQ-- 594

Db        478 LGPLQRAFWLDISHNHLETLAEGLFSSLGR-VRYLSLRNNS----------LQTFSPQPG 526

Qy        595 -KQFLVNVEQMTCATPVE-------MNTSLVLDFNNSTC--------YMYKTIISVSVVS 638

Db        527 LERLWLDANPWDCSCPLKALRDFALQNPGVVPRFVQTVCEGDDCQPVYTYNNITCAGPAN 586

Qy        639 V 639

Db        587 V 587
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RESULT 9
US-08-487-072A-50
; Sequence 50, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,072A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

```
;       NAME:  MURASHIGE, KATE H.
;       REGISTRATION NUMBER:  29,959
;       REFERENCE/DOCKET NUMBER:  2550-0025.20
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 887-1500
;       TELEFAX:  (202) 887-0763
;   INFORMATION FOR SEQ ID NO:  50:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  603 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       INDIVIDUAL ISOLATE:  Insulin-like growth factor bind.
;       INDIVIDUAL ISOLATE:  pro. complex-rat, Fig. 33
US-08-487-072A-50

  Query Match             7.3%;  Score 317.5;  DB 4;  Length 603;
  Best Local Similarity   24.1%;  Pred. No. 2.6e-19;
  Matches  159;  Conservative   86;  Mismatches  223;  Indels  193;  Gaps   24;

Qy         39 CMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWH 98
Db         60 CSSKNLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALL 119

Qy         99 GLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAH 158
Db        120 GLQNLYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGW 179

Qy        159 NF--------------IHSCKL---------PAYFSNLTNLVHVDLSYNYIQTITVNDLQ 195
Db        180 NSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSVKANVFV 239

Qy        196 FLRENPQV-NLSLDMSLNPIDFIQDQAFQGIK-LHELTLRGNFNSSNIMKTCLQNLAGLH 253
Db        240 HL---PRLQKLYLDRNL--ITAVAPGAFLGMKALRWLDLSHN-RVAGLMEDTFPGLLGLH 293

Qy        254 VHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSL 313
Db        294 VLR-----------------------------------------------LAHNAIASL 305

Qy        314 AGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNK----GSISFKKVA 369
Db        306 R----------PRTFK----------------DLHFLEELQLGHNRIRQLGERTFE--G 336

Qy        370 LPSLSYLDLSRNAL------SFSGCCSYS--DLGTNSLRHLDLSFNGAIIMSANFMGLEE 421
Db        337 LGQLEVLTLNDNQITEVRVGAFSGLFNVAVMNLSGNCLRSLP---------ERVFQGLDK 387

Qy        422 LQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSF 481
Db        388 LHSLHLEHSCLGHVRLHT-----------------------FAGLSGLRRLFL----- 417

Qy        482 KDNTLSNV----FANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSH 537
Db        418 RDNSISSIEEQSLAGLSELLELDLTTNRLTHLPRQLFQGLGHLEYLLLSYNQLTTLSAEV 477

Qy        538 YNQLYSLSTLDCSFNRIET-SKGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQ-- 594
Db        478 LGPLQRAFWLDISHNHLETLAEGLFSSLGR-VRYLSLRNNS----------LQTFSPQPG 526

Qy        595 -KQFLVNVEQMTCATPVE-------MNTSLVLDFNNSTC--------YMYKTIISVSVVS 638
Db        527 LERLWLDANPWDCSCPLKALRDFALQNPGVVPRFVQTVCEGDDCQPVYTYNNITCAGPAN 586

Qy        639 V 639
Db        587 V 587

RESULT 10
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US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
;  APPLICANT: Holtzman, Douglas A.
;  TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION: THEREFOR
;  FILE REFERENCE: MEI-019
;  CURRENT APPLICATION NUMBER: US/09/063,950C
;  CURRENT FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 605
;   TYPE: PRT
;   ORGANISM: Papio hamadryas
US-09-063-950-5

  Query Match             7.3%;  Score 316.5;  DB 3;  Length 605;
  Best Local Similarity   22.2%;  Pred. No. 3.2e-19;
  Matches  147;  Conservative   89;  Mismatches  238;  Indels  189;  Gaps   17;

Qy         32 VPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIET 91
Db         53 VNELSVFCSSRNLTRLPDGIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGS 112

Qy         92 IEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITL 151
Db        113 LEPQALLGLENLCHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLED--------- 163

Qy        152 KKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMSL 211
Db        164 ---------------GLFEGLGNLWDLNLGWNSLAV---------------------- 184

Qy        212 NPIDFIQDQAFQGI-KLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEI 270
Db        185 -----LPDAAFRGLGGLRELVLAGN-----------------------------RLAY 208

Qy        271 FEPSIMEGLC-----DVTIDEFRLTYTNDFSD--DIVKFHCLANVSAMSLAGVSIKYLED 323
Db        209 LQPALFSGLAELRELDLSRNALRAIKANVFAQLPRLQKLYLDRNLIAAVAPGA------- 261

Qy        324 VPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNK--GSISFKKVALPSLSYLDLSRN 381
Db        262 ----------------------FLGLKALRWLDLSHNRVAGLLEDTFPGLLGLRVLRLSHN 300

Qy        382 ALSFSGCCSYSD--------LGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLK 433
Db        301 AIASLRPRTFEDLHFLEELQLGHNRIRQL---------AERSFEGLGQLEVLTLDHNQLQ 351

Qy        434 RVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNS------------- 480
Db        352 EV-KVGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFAGLS 410

Qy        481 ------FKDNTLSNVFANT----TNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNL 530
Db        411 GLRRLFLKDNGLVGIEEQSLWGLAELLELDLTSNQLTHLPHQLFQGLGKLEYLLLSHNRL 470

Qy        531 LFLDSSHYNQLYSLSTLDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKFLQ- 589
Db        471 AELPADALGPLQRAFWLDVSHNRLEALPGSLLASLGRLRYLNLRNNSLRTFTPQPPGLER 530

Qy        590 -WVKEQKQFLVNVEQMTCATPVE-------MNTSLVLDFNNSTC---------YMYKTII 632
Db        531 LWLEG--------NPWDCSCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPVYTYNNIT 582

Qy        633 SVS 635
Db        583 CAS 585

RESULT 11
US-08-190-802A-49
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; Sequence 49, Application US/08190802A
; Patent No. 5519003
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  P.O. Box 60850
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306-0850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/190,802A
;      FILING DATE:  01-FEB-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fabian, Gary R.
;      REGISTRATION NUMBER:  33,875
;      REFERENCE/DOCKET NUMBER:  8600-0139
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-190-802A-49

  Query Match             6.7%;  Score 291.5;  DB 1;  Length 605;
  Best Local Similarity   22.0%;  Pred. No. 5.3e-17;
  Matches  147;  Conservative   86;  Mismatches  233;  Indels  201;  Gaps   17;

Qy         39 CMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWH 98
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy         99 GLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAH 158
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        159 NFIH----------------------SCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQ 195
Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKAN--V 237

Qy        196 FLRENPQVNLSLDMSLNPIDFIQDQAFQGIK-LHELTLRGNFNSSNIMKTCLQNLAGLHV 254
Db        238 FVQLPRLQKLYLDRNL--IAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRV 294

Qy        255 HRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSLA 314
Db        295 LRL-------------------------------------------------SHNAIA 303

Qy        315 GVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLS 374
Db        304 SLR-------PRTFK----------------DLHFLEEL------------------- 319

Qy        375 YLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKR 434
                                  || | :| |           :| || :|: |   |: |:
Db        320 -----------------QLGHNRIRQL---------AERSFEGLGQLEVLTLDHNQLQE 352

Qy        435 VTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNS-------------- 480
              | :  ||| |  :  :::|    :   : :| ||  |::| : |:
Db        353 V-KAGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSG 411

Qy        481 -----FKDNTLSNVFANT----TNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLL 531
                  ||| |   :   :      |  |||:  ||  :   :|  | :|: | :| | | |
Db        412 LRRLFLKDNGLVGIEEQSLWGLAELLELDLTSNQLTHLPHRLFQGLGKLEYLLLSRNRLA 471

Qy        532 FLDSSHYNQLYSLSTLDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKFLQ-- 589
              | :      |      || | ||:|     |       | : :| |||:          |:
Db        472 ELPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNNSLRTFTPQPPGLERL 531

Qy        590 WVKEQKQFLVNVEQMTCATPVE-------MNTSLVLDFNNSTC---------YMYKTIIS 633
              |::             |  |::       | | | |  | : |         | | |
Db        532 WLEG--------NPWDCGCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPAYTYNNITC 583

Qy        634 VSVVSVI 640
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Db        584 ASPPEVV 590


RESULT 12
US-08-477-346-49
; Sequence 49, Application US/08477346
; Patent No. 6262023
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,346
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/487,072
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-477-346-49
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  Query Match             6.7%;  Score 291.5;  DB 3;  Length 605;
  Best Local Similarity   22.0%;  Pred. No. 5.3e-17;
  Matches  147;  Conservative   86;  Mismatches  233;  Indels  201;  Gaps  17;

Qy         39 CMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWH 98
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy         99 GLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAH 158
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        159 NFIH----------------------SCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQ 195
Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKAN--V 237

Qy        196 FLRENPQVNLSLDMSLNPIDFIQDQAFQGIK-LHELTLRGNFNSSNIMKTCLQNLAGLHV 254
Db        238 FVQLPRLQKLYLDRNL--IAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRV 294

Qy        255 HRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSLA 314
Db        295 LRL-----------------------------------------------------SHNAIA 303

Qy        315 GVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLS 374
Db        304 SLR-------PRTFK----------------DLHFLEEL---------------------- 319

Qy        375 YLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKR 434
Db        320 ------------------QLGHNRIRQL---------AERSFEGLGQLEVLTLDHNQLQE 352

Qy        435 VTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNS-------------- 480
Db        353 V-KAGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSG 411

Qy        481 -----FKDNTLSNVFANT----TNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLL 531
Db        412 LRRLFLKDNGLVGIEEQSLWGLAELLELDLTSNQLTHLPHRLFQGLGKLEYLLLSRNRLA 471

Qy        532 FLDSSHYNQLYSLSTLDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKFLQ-- 589
Db        472 ELPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNNSLRTFTPQPPGLERL 531

Qy        590 WVKEQKQFLVNVEQMTCATPVE-------MNTSLVLDFNNSTC---------YMYKTIIS 633
Db        532 WLEG--------NPWDCGCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPAYTYNNITC 583

Qy        634 VSVVSVI 640
Db        584 ASPPEVV 590


RESULT 13
US-08-473-089-49
; Sequence 49, Application US/08473089
; Patent No. 6342368
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/473,089
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-473-089-49

  Query Match             6.7%;  Score 291.5;  DB 3;  Length 605;
  Best Local Similarity   22.0%;  Pred. No. 5.3e-17;
  Matches  147;  Conservative   86;  Mismatches  233;  Indels  201;  Gaps  17;

Qy         39 CMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWH 98
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy         99 GLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAH 158
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        159 NFIH----------------------SCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQ 195
Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKAN--V 237

Qy        196 FLRENPQVNLSLDMSLNPIDFIQDQAFQGIK-LHELTLRGNFNSSNIMKTCLQNLAGLHV 254
Db        238 FVQLPRLQKLYLDRNL--IAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRV 294

Qy        255 HRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSLA 314
Db        295 LRL-----------------------------------------------------SHNAIA 303

Qy        315 GVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLS 374
Db        304 SLR-------PRTFK----------------DLHFLEEL---------------------- 319

Qy        375 YLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKR 434
Db        320 ------------------QLGHNRIRQL---------AERSFEGLGQLEVLTLDHNQLQE 352

Qy        435 VTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNS-------------- 480
Db        353 V-KAGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSG 411

Qy        481 -----FKDNTLSNVFANT----TNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLL 531
Db        412 LRRLFLKDNGLVGIEEQSLWGLAELLELDLTSNQLTHLPHRLFQGLGKLEYLLLSRNRLA 471

Qy        532 FLDSSHYNQLYSLSTLDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKFLQ-- 589
Db        472 ELPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNNSLRTFTPQPPGLERL 531

Qy        590 WVKEQKQFLVNVEQMTCATPVE-------MNTSLVLDFNNSTC---------YMYKTIIS 633
Db        532 WLEG--------NPWDCGCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPAYTYNNITC 583
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Qy        634 VSVVSVI 640
              |   |:
Db        584 ASPPEVV 590


RESULT 14
US-08-487-072A-49
; Sequence 49, Application US/08487072A
; Patent No. 6423684
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    APPLICANT:  Ron, Dorit
;    TITLE OF INVENTION:  WD-40 - Derived Peptides and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  265
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Avenue, NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1812
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,072A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURASHIGE, KATE H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2550-0025.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  605 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  Insulin-like growth factor binding
;      INDIVIDUAL ISOLATE:  protein complex, Fig. 32
US-08-487-072A-49

  Query Match             6.7%;  Score 291.5;  DB 4;  Length 605;
  Best Local Similarity   22.0%;  Pred. No. 5.3e-17;
  Matches  147;  Conservative   86;  Mismatches  233;  Indels  201;  Gaps   17;

Qy         39 CMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWH 98
              |  : |:::|| :|  |: : |  | |  :   :| | | | :|:|   :: ::| :|
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy         99 GLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAH 158
              || :| :| |  | ::| : |:|:   :| :|     :|: ||      | :|  ||:
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        159 NFIH----------------------SCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQ 195
              | :                      :   || || |  |  :||| | :: |  |
Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKAN--V 237

Qy        196 FLRENPQVNLSLDMSLNPIDFIQDQAFQGIK-LHELTLRGNFNSSNIMKTCLQNLAGLHV 254
              |::      | || :|  |  :   || |:| |  | |  |   : :::     | || |
Db        238 FVQLPRLQKLYLDRNL--IAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRV 294

Qy        255 HRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSLA 314
              ||                                                  | ::|
Db        295 LRL----------------------------------------------------SHNAIA 303

Qy        315 GVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLS 374
              :        |: ||                 || ||: |
Db        304 SLR-------PRTFK----------------DLHFLEEL-------------------- 319

Qy        375 YLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKR 434
                                  || | :| |            :| || :|: |   |: |:
Db        320 -----------------QLGHNRIRQL---------AERSFEGLGQLEVLTLDHNQLQE 352

Qy        435 VTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNS-------------- 480
              | :  ||| |  :  :::|     :   : :| ||  |::| : |:
Db        353 V-KAGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSG 411

Qy        481 -----FKDNTLSNVFANT----TNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLL 531
                  ||| |  :   :       |  |||:  ||  :   :|  | :|: | :| | |
Db        412 LRRLFLKDNGLVGIEEQSLWGLAELLELDLTSNQLTHLPHRLFQGLGKLEYLLLSRNRLA 471

Qy        532 FLDSSHYNQLYSLSTLDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKFLQ-- 589
              | :       |     || | ||:|     |       | : :| |||:          |:
Db        472 ELPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNNSLRTFTPQPPGLERL 531

Qy        590 WVKEQKQFLVNVEQMTCATPVE-------MNTSLVLDFNNSTC---------YMYKTIIS 633
              |::           |  |::       | | |  | : |           | | |
Db        532 WLEG--------NPWDCGCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPAYTYNNITC 583

Qy        634 VSVVSVI 640
              |   |:
Db        584 ASPPEVV 590


RESULT 15
US-09-538-092-1087
; Sequence 1087, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1087
;   LENGTH: 605
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number P35858
US-09-538-092-1087

  Query Match             6.7%;  Score 291.5;  DB 4;  Length 605;
  Best Local Similarity   22.0%;  Pred. No. 5.3e-17;
  Matches  147;  Conservative   86;  Mismatches  233;  Indels  201;  Gaps   17;

Qy         39 CMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWH 98
              |  : |:::|| :|  |: : |  | |  :   :| | | | :|:|   :: ::| :|
Db         60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy         99 GLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAH 158
              || :| :| |  | ::| : |:|:   :| :|     :|: ||      | :|  ||:
Db        120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy        159 NFIH----------------------SCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQ 195
              | :                      :   || || |  |  :||| | :: |  |
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Db        180 NSLAVLPDAAFRGLGSLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKAN--V 237

Qy        196 FLRENPQVNLSLDMSLNPIDFIQDQAFQGIK-LHELTLRGNFNSSNIMKTCLQNLAGLHV 254

Db        238 FVQLPRLQKLYLDRNL--IAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRV 294

Qy        255 HRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSLA 314

Db        295 LRL-----------------------------------------------------SHNAIA 303

Qy        315 GVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLS 374

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Qy        375 YLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKR 434

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Qy        435 VTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNS-------------- 480

Db        353 V-KAGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSG 411

Qy        481 -----FKDNTLSNVFANT----TNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLL 531

Db        412 LRRLFLKDNGLVGIEEQSLWGLAELLELDLTSNQLTHLPHRLFQGLGKLEYLLLSRNRLA 471

Qy        532 FLDSSHYNQLYSLSTLDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKFLQ-- 589

Db        472 ELPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNNSLRTFTPQPPGLERL 531

Qy        590 WVKEQKQFLVNVEQMTCATPVE-------MNTSLVLDFNNSTC---------YMYKTIIS 633

Db        532 WLEG--------NPWDCGCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPAYTYNNITC 583

Qy        634 VSVVSVI 640

Db        584 ASPPEVV 590
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Search completed: March 12, 2005, 19:59:07
Job time : 24.9539 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:55:29 ; Search time 73.8956 Seconds
(without alignments)
3727.157 Million cell updates/sec

Title: US-09-396-985B-99
Perfect score: 4345
Sequence: 1 MMPPWLLARTLIMALFFSCL.....GKASNPEQTAEEEQETATWT 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2829.5	65.1	837	10	US-09-950-041-26	Sequence 26, Appl
2	2730.5	62.8	799	10	US-09-950-041-8	Sequence 8, Appli
3	2730.5	62.8	799	14	US-10-128-166-7	Sequence 7, Appli
4	2730.5	62.8	799	16	US-10-732-563-8	Sequence 8, Appli
5	2730.5	62.8	799	16	US-10-732-796A-8	Sequence 8, Appli
6	619.5	14.3	661	13	US-10-114-893-10	Sequence 10, Appl
7	619.5	14.3	661	15	US-10-038-854-134	Sequence 134, App
8	612.5	14.1	661	15	US-10-038-854-135	Sequence 135, App
9	612.5	14.1	661	15	US-10-037-417-107	Sequence 107, App
10	580	13.3	1032	10	US-09-954-987B-192	Sequence 192, App
11	580	13.3	1032	14	US-10-272-502A-31	Sequence 31, Appl
12	580	13.3	1032	15	US-10-407-952-32	Sequence 32, Appl
13	559	12.9	1059	10	US-09-954-987B-187	Sequence 187, App
14	559	12.9	1059	15	US-10-407-952-30	Sequence 30, Appl
15	559	12.9	1059	17	US-10-753-267-30	Sequence 30, Appl
16	557	12.8	1041	9	US-09-168-978-3	Sequence 3, Appli
17	557	12.8	1041	9	US-09-978-295A-498	Sequence 498, App
18	557	12.8	1041	9	US-09-978-697-498	Sequence 498, App
19	557	12.8	1041	9	US-09-978-192A-498	Sequence 498, App
20	557	12.8	1041	9	US-09-999-832A-498	Sequence 498, App
21	557	12.8	1041	10	US-09-978-189-498	Sequence 498, App
22	557	12.8	1041	10	US-09-978-608A-498	Sequence 498, App
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26	557	12.8	1041	10	US-09-978-564A-498	Sequence 498, App
27	557	12.8	1041	10	US-09-999-833A-498	Sequence 498, App
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29	557	12.8	1041	10	US-09-978-824-498	Sequence 498, App
30	557	12.8	1041	10	US-09-918-585A-498	Sequence 498, App
31	557	12.8	1041	10	US-09-999-834A-498	Sequence 498, App
32	557	12.8	1041	10	US-09-978-423A-498	Sequence 498, App
33	557	12.8	1041	10	US-09-978-193A-498	Sequence 498, App
34	557	12.8	1041	10	US-09-999-830A-498	Sequence 498, App
35	557	12.8	1041	10	US-09-978-757A-498	Sequence 498, App
36	557	12.8	1041	10	US-09-978-187B-498	Sequence 498, App
37	557	12.8	1041	10	US-09-978-643A-498	Sequence 498, App
38	557	12.8	1041	10	US-09-978-375A-498	Sequence 498, App
39	557	12.8	1041	10	US-09-978-298A-498	Sequence 498, App
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41	557	12.8	1041	10	US-09-978-681A-498	Sequence 498, App
42	557	12.8	1041	10	US-09-978-194A-498	Sequence 498, App
43	557	12.8	1041	10	US-09-999-829A-498	Sequence 498, App
44	557	12.8	1041	10	US-09-978-299A-498	Sequence 498, App
45	557	12.8	1041	10	US-09-978-544A-498	Sequence 498, App

ALIGNMENTS

RESULT 1
US-09-950-041-26
; Sequence 26, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XK1
; CURRENT APPLICATION NUMBER: US/09/950,041
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-26

Query Match 65.1%; Score 2829.5; DB 10; Length 837;

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  Best Local Similarity   67.7%;  Pred. No. 3e-224;
  Matches  556;  Conservative  101;  Mismatches  159;  Indels    5;  Gaps    5;

Qy          7 LARTLIMAL-FFSCLTPGSLNPCIEVVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPL 65
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Db          6 LAGTLIPAMAFLSCVRPESWEPCVE-VPNITYQCMELNFYKIPDNLPFSTKNLDLSFNPL 64

Qy         66 KILKSYSFSNFSELQWLDLSRCEIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLT 125
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Db         65 RHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQSLSHLSTLILTGNPIQSLALGAFSGLS 124

Qy        126 SLENLVAVETKLASLESFPIGQLITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNY 185
              ||: |||||| |||||:|||| | |||:|||||| | | ||| |||||||| |:||| |
Db        125 SLQKLVAVETNLASLENFPIGHLKTLKELNVAHNLIQSFKLPEYFSNLTNLEHLDLSSNK 184

Qy        186 IQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTC 245
              ||:|   ||: | : | :|||||:||||::|||  ||: |:||:|||| ||:| |:|||| 
Db        185 IQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQPGAFKEIRLHKLTLRNNFDSLNVMKTC 244

Qy        246 LQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVK-FHC 304
              :| |||| ||||:||||::| ||| |: | :||||::||:|||| | : : |||:  |:| 
Db        245 IQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGLCNLTIEEFRLAYLDYYLDDIIDLFNC 304

Qy        305 LANVSAMSLAGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSIS 364
              | |||: ||  |:|: ::|   :| || | :: |:  ||||| |  || || | |||  : 
Db        305 LTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNCKFGQFPTLKLKSLKRLTFTSNKGGNA 364

Qy        365 FKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQH 424
              | :| |||| :|||||| ||| |||| || || ||::|||||| | ||:||:|||:|:|
Db        365 FSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTSLKYLDLSFNGVITMSSNFLGLEQLEH 424

Qy        425 LDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDN 484
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Qy        485 TLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSL 544
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Qy        604 MTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVVSVIVVSTVAFLIYHFYFHLILIAGCK 663
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Db        605 MECATPSDKQGMPVLSL-NITCQMNKTIIGVSVLSVLVVSVVAVLVYKFYFHLMLLAGCI 663

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RESULT 2
US-09-950-041-8
; Sequence 8, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
;  APPLICANT: Hardiman, Gerard T.
;  APPLICANT:  Rock, Fernando L.
;  APPLICANT:  Bazan, J. Fernando
;  APPLICANT:  Kastelein, Robert A.
;  APPLICANT:  Ho, Stephen W.K.
;  APPLICANT:  Liu, Yong-Jun
;  TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
;  FILE REFERENCE: DX0724XK1
;  CURRENT APPLICATION NUMBER: US/09/950,041
;  CURRENT FILING DATE:  2002-05-06
;  PRIOR APPLICATION NUMBER: 09/728,540
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 60/207,558
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 09/073,363
;  PRIOR FILING DATE: 1999-06-05
;  PRIOR APPLICATION NUMBER: 60/044,293
;  PRIOR FILING DATE: 1997-05-07
;  PRIOR APPLICATION NUMBER: 60/072,212
;  PRIOR FILING DATE: 1998-01-22
;  PRIOR APPLICATION NUMBER: 60/076,947
;  PRIOR FILING DATE: 1998-03-05
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-950-041-8

  Query Match             62.8%;  Score 2730.5;  DB 10;  Length 799;
  Best Local Similarity   67.9%;  Pred. No. 4.2e-216;
  Matches  534;  Conservative   98;  Mismatches  152;  Indels    3;  Gaps    3;

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Qy        100 LHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAHN 159
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Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        220 QAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGL 279
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Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        280 CDVTIDEFRLTYTNDFSDDIVK-FHCLANVSAMSLAGVSIKYLEDVPKHFKWQSLSIIRC 338
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Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        339 QLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNS 398
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Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        399 LRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTK 458
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Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        459 IDFDGIFLGLTSLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLH 518
              : |:||| ||:||  |||||||::| | ::|    |||||||:|||||:|   |::|
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        519 RLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIETS-KGILQHFPKSLAFFNLTNNS 577
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Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        578 VACICEHQKFLQWVKEQKQFLVNVEQMTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVV 637
              || |||| ||||:|:|:| || ||:| |||| :     ||   | || | |||| |||:
Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVL 599

Qy        638 SVIVVSTVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEG 697
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Db        600 SVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEG 659

Qy        698 VPRFHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQF 757
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Db        660 VPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQF 719
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Qy        758 LSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNPLGRHIFWRRLKNALLDGK 817
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RESULT 3
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US20030077279A1
; GENERAL INFORMATION:
;  APPLICANT: ARDITI, MOSHE
;  APPLICANT:  RAJAVASHISTH, TRIPATHI
;  APPLICANT:  SHAH, PREDIMAN K.
;  TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
;  TITLE OF INVENTION:  TOLL-LIKE RECEPTOR-4
;  FILE REFERENCE: 81476-0255398
;  CURRENT APPLICATION NUMBER: US/10/128,166
;  CURRENT FILING DATE:  2002-04-23
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-128-166-7

  Query Match             62.8%;  Score 2730.5;  DB 14;  Length 799;
  Best Local Similarity   67.9%;  Pred. No. 4.2e-216;
  Matches  534;  Conservative   98;  Mismatches  152;  Indels    3;  Gaps    3;

Qy         40 MDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWHG 99
              |:    |:||::| ||||:|||||||: | |||| :| ||| ||||||||:|||| |:
Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy        100 LHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAHN 159
              | ||| |||||||||| : |:||||:||: |||||| |||||:|||| | |||:||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        160 FIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQD 219
              |.| ||| |||||||| |:||| | ||:|   ||: | : | :|||||:||||::|||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        220 QAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGL 279
              ||: |:||:|||| ||:| |:||||:| |||| ||||:||||::| ||| |: | :|||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        280 CDVTIDEFRLTYTNDFSDDIVK-FHCLANVSAMSLAGVSIKYLEDVPKHFKWQSLSIIRC 338
              |::||:|||| | : : |||:  |:|| |||: ||  |:|: ::|   :| || | :: |
Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        339 QLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNS 398
              : ||||| |  || || | |||  :| :| |||| :|||||| ||| |||| || || |
Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        399 LRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTK 458
              |::|||||| | ||:||:|||:|:|||||| ||:::||| |||| |:|||||:|:|:
Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        459 IDFDGIFLGLTSLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLH 518
              : |:||| ||:|| |||||||::| | ::|    |||||||:|||||:|   |::|
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        519 RLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIETS-KGILQHFPKSLAFFNLTNNS 577
              ||:|||||||   ||:  |  | ||  || | | || |  ||||| |||| ||| |
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        578 VACICEHQKFLQWVKEQKQFLVNVEQMTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVV 637
              || |||| ||||:|:|:| || ||:| |||| :     ||   | || | |||| |||:

Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVL 599

Qy        638 SVIVVSTVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEG 697
              ||:||| || |:| |||||:|:||| || |||:||||||||||:||||||||||||||
Db        600 SVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEG 659

Qy        698 VPRFHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQF 757
              || | |||||||||||||||||| |||||||||||||:|||||||||||||||||||||
Db        660 VPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQF 719

Qy        758 LSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNPLGRHIFWRRLKNALLDGK 817
              ||||:|||||||:||||:|||||||||||||||||||||||: ||||||||||: ||||||
Db        720 LSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGK 779

Qy        818 ASNPEQT 824
              : ||| |
Db        780 SWNPEGT 786


RESULT 4
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
;  APPLICANT: Gupta, Shalley K.
;  APPLICANT:  Ghosh, Tarun K.
;  APPLICANT:  Fink, Jason R.
;  TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
;  FILE REFERENCE: 58183WO0003
;  CURRENT APPLICATION NUMBER: US/10/732,563
;  CURRENT FILING DATE:  2003-12-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-732-563-8

  Query Match             62.8%;  Score 2730.5;  DB 16;  Length 799;
  Best Local Similarity   67.9%;  Pred. No. 4.2e-216;
  Matches  534;  Conservative   98;  Mismatches  152;  Indels    3;  Gaps    3;

Qy         40 MDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWHG 99
              |:    |:||::| ||||:|||||||: | |||| :| ||| ||||||||:|||| |:
Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy        100 LHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAHN 159
              | ||| |||||||||| : |:||||:||: |||||| |||||:|||| | |||:||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        160 FIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQD 219
              | | ||| |||||||| |:||| | ||:|   ||: | : | :|||||:||||::|||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        220 QAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGL 279
              ||: |:||:|||| ||:| |:||||:| |||| ||||:||||::| ||| |: | :|||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        280 CDVTIDEFRLTYTNDFSDDIVK-FHCLANVSAMSLAGVSIKYLEDVPKHFKWQSLSIIRC 338
              |::||:|||| | : : |||:  |:|| |||: ||  |:|: ::|   :| || | :: |
Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        339 QLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNS 398
              : ||||| |  || || | |||  :| :| |||| :|||||| ||| |||| || || |
Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        399 LRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTK 458
              |::|||||| | ||:||:|||:|:|||||| ||:::||| |||| |:|||||:|:|:
Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        459 IDFDGIFLGLTSLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLH 518
              : |:||| ||:|| |||||||::| | ::|    |||||||:|||||:|   |::|
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Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        519 RLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIETS-KGILQHFPKSLAFFNLTNNS 577
              ||:|||||||    ||:  |  | ||  || | | | || |  ||||| |||| ||| |
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        578 VACICEHQKFLQWVKEQKQFLVNVEQMTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVV 637
              || |||| ||||:|:|:| || ||:| |||| :      ||    | || | |||| |||:
Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVL 599

Qy        638 SVIVVSTVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEG 697
              ||:||| || |:| |||||:|:||| || |||:||||||||||||:|||||||||||||||
Db        600 SVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEG 659

Qy        698 VPRFHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQF 757
              || | |||||||||||||||||| |||||||||||||:|||||||||||||||||||||
Db        660 VPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQF 719

Qy        758 LSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNPLGRHIFWRRLKNALLDGK 817
              ||||:|||||||:||||:|||||||||||||||||||: |||||||||: ||||||
Db        720 LSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGK 779

Qy        818 ASNPEQT 824
              : ||| |
Db        780 SWNPEGT 786


RESULT 5
US-10-732-796A-8
; Sequence 8, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
;  APPLICANT: Gupta, Shalley K.
;  APPLICANT:  Ghosh, Tarun K.
;  APPLICANT:  Fink, Jason R.
;  TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
;  FILE REFERENCE: 58182US004
;  CURRENT APPLICATION NUMBER: US/10/732,796A
;  CURRENT FILING DATE:  2003-12-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
;   LENGTH: 799
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-732-796A-8

  Query Match             62.8%;  Score 2730.5;  DB 16;  Length 799;
  Best Local Similarity   67.9%;  Pred. No. 4.2e-216;
  Matches  534;  Conservative   98;  Mismatches  152;  Indels    3;  Gaps    3;

Qy         40 MDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWHG 99
              |:    |:||::| ||||:|||||||: | |||| :| ||| |||||||:|||| |:
Db          1 MELNFYKIPDNLPFSTKNLDLSFNPLRHLGSYSFFSFPELQVLDLSRCEIQTIEDGAYQS 60

Qy        100 LHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAHN 159
              | ||| |||||||||| : |:||||:||: |||||| |||||:|||| | |||:||||||
Db         61 LSHLSTLILTGNPIQSLALGAFSGLSSLQKLVAVETNLASLENFPIGHLKTLKELNVAHN 120

Qy        160 FIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQD 219
              | | ||| |||||||| |:||| | ||:|   ||: | : | :|||||:||||::|||
Db        121 LIQSFKLPEYFSNLTNLEHLDLSSNKIQSIYCTDLRVLHQMPLLNLSLDLSLNPMNFIQP 180

Qy        220 QAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGL 279
              ||: |:|||:|||| ||:| |:||||:| |||| ||||:||||::| ||| |: | :|||
Db        181 GAFKEIRLHKLTLRNNFDSLNVMKTCIQGLAGLEVHRLVLGEFRNEGNLEKFDKSALEGL 240

Qy        280 CDVTIDEFRLTYTNDFSDDIVK-FHCLANVSAMSLAGVSIKYLEDVPKHFKWQSLSIIRC 338
              |::||:|||| | : : |||:  |:|| |||: ||  |:|: ::|   :| || | :: |
Db        241 CNLTIEEFRLAYLDYYLDDIIDLFNCLTNVSSFSLVSVTIERVKDFSYNFGWQHLELVNC 300

Qy        339 QLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNS 398
              :  ||||| |  || || | |||  :| :| |||| :|||||| ||| |||| || || |
Db        301 KFGQFPTLKLKSLKRLTFTSNKGGNAFSEVDLPSLEFLDLSRNGLSFKGCCSQSDFGTTS 360

Qy        399 LRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTK 458
              |::|||||| | ||:||:|||:|:|||||| ||:::||| |||| |:|||||:|:|:
Db        361 LKYLDLSFNGVITMSSNFLGLEQLEHLDFQHSNLKQMSEFSVFLSLRNLIYLDISHTHTR 420

Qy        459 IDFDGIFLGLTSLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLSKCQLEQISWGVFDTLH 518
              : |:||| ||:||  |||||||::| | ::|    ||||||||:|||||:|   |::|
Db        421 VAFNGIFNGLSSLEVLKMAGNSFQENFLPDIFTELRNLTFLDLSQCQLEQLSPTAFNSLS 480

Qy        519 RLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIETS-KGILQHFPKSLAFFNLTNNS 577
              ||:|||||||    ||:  |  | ||  || | | | || |  ||||| |||| ||| |
Db        481 SLQVLNMSHNNFFSLDTFPYKCLNSLQVLDYSLNHIMTSKKQELQHFPSSLAFLNLTQND 540

Qy        578 VACICEHQKFLQWVKEQKQFLVNVEQMTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVV 637
              || |||| ||||:|:|:| || ||:| |||| :      ||    | || | |||| |||:
Db        541 FACTCEHQSFLQWIKDQRQLLVEVERMECATPSDKQGMPVLSL-NITCQMNKTIIGVSVL 599

Qy        638 SVIVVSTVAFLIYHFYFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWVRNELVKNLEEG 697
              ||:||| || |:| |||||:|:||| || |||:||||||||||||:|||||||||||||||
Db        600 SVLVVSVVAVLVYKFYFHLMLLAGCIKYGRGENIYDAFVIYSSQDEDWVRNELVKNLEEG 659

Qy        698 VPRFHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQF 757
              || | |||||||||||||||||| |||||||||||||:|||||||||||||||||||||
Db        660 VPPFQLCLHYRDFIPGVAIAANIIHEGFHKSRKVIVVVSQHFIQSRWCIFEYEIAQTWQF 719

Qy        758 LSSRSGIIFIVLEKVEKSLLRQQVELYRLLSRNTYLEWEDNPLGRHIFWRRLKNALLDGK 817
              ||||:|||||||:||||:|||||||||||||||||||: |||||||||: ||||||
Db        720 LSSRAGIIFIVLQKVEKTLLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRRLRKALLDGK 779

Qy        818 ASNPEQT 824
              : ||| |
Db        780 SWNPEGT 786


RESULT 6
US-10-114-893-10
; Sequence 10, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
;  APPLICANT: Jacobs, Kenneth
;  APPLICANT: McCoy, John M.
;  APPLICANT: LaVallie, Edward R.
;  APPLICANT: Collins-Racie, Lisa A.
;  APPLICANT: Evans, Cheryl
;  APPLICANT: Merberg, David
;  APPLICANT: Treacy, Maurice
;  APPLICANT: Bowman, Michael R.
;  APPLICANT: Spaulding, Vikki
;  APPLICANT: Carlin-Duckett, McKeough
;  APPLICANT: Kelleher, Kerry S.
;  APPLICANT: Genetics Institute, Inc.
;  TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
;  FILE REFERENCE: GI 6000-10A
;  CURRENT APPLICATION NUMBER: US/10/114,893
;  CURRENT FILING DATE: 2002-04-02
;  EARLIER APPLICATION NUMBER: 09/413,232
;  EARLIER FILING DATE: 1999-10-06
;  NUMBER OF SEQ ID NOS: 321
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 661
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-114-893-10

  Query Match             14.3%;  Score 619.5;  DB 13;  Length 661;
  Best Local Similarity   28.6%;  Pred. No. 5.2e-42;
  Matches  187;  Conservative   126;  Mismatches  296;  Indels   45;  Gaps   18;

Qy         28 CIEVVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRC 87
              |||   | || | :  ||::|| :|::|: :: ||| |  : : :||    | :|||:||
Db         28 CIEKEANKTYNCENLGLSEIPDTLPNTTEFLEFSFNFLPTIHNRTFSRLMNLTFLDLTRC 87
```

```
Qy          88 EIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQ 147
               :|  |  :  :   | || |:|||||:   :  | :|  ||::|  ::| :::||  |:
Db          88 QINWIHEDTFQSHHQLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEFIPVHN 147

Qy         148 LITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSL 207
               |  |: | :  | | | | |    || :|   | |  |:  |:: | :   :||||
Db         148 LENLESLYLGSNHISSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--AINLSL 204

Qy         208 DMSLNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERN 267
               : : | :  |:  ||        |  | | | |    |||         | || |:|  :
Db         205 NFNGNNVKGIELGAFDSTVFQSLNFGGTPNLSVIFNG-LQNST---TQSLWLGTFEDIDD 260

Qy         268 LEIFEPSIMEGLCDVTIDEFRLTYTNDFSD-DIVKFHCLANVSAMSLAGVSIKYLEDVPK 326
                :|   ::::|||:::::   |   : |||     | |   :  : |      :|: :|
Db         261 EDI-SSAMLKGLCEMSVESLNL-QEHRFSDISSTTFQCFTQLQELDLTAT---HLKGLPS 315

Qy         327 HFKWQSLSIIR----------CQLK--QFPTLDLPFLKSLTLTMNKGSISFKKVALPS 372
                 |   |::::             ||:    ||:|   :::     :: |    :|  | :
Db         316 GMK--GLNLLKKLVLSVNHFDQLCQISAANFPSLTHLYIRGNVKKLHLGVGCLEK--LGN 371

Qy         373 LSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAI-IMSANFMGLEELQHLDFQHST 431
               |  |||| | :  | |||      : |: |:|| |  : : |  |    :|: ||   :
Db         372 LQTLDLSHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKECPQLELLDLAFTR 431

Qy         432 LKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDNTL--SNV 489
               |      | | :|  |  |:::|         :  ||  |  | : || |:| |:  :|:
Db         432 LHINAPQSPFQNLHFLQVLNLTYCFLDTSNQHLLAGLPVLRHLNLKGNHFQDGTITKTNL 491

Qy         490 FANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLL--FLDS-SHYNQLYSLST 546
                    :|  | || | |   |    | :| ::  :::|||:|    :|| ||   :|
Db         492 LQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHNSLTCDSIDSLSHLKGIY---- 547

Qy         547 LDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQMTC 606
               |: : | |      |         :  ||::| : | | :  || | ||    |  |: ||
Db         548 LNLAANSINIISPRLLPILSQQSTINLSHNPLDCTCSNIHFLTWYKENLHKLEGSEETTC 607

Qy         607 ATPVEMN----TSLVLDFNNSTCYMYKTIISVSVVSVIVVSTVAFLIYHFYFHL 656
               | |  :      : : |    :   ::  |: : ::::::   | :|:   | |:
Db         608 ANPPSLRGVKLSDVKLSCGITAIGIFFLIVFLLLLAILLFFAVKYLLRWKYQHI 661
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RESULT 7
US-10-038-854-134
; Sequence 134, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-854-134

Query Match 14.3%; Score 619.5; DB 15; Length 661;
Best Local Similarity 28.6%; Pred. No. 5.2e-42;
Matches 187; Conservative 126; Mismatches 296; Indels 45; Gaps 18;

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Qy          28 CIEVVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRC 87
               |||   | || | :  ||::|| :|::|: :: ||| |  : : :||    | :|||:||
Db          28 CIEKEANKTYNCENLGLSEIPDTLPNTTEFLEFSFNFLPTIHNRTFSRLMNLTFLDLTRC 87

Qy          88 EIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQ 147
               :|  | :  :   | || |:|||||:   :  | :|  ||::|  ::| :::||  |:
Db          88 QINWIHEDTFQSHHQLSTLVLTGNPLIFMAETSLNGPKSLKHLFLIQTGISNLEFIPVHN 147

Qy         148 LITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSL 207
               |  |: | :  | | | | |    || :|   | |  |:  |:: | :   :||||
Db         148 LENLESLYLGSNHISSIKFPKDFP-ARNLKVLDFQNNAIHYISREDMRSLEQ--AINLSL 204

Qy         208 DMSLNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERN 267
               : : | :  |:  ||        |  | | | |    |||         | || |:|  :
Db         205 NFNGNNVKGIELGAFDSTVFQSLNFGGTPNLSVIFNG-LQNST---TQSLWLGTFEDIDD 260

Qy         268 LEIFEPSIMEGLCDVTIDEFRLTYTNDFSD-DIVKFHCLANVSAMSLAGVSIKYLEDVPK 326
                :|   ::::|||:::::   |   : |||     | |   :  : |      :|: :|
Db         261 EDI-SSAMLKGLCEMSVESLNL-QEHRFSDISSTTFQCFTQLQELDLTAT---HLKGLPS 315

Qy         327 HFKWQSLSIIR----------CQLK--QFPTLDLPFLKSLTLTMNKGSISFKKVALPS 372
                 |   |::::             ||:    ||:|   :::     :: |    :|  | :
Db         316 GMK--GLNLLKKLVLSVNHFDQLCQISAANFPSLTHLYIRGNVKKLHLGVGCLEK--LGN 371

Qy         373 LSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAI-IMSANFMGLEELQHLDFQHST 431
               |  |||| | :  | |||      : |: |:|| |  : : |  |    :|: ||   :
Db         372 LQTLDLSHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKECPQLELLDLAFTR 431

Qy         432 LKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDNTL--SNV 489
               |      | | :|  |  |:::|         :  ||  |  | : || |:| |:  :|:
Db         432 LHINAPQSPFQNLHFLQVLNLTYCFLDTSNQHLLAGLPVLRHLNLKGNHFQDGTITKTNL 491

Qy         490 FANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLL--FLDS-SHYNQLYSLST 546
                    :|  | || | |   |    | :| ::  :::|||:|    :|| ||   :|
Db         492 LQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVDLSHNSLTCDSIDSLSHLKGIY---- 547
```

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Qy        547 LDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQMTC 606
              |: : | |       |       :  ||::| : | | :  || | ||    |   |: ||
Db        548 LNLAANSINIISPRLLPILSQQSTINLSHNPLDCTCSNIHFLTWYKENLHKLEGSEETTC 607

Qy        607 ATPVEMN----TSLVLDFNNSTCYMYKTIISVSVVSVIVVSTVAFLIYHFYFHL 656
              | |  :     : : |    :   ::  |: : ::::::   | :|:   | |:
Db        608 ANPPSLRGVKLSDVKLSCGITAIGIFFLIVFLLLLAILLFFAVKYLLRWKYQHI 661


RESULT 8
US-10-038-854-135
; Sequence 135, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
;  APPLICANT: Spytek, Kimberly A
;  APPLICANT:  Li, Li
;  APPLICANT:  Wolenc, Adam R
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Eisen, Andrew J
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Tchernev, Velizar
;  APPLICANT:  Spaderna, Steven K
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Gusev, Vladimir Y
;  APPLICANT:  Gangolli, Esha A
;  APPLICANT:  Guo, Xiaojia S
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Edinger, Shlomit R
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  MacDougall, John R
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-230
;  CURRENT APPLICATION NUMBER: US/10/038,854
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: 60/258,928
;  PRIOR FILING DATE: 2000-12-29
;  PRIOR APPLICATION NUMBER: 60/259,415
;  PRIOR FILING DATE: 2001-01-02
;  PRIOR APPLICATION NUMBER: 60/259,785
;  PRIOR FILING DATE: 2001-01-04
;  PRIOR APPLICATION NUMBER: 60/269,814
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: 60/279,832
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/279,833
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/279,863
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/283,889
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,447
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: 60/286,683
;  PRIOR FILING DATE: 2001-04-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 411
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
;   LENGTH: 661
;   TYPE: PRT
;   ORGANISM: Mus musculus

US-10-038-854-135

  Query Match             14.1%;  Score 612.5;  DB 15;  Length 661;
  Best Local Similarity   27.0%;  Pred. No. 2e-41;
  Matches  182;  Conservative  129;  Mismatches  313;  Indels   49;  Gaps   16;

Qy         12 IMALFF-SC-LTPGSLNPCIEVVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILK 69
              ::|||  ||  |  |   |||  | || | :  |:::|  :|:||: :: ||| |  ::
Db         10 LVALFLASCRATTSSDQKCIEKEVNKTYNCENLGLNEIPGTLPNSTECLEFSFNVLPTIQ 69

Qy         70 SYSFSNFSELQWLDLSRCEIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLEN 129
              : :||    | :|||:||:|  | :  :   | |  |:|| ||:   :  : ||  :|::
Db         70 NTTFSRLINLTFLDLTRCQIYWIHEDTFQSQHRLDTLVLTANPLIFMAETALSGPKALKH 129

Qy        130 LVAVETKLASLESFPIGQLITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTI 189
              |  ::| ::|::  |:    ||: | :  | | | |||  |      |  :|   | |  :
Db        130 LFFIQTGISSIDFIPLHNQKTLESLYLGSNHISSIKLPKGFPT-EKLKVLDFQNNAIHYL 188

Qy        190 TVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNL 249
              :  |:  |::    ||||::: | |  |:  ||       |   ||  :  :    : |
Db        189 SKEDMSSLQQ--ATNLSLNLNGNDIAGIEPGAFDSAVFQSL----NFGGTQNLLVIFKGL 242

Qy        250 AGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVS 309
              :  | || |:|  : :|  |:: ||||:::::   |      |:     ||| : :
Db        243 KNSTIQSLWLGTFEDMDDEDI-SPAVFEGLCEMSVESINLQKHYFFNISSNTFHCFSGLQ 301

Qy        310 AMSLAGVSIKYLEDVPKHF-------------KWQSLSIIRCQL--KQFPTLDLPFLKS 353
              : |     :| ::|                 |:::|    ||:    ||:|    :|
Db        302 ELDLTAT---HLSELPSGLVGLSTLKKLVLSANKFENL----CQISASNFPSLTHLSIKG 354

Qy        354 LTLTMNKGSISFKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMS 413
              |  :  |:   :   | :|  |||| : :  | ||:      : |: |:||:|  : :
Db        355 NTKRLELGTGCLEN--LENLRELDLSHDDIETSDCCNLQLRNLSHLQSLNLSYNEPLSLK 412

Qy        414 AN-FMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLN 472
              |    :|: ||   : ||     | | :|  |  |::|::   |  : :| || :|
Db        413 TEAFKECPQLELLDLAFTRLKVKDAQSPFQNLHLLKVLNLSHSLLDISSEQLFDGLPALQ 472

Qy        473 TLKMAGNSFKDNTL--SNVFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNL 530
              | : || |   :  :|      |  | || | |  |    | :|  :  :::||| |
Db        473 HLNLQGNHFPKGNIQKTNSLQTLGRLEILVLSFCDLSSIDQHAFTSLKMMNHVDLSHNRL 532

Qy        531 LFLD---SSHYNQLYSLSTLDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKF 587
                    ||   :|    |: : | |       |          ||  | : | | :  |
Db        533 TSSSIEALSHLKGIY----LNLASNHISIILPSLLPILSQQRTINLRQNPLDCTCSNIYF 588

Qy        588 LQWVKEQKQFLVNVEQMTCATPVEMN----TSLVLDFNNSTCYMYKTIISVSVVSVIVVS 643
              |:| ||  | | : |   | |  :     : : |  : :   ::  |: : | :::::
Db        589 LEWYKENMQKLEDTEDTLCENPPLLRGVRLSDVTLSCSMAAVGIFFLIVFLLVFAILLIF 648

Qy        644 TVAFLIYHFYFHL 656
              | : :   | |:
Db        649 AVKYFLRWKYQHI 661


RESULT 9
US-10-037-417-107
; Sequence 107, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
;  APPLICANT: Kekuda, Ramesh
;  APPLICANT:  Alsobrook II, John P
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Li, Li
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Edinger, Shlomit R
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;  APPLICANT:  Sciore, Paul
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Rothenberg, Mark
;  APPLICANT:  Stone, David J
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Anderson, David W
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Eisen, Andrew J
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-235
;  CURRENT APPLICATION NUMBER: US/10/037,417
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: 60/260,018
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: 60/260,360
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/272,411
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/272,817
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: 60/291,186
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: 60/303,231
;  PRIOR FILING DATE: 2001-07-05
;  PRIOR APPLICATION NUMBER: 60/305,060
;  PRIOR FILING DATE: 2001-07-12
;  PRIOR APPLICATION NUMBER: 60/318,405
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/318,700
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
;   LENGTH: 661
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-037-417-107

  Query Match             14.1%;  Score 612.5;  DB 15;  Length 661;
  Best Local Similarity   27.0%;  Pred. No. 2e-41;
  Matches  182;  Conservative  129;  Mismatches  313;  Indels   49;  Gaps   16;

Qy          12 IMALFF-SC-LTPGSLNPCIEVVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILK 69
               ::|||  ||  |  |   |||   | || | :  |:::|  :|:||: :: ||| |  ::
Db          10 LVALFLASCRATTSSDQKCIEKEVNKTYNCENLGLNEIPGTLPNSTECLEFSFNVLPTIQ 69

Qy          70 SYSFSNFSELQWLDLSRCEIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLEN 129
               : :||    | :|||:||:|  | :  :   | |  |:|| ||:  :  : ||  :|::
Db          70 NTTFSRLINLTFLDLTRCQIYWIHEDTFQSQHRLDTLVLTANPLIFMAETALSGPKALKH 129

Qy         130 LVAVETKLASLESFPIGQLITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTI 189
               |  ::| ::|::  |:    ||: | :  | | | ||| |     | :|  | | :
Db         130 LFFIQTGISSIDFIPLHNQKTLESLYLGSNHISSIKLPKGFPT-EKLKVLDFQNNAIHYL 188

Qy         190 TVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNL 249
               :  |:  |::    ||||::: | |  |:  ||        |    ||  :  :    : |
Db         189 SKEDMSSLQQ--ATNLSLNLNGNDIAGIEPGAFDSAVFQSL----NFGGTQNLLVIFKGL 242

Qy         250 AGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVS 309
                 :  | || |:|  : :|  |:: |||||:::::  |     |:     ||| : :
Db         243 KNSTIQSLWLGTFEDMDDEDI-SPAVFEGLCEMSVESINLQKHYFFNISSNTFHCFSGLQ 301

Qy         310 AMSLAGVSIKYLEDVPKHF-------------KWQSLSIIRCQL--KQFPTLDLPFLKS 353
                : |      :| ::|              |:::|    ||:    ||:|    :|
Db         302 ELDLTAT---HLSELPSGLVGLSTLKKLVLSANKFENL----CQISASNFPSLTHLSIKG 354

Qy         354 LTLTMNKGSISFKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMS 413
                 |  :  |:   :   | :|  |||| : :  | ||:      : |: |:||:|  : :

Db         355 NTKRLELGTGCLEN--LENLRELDLSHDDIETSDCCNLQLRNLSHLQSLNLSYNEPLSLK 412

Qy         414 AN-FMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLN 472
                 |    :|: ||   : ||      | | :|  |  |::|::   |  : :| || :|
Db         413 TEAFKECPQLELLDLAFTRLKVKDAQSPFQNLHLLKVLNLSHSLLDISSEQLFDGLPALQ 472

Qy         473 TLKMAGNSFKDNTL--SNVFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNL 530
                | : || |    :  :|      |  | || | |   |    | :|  :  :::||| |
Db         473 HLNLQGNHFPKGNIQKTNSLQTLGRLEILVLSFCDLSSIDQHAFTSLKMMNHVDLSHNRL 532

Qy         531 LFLD---SSHYNQLYSLSTLDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKF 587
                    ||   :|    |: : | |       |           ||  | : | | :  |
Db         533 TSSSIEALSHLKGIY----LNLASNHISIILPSLLPILSQQRTINLRQNPLDCTCSNIYF 588

Qy         588 LQWVKEQKQFLVNVEQMTCATPVEMN----TSLVLDFNNSTCYMYKTIISVSVVSVIVVS 643
               |:| ||  | | : |   |  |  :     : : |  : :   ::  |: : | :::::
Db         589 LEWYKENMQKLEDTEDTLCENPPLLRGVRLSDVTLSCSMAAVGIFFLIVFLLVFAILLIF 648

Qy         644 TVAFLIYHFYFHL 656
                | : :   | |:
Db         649 AVKYFLRWKYQHI 661


RESULT 10
US-09-954-987B-192
; Sequence 192, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
;  APPLICANT: Stefan Bauer
;  APPLICANT:  Grayson B. Lipford
;  APPLICANT:  Hermann Wagner
;  TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
;  TITLE OF INVENTION:  CpG-BASED IMMUNO-AGONIST/ANTAGONIST
;  FILE REFERENCE: C1041/7016 (AWS)
;  CURRENT APPLICATION NUMBER: US/09/954,987B
;  CURRENT FILING DATE:  2001-09-17
;  PRIOR APPLICATION NUMBER: US 60/233,035
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/263,657
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: US 60/291,726
;  PRIOR FILING DATE: 2001-05-17
;  PRIOR APPLICATION NUMBER: US 60/300,210
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 230
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 192
;   LENGTH: 1032
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-954-987B-192

  Query Match             13.3%;  Score 580;  DB 10;  Length 1032;
  Best Local Similarity   23.8%;  Pred. No. 1.8e-38;
  Matches  253;  Conservative  160;  Mismatches  350;  Indels  298;  Gaps   43;

Qy           2 MPP--WLLARTLIM-----ALFFSCLTPGSLNPCIEVVPN--ITYQCMDQKLSKVPDDIP 52
                |||  |:|    ::     |:|       |  || |:  |  :  :|  ::| :|| |
Db           4 MPPQSWILTCFCLLSSGTSAIFHKANYSRSY-PCDEIRHNSLVIAECNHRQLHEVPQTIG 62

Qy          53 SSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIE----------TIEDKAWHGLHH 102
                |||||  :  :   ||      |  :||:    :           | : |    | :
Db          63 KYVTNIDLSDNAITHITKESFQKLQNLTKIDLNHNAKQQHPNENKNGMNITEGALLSLRN 122

Qy         103 LSNLILTGNPIQSFS---PGSFSGLTSLENLVAVETK-----LASLESFPIG-------- 146
               |: |:|  | : :     | |   |: ::| :   ||     | :||   :|
Db         123 LTVLLLEDNQLYTIPAGLPESLKELSLIQNNIFQVTKNNTFGLRNLERLYLGWNCYFKCN 182

Qy         147 -----------QLITLKKLNVAHN--FIHSCKLPA------------------------ 168
                          || || |::: |  |    |||:
Db         183 QTFKVEDGAFKNLIHLKVLSLSFNNLFYVPPKLPSSLRKLFLSNAKIMNITQEDFKGLEN 242

Qy         169 ----------------------------------------------------------YF 170
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Db        243 LTLLDLSGNCPRCYNAPFPCTPCKENSSIHIHPLAFQSLTQLLYLNLSSTSLRTIPSTWF 302

Qy        171 SNLTNLVHVDLSYNY-IQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHE 229

Db        303 ENLSNLKELHLEFNYLVQEIASG--AFLTKLPSLQI-LDLSFN---FQYKEYLQFINI-- 354

Qy        230 LTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRL 289

Db        355 --------SSNFSK--LRSLKKLHLRGYVFRELKKKH----FEH--LQSLPNLATINLGI 398

Qy        290 TYTNDFSDDIVKFHCLANVSAMSLAGVSIKYLEDVPKHFKWQS-----LS---------- 334

Db        399 NFIEKI--DFKAFQNFSKLDVIYLSGNRIASVLDGTDYSSWRNRLRKPLSTDDDEFDPHV 456

Qy        335 --------IIRCQLKQF-PTLDLPF---------------LKSLTLTMNKGSISFKKV- 368

Db        457 NFYHSTKPLIKPQCTAYGKALDLSLNNIFIIGKSQFEGFQDIACLNLSFNANTQVFNGTE 516

Qy        369 --ALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSAN-------FMGL 419

Db        517 FSSMPHIKYLDLTNNRLDFDDNNAFSDL--HDLEVLDLSHNAHYFSIAGVTHRLGFIQNL 574

Qy        420 EELQHLDFQHSTLKRVTE----------------------------FSAFLSLEKLLY 449

Db        575 INLRVLNLSHNGIYTLTEESELKSISLKELVFSGNRLDHLWNANDGKYWSIFKSLQNLIR 634

Qy        450 LDISYTNTKIDFDGIFLGL-TSLNTLKMAGNS--FKDNTLSNVFANTTNLTFLDLSKCQL 506

Db        635 LDLSYNNLQQIPNGAFLNLPQSLQELLISGNKLRFFNWTLLQYF---PHLHLLDLSRNEL 691

Qy        507 EQISWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIE-TSKGILQHFP 565

Db        692 YFLPNCLSKFAHSLETLLLSHNHFSHLPSGFLSEARNLVHLDLSFNTIKMINKSSLQTKM 751

Qy        566 K-SLAFFNLTNNSVACICEHQKFLQWVKEQKQF----LVNVEQMTCATPVEMNTSLVLDF 620

Db        752 KTNLSILELHGNYFDCTCDISDFRSWLDENLNITIPKLVNV---ICSNPGDQKSKSIMSL 808

Qy        621 NNSTCYMYKTIISVSVVSVIVVSTV--AFLIYH-------FYFHL--ILIAGCKKYSRGE 669

Db        809 DLTTCVSDTTAAVLFFLTFLTTSMVMLAALVHHLFYWDVWFIYHMCSAKLKGYRTSSTSQ 868

Qy        670 SIYDAFVIYSSQN---EDWVRNELVKNLEEGVPR-FHLCLHYRDFIPGVAIAANIIQEGF 725

Db        869 TFYDAYISYDTKDASVTDWVINELRYHLEESEDKSVLLCLEERDWDPGLPIIDNLMQ-SI 927

Qy        726 HKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLS------------SRSGIIFIVLEKVE 773

Db        928 NQSKKTIFVLTKKY------------AKSWNFKTAFYLALQRLMDENMDVIIFILLEPVL 975

Qy        774 KSLLRQQVELYRLLSRNTYLEWEDNPLGRHIFWRRLKNALL 814

Db        976 Q--YSQYLRLRQRICKSSILQWPNNPKAENLFWQSLKNVVL 1014
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RESULT 11
US-10-272-502A-31
; Sequence 31, Application US/10272502A
; Publication No. US20030139364A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Vollmer, Jorg
; APPLICANT: Bauer, Stefan
; APPLICANT: Jurk, Marion
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ENHANCING IMMUNE RESPONSES USING
; TITLE OF INVENTION: IMIDAZOQUINOLINE COMPOUNDS
; FILE REFERENCE: C01039.70065.US
; CURRENT APPLICATION NUMBER: US/10/272,502A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,208
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-272-502A-31

Query Match 13.3%; Score 580; DB 14; Length 1032;
Best Local Similarity 23.8%; Pred. No. 1.8e-38;
Matches 253; Conservative 160; Mismatches 350; Indels 298; Gaps 43;

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Qy          2 MPP--WLLARTLIM-----ALFFSCLTPGSLNPCIEVVPN--ITYQCMDQKLSKVPDDIP 52

Db          4 MPPQSWILTCFCLLSSGTSAIFHKANYSRSY-PCDEIRHNSLVIAECNHRQLHEVPQTIG 62

Qy         53 SSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIE----------TIEDKAWHGLHH 102

Db         63 KYVTNIDLSDNAITHITKESFQKLQNLTKIDLNHNAKQQHPNENKNGMNITEGALLSLRN 122

Qy        103 LSNLILTGNPIQSFS---PGSFSGLTSLENLVAVETK-----LASLESFPIG-------- 146

Db        123 LTVLLLEDNQLYTIPAGLPESLKELSLIQNNIFQVTKNNTFGLRNLERLYLGWNCYFKCN 182

Qy        147 ----------QLITLKKLNVAHN--FIHSCKLPA------------------------ 168

Db        183 QTFKVEDGAFKNLIHLKVLSLSFNNLFYVPPKLPSSLRKLFLSNAKIMNITQEDFKGLEN 242

Qy        169 ----------------------------------------------------------YF 170

Db        243 LTLLDLSGNCPRCYNAPFPCTPCKENSSIHIHPLAFQSLTQLLYLNLSSTSLRTIPSTWF 302

Qy        171 SNLTNLVHVDLSYNY-IQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHE 229

Db        303 ENLSNLKELHLEFNYLVQEIASG--AFLTKLPSLQI-LDLSFN---FQYKEYLQFINI-- 354

Qy        230 LTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRL 289

Db        355 --------SSNFSK--LRSLKKLHLRGYVFRELKKKH----FEH--LQSLPNLATINLGI 398

Qy        290 TYTNDFSDDIVKFHCLANVSAMSLAGVSIKYLEDVPKHFKWQS-----LS---------- 334

Db        399 NFIEKI--DFKAFQNFSKLDVIYLSGNRIASVLDGTDYSSWRNRLRKPLSTDDDEFDPHV 456

Qy        335 --------IIRCQLKQF-PTLDLPF---------------LKSLTLTMNKGSISFKKV- 368

Db        457 NFYHSTKPLIKPQCTAYGKALDLSLNNIFIIGKSQFEGFQDIACLNLSFNANTQVFNGTE 516

Qy        369 --ALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSAN-------FMGL 419

Db        517 FSSMPHIKYLDLTNNRLDFDDNNAFSDL--HDLEVLDLSHNAHYFSIAGVTHRLGFIQNL 574

Qy        420 EELQHLDFQHSTLKRVTE----------------------------FSAFLSLEKLLY 449

Db        575 INLRVLNLSHNGIYTLTEESELKSISLKELVFSGNRLDHLWNANDGKYWSIFKSLQNLIR 634

Qy        450 LDISYTNTKIDFDGIFLGL-TSLNTLKMAGNS--FKDNTLSNVFANTTNLTFLDLSKCQL 506

Db        635 LDLSYNNLQQIPNGAFLNLPQSLQELLISGNKLRFFNWTLLQYF---PHLHLLDLSRNEL 691

Qy        507 EQISWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIE-TSKGILQHFP 565

Db        692 YFLPNCLSKFAHSLETLLLSHNHFSHLPSGFLSEARNLVHLDLSFNTIKMINKSSLQTKM 751

Qy        566 K-SLAFFNLTNNSVACICEHQKFLQWVKEQKQF----LVNVEQMTCATPVEMNTSLVLDF 620

Db        752 KTNLSILELHGNYFDCTCDISDFRSWLDENLNITIPKLVNV---ICSNPGDQKSKSIMSL 808

Qy        621 NNSTCYMYKTIISVSVVSVIVVSTV--AFLIYH-------FYFHL--ILIAGCKKYSRGE 669

Db        809 DLTTCVSDTTAAVLFFLTFLTTSMVMLAALVHHLFYWDVWFIYHMCSAKLKGYRTSSTSQ 868
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Qy        670 SIYDAFVIYSSQN---EDWVRNELVKNLEEGVPR-FHLCLHYRDFIPGVAIAANIIQEGF 725
              : |||:: | :::    ||| |||  :|||   :   |||  ||: ||: |  |::|
Db        869 TFYDAYISYDTKDASVTDWVINELRYHLEESEDKSVLLCLEERDWDPGLPIIDNLMQ-SI 927

Qy        726 HKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLS-----------SRSGIIFIVLEKVE 773
              ::|:| | |::: :             |::| | :           :  ||||:|| |
Db        928 NQSKKTIFVLTKKY-----------AKSWNFKTAFYLALQRLMDENMDVIIFILLEPVL 975

Qy        774 KSLLRQQVELYRLLSRNTYLEWEDNPLGRHIFWRRLKNALL 814
              :    | : | : : ::: |:| :||   ::||: ||| :|
Db        976 Q--YSQYLRLRQRICKSSILQWPNNPKAENLFWQSLKNVVL 1014
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RESULT 12
US-10-407-952-32
; Sequence 32, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Bauer, Stefan
; TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligoribonucleotides
; FILE REFERENCE: C01041.70037.US
; CURRENT APPLICATION NUMBER: US/10/407,952
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-407-952-32

Query Match 13.3%; Score 580; DB 15; Length 1032;
Best Local Similarity 23.8%; Pred. No. 1.8e-38;
Matches 253; Conservative 160; Mismatches 350; Indels 298; Gaps 43;

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Qy          2 MPP--WLLARTLIM-----ALFFSCLTPGSLNPCIEVVPN--ITYQCMDQKLSKVPDDIP 52
              |||  |:|    ::    |:|      |  || |:  |  :  :|  ::| :||  |
Db          4 MPPQSWILTCFCLLSSGTSAIFHKANYSRSY-PCDEIRHNSLVIAECNHRQLHEVPQTIG 62

Qy         53 SSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIE----------TIEDKAWHGLHH 102
              |||||| :  :   ||     | :|||:   :           | : |   | :
Db         63 KYVTNIDLSDNAITHITKESFQKLQNLTKIDLNHNAKQQHPNENKNGMNITEGALLSLRN 122

Qy        103 LSNLILTGNPIQSFS---PGSFSGLTSLENLVAVETK-----LASLESFPIG-------- 146
              |: |:|  | : :     | |   |: ::| :   ||     | :||   :|
Db        123 LTVLLLEDNQLYTIPAGLPESLKELSLIQNNIFQVTKNNTFGLRNLERLYLGWNCYFKCN 182

Qy        147 -----------QLITLKKLNVAHN--FIHSCKLPA------------------------ 168
                        || || |::: |  |    |||:
Db        183 QTFKVEDGAFKNLIHLKVLSLSFNNLFYVPPKLPSSLRKLFLSNAKIMNITQEDFKGLEN 242

Qy        169 ------------------------------------------------------YF 170
                                                                     :|
Db        243 LTLLDLSGNCPRCYNAPFPCTPCKENSSIHIHPLAFQSLTQLLYLNLSSTSLRTIPSTWF 302

Qy        171 SNLTNLVHVDLSYNY-IQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHE 229
              ||:||  : | :|| :| |      || : | : : ||:| |   |  :  | | :
Db        303 ENLSNLKELHLEFNYLVQEIASG--AFLTKLPSLQI-LDLSFN---FQYKEYLQFINI-- 354

Qy        230 LTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRL 289
                  |||  |  |:|  ||:   :  | | :     ||   :: | ::     :
Db        355 --------SSNFSK--LRSLKKLHLRGYVFRELKKKH----FEH--LQSLPNLATINLGI 398

Qy        290 TYTNDFSDDIVKFHCLANVSAMSLAGVSIKYLEDVPKHFKWQS-----LS---------- 334
              :      |   |   : :  : |:|  |  : |   :  |::     ||
Db        399 NFIEKI--DFKAFQNFSKLDVIYLSGNRIASVLDGTDYSSWRNRLRKPLSTDDDEFDPHV 456

Qy        335 --------IIRCQLKQF-PTLDLPF---------------LKSLTLTMNKGSISFKKV- 368
```

```
Db        457 NFYHSTKPLIKPQCTAYGKALDLSLNNIFIIGKSQFEGFQDIACLNLSFNANTQVFNGTE 516

Qy        369 --ALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSAN-------FMGL 419
                ::| : ||||: | | |    ::|||  : |  |||| |       |          |
Db        517 FSSMPHIKYLDLTNNRLDFDDNNAFSDL--HDLEVLDLSHNAHYFSIAGVTHRLGFIQNL 574

Qy        420 EELQHLDFQHSTLKRVTE-----------------------------FSAFLSLEKLLY 449
              |: |:  |: :  :||                             :| | ||: |:
Db        575 INLRVLNLSHNGIYTLTEESELKSISLKELVFSGNRLDHLWNANDGKYWSIFKSLQNLIR 634

Qy        450 LDISYTNTKIDFDGIFLGL-TSLNTLKMAGNS--FKDNTLSNVFANTTNLTFLDLSKCQL 506
              ||:|| | :   :| || |  ||  | ::||   | : ||   |    :|  ||||: :|
Db        635 LDLSYNNLQQIPNGAFLNLPQSLQELLISGNKLRFFNWTLLQYF---PHLHLLDLSRNEL 691

Qy        507 EQISWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIE-TSKGILQHFP 565
                :   :    | |: | :|||:   | |   ::  :|  || ||| |:  :|  ||
Db        692 YFLPNCLSKFAHSLETLLLSHNHFSHLPSGFLSEARNLVHLDLSFNTIKMINKSSLQTKM 751

Qy        566 K-SLAFFNLTNNSVACICEHQKFLQWVKEQKQF----LVNVEQMTCATPVEMNTSLVLDF 620
              | :|:   |  |   | |:   |  |: |         ||||    |: | :  :  ::
Db        752 KTNLSILELHGNYFDCTCDISDFRSWLDENLNITIPKLVNV---ICSNPGDQKSKSIMSL 808

Qy        621 NNSTCYMYKTIISVSVVSVIVVSTV--AFLIYH-------FYFHL--ILIAGCKKYSRGE 669
              : :||    |   :  :: :  | |  | |::|       | :|:    :| | :  |  :
Db        809 DLTTCVSDTTAAVLFFLTFLTTSMVMLAALVHHLFYWDVWFIYHMCSAKLKGYRTSSTSQ 868

Qy        670 SIYDAFVIYSSQN---EDWVRNELVKNLEEGVPR-FHLCLHYRDFIPGVAIAANIIQEGF 725
              : |||:: | :::    ||| |||  :|||   :   |||  ||: ||: |  |::|
Db        869 TFYDAYISYDTKDASVTDWVINELRYHLEESEDKSVLLCLEERDWDPGLPIIDNLMQ-SI 927

Qy        726 HKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLS-----------SRSGIIFIVLEKVE 773
              ::|:| | |::: :             |::| | :           :  ||||:|| |
Db        928 NQSKKTIFVLTKKY-----------AKSWNFKTAFYLALQRLMDENMDVIIFILLEPVL 975

Qy        774 KSLLRQQVELYRLLSRNTYLEWEDNPLGRHIFWRRLKNALL 814
              :    | : | : : ::: |:| :||   ::||: ||| :|
Db        976 Q--YSQYLRLRQRICKSSILQWPNNPKAENLFWQSLKNVVL 1014
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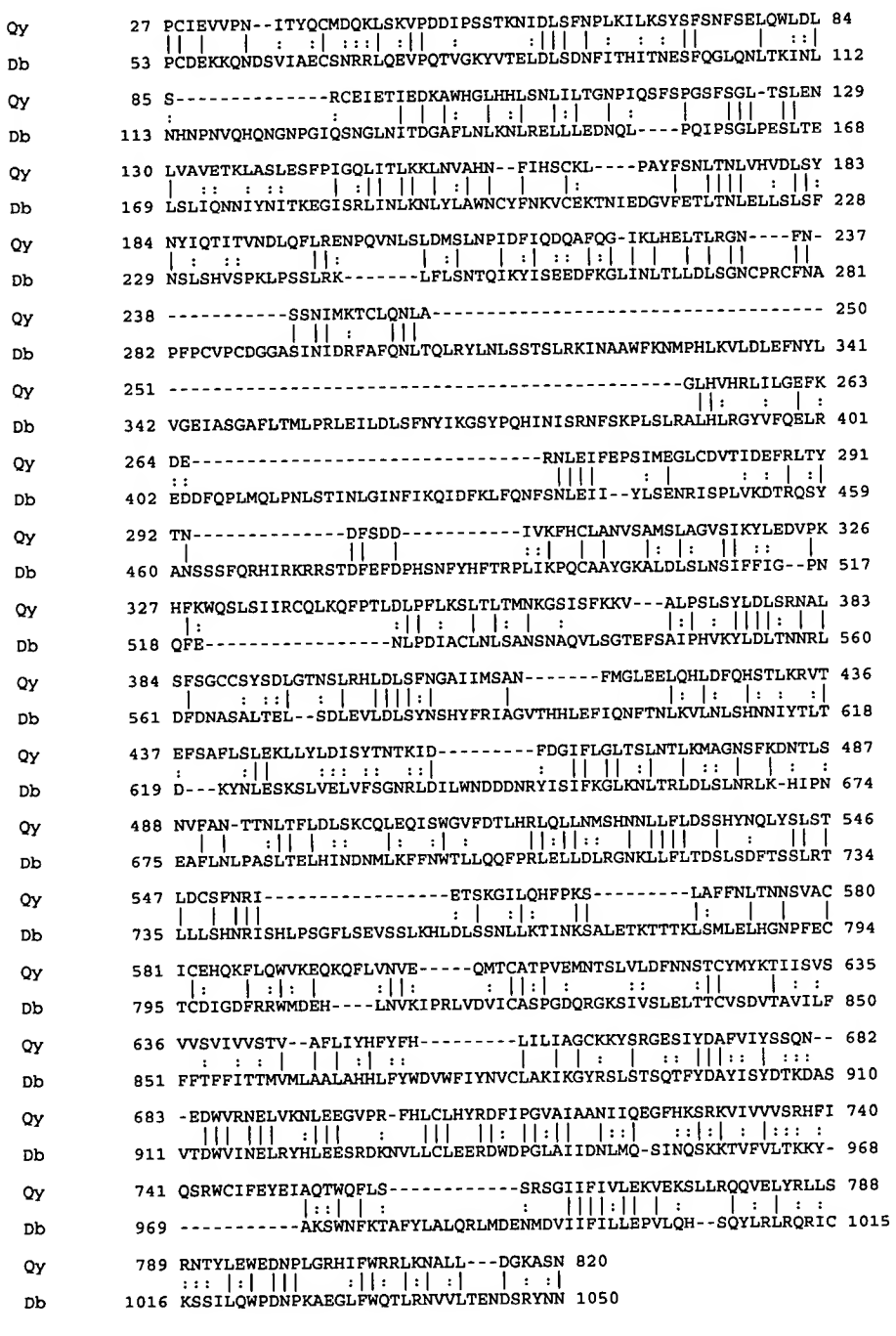
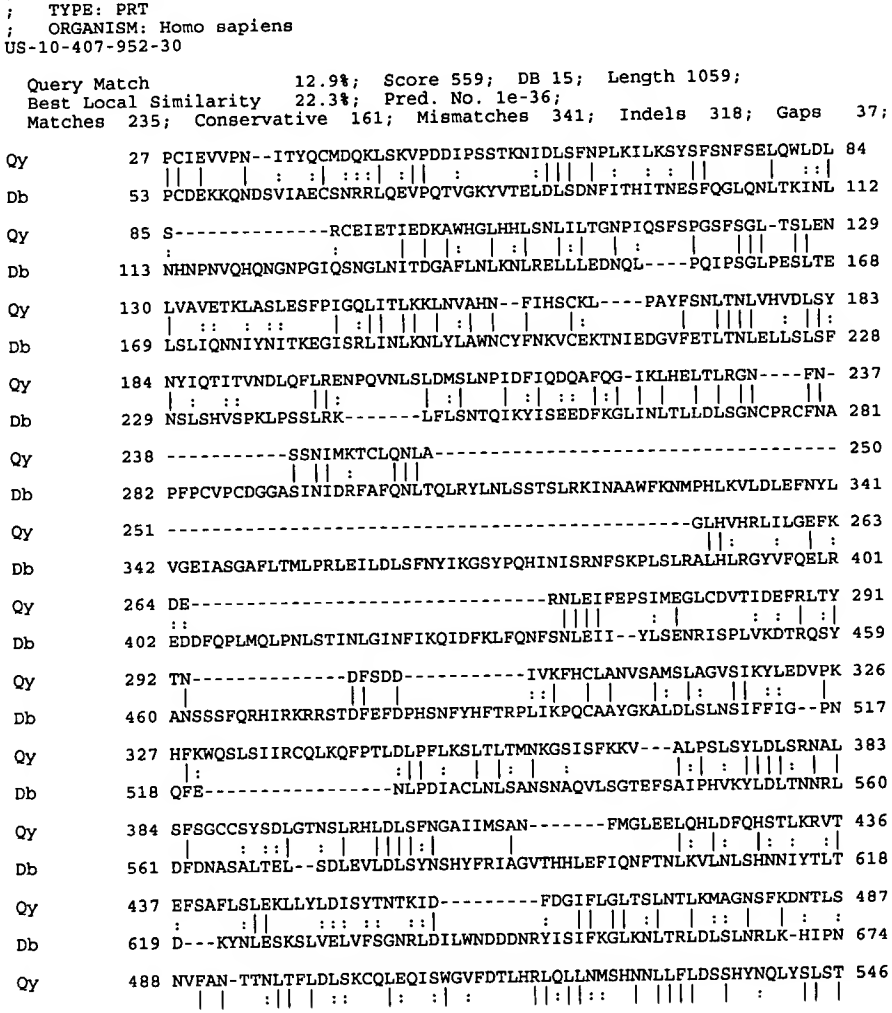
RESULT 13
US-09-954-987B-187
; Sequence 187, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
; APPLICANT: Stefan Bauer
; APPLICANT: Grayson B. Lipford
; APPLICANT: Hermann Wagner
; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
; TITLE OF INVENTION: CpG-BASED IMMUNO-AGONIST/ANTAGONIST
; FILE REFERENCE: C1041/7016 (AWS)
; CURRENT APPLICATION NUMBER: US/09/954,987B
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/233,035
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/263,657
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/291,726
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/300,210
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 1059
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-987B-187

Query Match 12.9%; Score 559; DB 10; Length 1059;
Best Local Similarity 22.3%; Pred. No. 1e-36;
Matches 235; Conservative 161; Mismatches 341; Indels 318; Gaps 37;



RESULT 14
US-10-407-952-30
; Sequence 30, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Bauer, Stefan
; TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligoribonucleotides
; FILE REFERENCE: C01041.70037.US
; CURRENT APPLICATION NUMBER: US/10/407,952
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 1059
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-407-952-30

Query Match 12.9%; Score 559; DB 15; Length 1059;
Best Local Similarity 22.3%; Pred. No. 1e-36;
Matches 235; Conservative 161; Mismatches 341; Indels 318; Gaps 37;



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Db        675 EAFLNLPASLTELHINDNMLKFFNWTLLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRT 734

Qy        547 LDCSFNRI----------------ETSKGILQHFPKS---------LAFFNLTNNSVAC 580
              |  | |||                : |  :|:   ||         |:   |  | :|
Db        735 LLLSHNRISHLPSGFLSEVSSLKHLDLSSNLLKTINKSALETKTTTKLSMLELHGNPFEC 794

Qy        581 ICEHQKFLQWVKEQKQFLVNVE-----QMTCATPVEMNTSLVLDFNNSTCYMYKTIISVS 635
              |:   | :|: |     :||:      : ||:| :      ::    :||    | : :
Db        795 TCDIGDFRRWMDEH----LNVKIPRLVDVICASPGDQRGKSIVSLELTTCVSDVTAVILF 850

Qy        636 VVSVIVVSTV--AFLIYHFYFH---------LILIAGCKKYSRGESIYDAFVIYSSQN-- 682
              :  : : |  | | :| ::          |  | | :  |  :: |||:: | :::
Db        851 FFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKIKGYRSLSTSQTFYDAYISYDTKDAS 910

Qy        683 -EDWVRNELVKNLEEGVPR-FHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFI 740
               ||| |||  :|||   :   |||  ||: ||:||  |::|   ::|:| : |::: :
Db        911 VTDWVINELRYHLEESRDKNVLLCLEERDWDPGLAIIDNLMQ-SINQSKKTVFVLTKKY- 968

Qy        741 QSRWCIFEYEIAQTWQFLS------------SRSGIIFIVLEKVEKSLLRQQVELYRLLS 788
                    |::| | :             :  ||||:|| | :    | : | : :
Db        969 -----------AKSWNFKTAFYLALQRLMDENMDVIIFILLEPVLQH--SQYLRLRQRIC 1015

Qy        789 RNTYLEWEDNPLGRHIFWRRLKNALL---DGKASN 820
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Db       1016 KSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNN 1050


RESULT 15
US-10-753-267-30
; Sequence 30, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc.
;  APPLICANT:  Stagliano, Nancy E.
;  APPLICANT:  Healy, Aileen
;  APPLICANT:  Acton, Susan L.
;  APPLICANT:  Galvin, Katherine M.
;  APPLICANT:  Donoghue, Mary A.
;  APPLICANT:  Rodrigue-Way, Amelie
;  APPLICANT:  Tomlinson, James E.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
;  TITLE OF INVENTION:  10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
;  TITLE OF INVENTION:  1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
;  TITLE OF INVENTION:  3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
;  TITLE OF INVENTION:  9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,
;  TITLE OF INVENTION:  44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
;  TITLE OF INVENTION:  32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
;  TITLE OF INVENTION:  42028, 112091, 13886, 13942, 1673, 54946 OR 2419
;  FILE REFERENCE: MPI03-003P1RNOMNIM
;  CURRENT APPLICATION NUMBER: US/10/753,267
;  CURRENT FILING DATE:  2004-01-08
;  PRIOR APPLICATION NUMBER: US 60/439,683
;  PRIOR FILING DATE: 2003-01-13
;  PRIOR APPLICATION NUMBER: US 60/445,216
;  PRIOR FILING DATE: 2003-02-05
;  PRIOR APPLICATION NUMBER: US 60/448,036
;  PRIOR FILING DATE: 2003-02-18
;  PRIOR APPLICATION NUMBER: US 60/454,189
;  PRIOR FILING DATE: 2003-03-12
;  PRIOR APPLICATION NUMBER: US 60/457,541
;  PRIOR FILING DATE: 2003-03-25
;  PRIOR APPLICATION NUMBER: US 60/466,411
;  PRIOR FILING DATE: 2003-04-29
;  PRIOR APPLICATION NUMBER: US 60/469,041
;  PRIOR FILING DATE: 2003-05-08
;  PRIOR APPLICATION NUMBER: US 60/477,414
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: US 60/478,560
;  PRIOR FILING DATE: 2003-06-13
;  PRIOR APPLICATION NUMBER: US 60/489,772
;  PRIOR FILING DATE: 2003-07-24
;  Remaining Prior Application data removed - See File Wrapper or PALM.

;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
;   LENGTH: 1059
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-753-267-30

  Query Match           12.9%;  Score 559;  DB 17;  Length 1059;
  Best Local Similarity   22.3%;  Pred. No. 1e-36;
  Matches  235;  Conservative  161;  Mismatches  341;  Indels  318;  Gaps   37;

Qy         27 PCIEVVPN--ITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDL 84
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Db         53 PCDEKKQNDSVIAECSNRRLQEVPQTVGKYVTELDLSDNFITHITNESFQGLQNLTKINL 112

Qy         85 S--------------RCEIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGL-TSLEN 129
              :              :     | | |:  | :|  |:|  | :    |   |||  ||
Db        113 NHNPNVQHQNGNPGIQSNGLNITDGAFLNLKNLRELLLEDNQL----PQIPSGLPESLTE 168

Qy        130 LVAVETKLASLESFPIGQLITLKKLNVAHN--FIHSCKL----PAYFSNLTNLVHVDLSY 183
              |  ::  : ::    | :|| || | :| |  |   |:        |  ||||  : ||:
Db        169 LSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLSF 228

Qy        184 NYIQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQG-IKLHELTLRGN----FN- 237
              | :  ::      ||:       | :|   | :| :: |:| | |  | | ||    ||
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Db        282 PFPCVPCDGGASINIDRFAFQNLTQLRYLNLSSTSLRKINAAWFKNMPHLKVLDLEFNYL 341

Qy        251 ------------------------------------------------GLHVHRLILGEFK 263
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Db        342 VGEIASGAFLTMLPRLEILDLSFNYIKGSYPQHINISRNFSKPLSLRALHLRGYVFQELR 401

Qy        264 DE-------------------------------RNLEIFEPSIMEGLCDVTIDEFRLTY 291
              ::                             ||||   : |     : : | :|
Db        402 EDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFSNLEII--YLSENRISPLVKDTRQSY 459

Qy        292 TN--------------DFSDD-----------IVKFHCLANVSAMSLAGVSIKYLEDVPK 326
                |              || |           ::|  | |   |: |:  || ::   |
Db        460 ANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFIG--PN 517

Qy        327 HFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKV---ALPSLSYLDLSRNAL 383
              |:                :|| :  | |: |  :          |:| : ||||: | |
Db        518 QFE----------------NLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRL 560

Qy        384 SFSGCCSYSDLGTNSLRHLDLSFNGAIIMSAN-------FMGLEELQHLDFQHSTLKRVT 436
              |    : ::|  : |  ||||:|      |              |: |:  |: : :|
Db        561 DFDNASALTEL--SDLEVLDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLT 618

Qy        437 EFSAFLSLEKLLYLDISYTNTKID---------FDGIFLGLTSLNTLKMAGNSFKDNTLS 487
              :     :||    ::: ::  ::|          :  || || :|  | :: |  | :  :
Db        619 D---KYNLESKSLVELVFSGNRLDILWNDDDNRYISIPKGLKNLTRLDLSLNRLK-HIPN 674

Qy        488 NVFAN-TTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSLST 546
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Db        675 EAFLNLPASLTELHINDNMLKFFNWTLLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRT 734

Qy        547 LDCSFNRI----------------ETSKGILQHFPKS---------LAFFNLTNNSVAC 580
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Qy        636 VVSVIVVSTV--AFLIYHFYFH---------LILIAGCKKYSRGESIYDAFVIYSSQN-- 682
              :  : : |  | | :| ::          |  | | :  |  :: |||:: | :::
Db        851 FFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKIKGYRSLSTSQTFYDAYISYDTKDAS 910

Qy        683 -EDWVRNELVKNLEEGVPR-FHLCLHYRDFIPGVAIAANIIQEGFHKSRKVIVVVSRHFI 740
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                 ||| |||  :|||   :   |||  ||: ||:||  |::|   ::|:| : |::: :
Db        911 VTDWVINELRYHLEESRDKNVLLCLEERDWDPGLAIIDNLMQ-SINQSKKTVFVLTKKY- 968

Qy        741 QSRWCIFEYEIAQTWQFLS----------SRSGIIFIVLEKVEKSLLRQQVELYRLLS 788
                      |::| | :            :   ||||:|| | :    | : | : :
Db        969 ----------AKSWNFKTAFYLALQRLMDENMDVIIFILLEPVLQH--SQYLRLRQRIC 1015

Qy        789 RNTYLEWEDNPLGRHIFWRRLKNALL---DGKASN 820
              ::: |:| |||    :||: |:| :|   | : :|
Db       1016 KSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNN 1050
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Job time : 79.8956 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 12, 2005, 19:34:01 ; Search time 21.5445 Seconds
(without alignments)
3729.074 Million cell updates/sec

Title: US-09-396-985B-99
Perfect score: 4345
Sequence: 1 MMPPWLLARTLIMALFFSCL.....GKASNPEQTAEEEQETATWT 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	457.5	10.5	786	2	T08664	Toll protein-like
3	406	9.3	1097	2	A29943	Toll protein precu
4	344	7.9	1389	2	T13852	gene wheeler prote
5	342	7.9	1385	2	T13887	tlr protein - frui
6	319.5	7.4	603	2	JC6128	insulin-like growt
7	317.5	7.3	603	2	JC1282	insulin-like growt
8	316.5	7.3	605	2	JC5239	insulin-like growt
9	315.5	7.3	1066	2	T15864	hypothetical prote
10	303.5	7.0	1134	1	A29944	chaoptin precursor
11	291.5	6.7	605	2	A41915	insulin-like growt
12	287.5	6.6	1531	2	T42218	slit-1 protein hom
13	283.5	6.5	1112	2	T10504	disease resistance
14	273	6.3	1469	2	B36665	slit protein 2 pre
15	273	6.3	1480	2	A36665	slit protein 1 pre
16	270	6.2	2026	1	OYBY	adenylate cyclase
17	269	6.2	1143	2	T10636	hypothetical prote
18	266.5	6.1	662	2	S42799	garp precursor - h
19	262.5	6.0	1091	2	A58532	glial cell membran
20	260.5	6.0	1523	2	T13953	MEGF5 protein - ra
21	257.5	5.9	1134	2	T04587	hypothetical prote
22	256	5.9	1120	2	B86479	hypothetical prote
23	255.5	5.9	994	2	H96510	probable disease r
24	255	5.9	907	2	JG0193	G protein-coupled
25	254.5	5.9	890	2	T00800	disease resistance
26	253.5	5.8	983	2	G84524	probable disease r
27	249.5	5.7	1027	2	B85089	receptor protein k
28	249.5	5.7	1051	2	T13174	gp150 protein - fr
29	247.5	5.7	603	2	T24315	hypothetical prote
30	247	5.7	907	2	JE0176	orphan G protein-c
31	244	5.6	1007	2	C84668	probable receptor-
32	243	5.6	1016	2	T30553	disease resistance
33	242	5.6	853	2	T17461	disease resistance
34	241.5	5.6	1109	2	T18536	receptor-like prot
35	241	5.5	741	2	T05250	probable disease r
36	240.5	5.5	1232	2	T05322	hypothetical prote
37	238	5.5	1039	2	T22117	hypothetical prote
38	235	5.4	1019	2	C96519	probable disease r
39	234	5.4	855	2	T17460	disease resistance
40	234	5.4	1068	2	H96769	hypothetical prote
41	230.5	5.3	910	2	G84648	probable disease r
42	230.5	5.3	1692	2	A33988	adenylate cyclase
43	230	5.3	1778	2	AF1116	internalin protein
44	226	5.2	1192	2	T48499	receptor-like prot
45	222.5	5.1	951	2	A96770	hypothetical prote

ALIGNMENTS

RESULT 1
I56258
RP105 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56258
R;Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995
A;Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a me
A;Reference number: I56258; MUID:95204928; PMID:7897216
A;Accession: I56258
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-661 <RES>
A;Cross-references: UNIPROT:Q62192; GB:D37797; NID:g761711; PIDN:BAA07043.1; PID:g761712

Query Match 14.1%; Score 612.5; DB 2; Length 661;
Best Local Similarity 27.0%; Pred. No. 3.3e-30;
Matches 182; Conservative 129; Mismatches 313; Indels 49; Gaps 16;

```
Qy         12 IMALFF-SC-LTPGSLNPCIEVVPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILK 69
              ::|||  ||  |  |   |||   | || | :  |:::|  :|:||: :: ||| |  ::
Db         10 LVALFLASCRATTSSDQKCIEKEVNKTYNCENLGLNEIPGTLPNSTECLEFSFNVLPTIQ 69

Qy         70 SYSFSNFSELQWLDLSRCEIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLEN 129
              : :||    | :|||:||:|  | :  :    | |  |:|| ||:   :  : ||  :|::
Db         70 NTTFSRLINLTFLDLTRCQIYWIHEDTFQSQHRLDTLVLTANPLIFMAETALSGPKALKH 129

Qy        130 LVAVETKLASLESFPIGQLITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTI 189
              |  ::| ::|::  |:    ||: | :  | | | |||  |     |  :|   | |  :
Db        130 LFFIQTGISSIDFIPLHNQKTLESLYLGSNHISSIKLPKGFPT-EKLKVLDFQNNAIHYL 188

Qy        190 TVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNL 249
              :  |:  |::   ||||::: | |  |:  ||      |    ||  :  :   : |
Db        189 SKEDMSSLQQ--ATNLSLNLNGNDIAGIEPGAFDSAVFQSL----NFGGTQNLLVIFKGL 242

Qy        250 AGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVS 309
              :  | || |:|  : :|  |:: ||||:::::  |     |:     ||| : :
Db        243 KNSTIQSLWLGTFEDMDDEDI-SPAVFEGLCEMSVESINLQKHYFFNISSNTFHCFSGLQ 301

Qy        310 AMSLAGVSIKYLEDVPKHF----------KWQSLSIIRCQL--KQFPTLDLPFLKS 353
              : |     :| ::|                |:::|    ||:    ||:|    :|
Db        302 ELDLTAT---HLSELPSGLVGLSTLKKLVLSANKFENL----CQISASNFPSLTHLSIKG 354

Qy        354 LTLTMNKGSISFKKVALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMS 413
              |  :  |:   :  | :|  |||| : :  | ||:      : |: |:||:|  : :
Db        355 NTKRLELGTGCLEN--LENLRELDLSHDDIETSDCCNLQLRNLSHLQSLNLSYNEPLSLK 412

Qy        414 AN-FMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLN 472
              |    :|: ||   : ||     | | :|  |  |::|::   |  : :| || :|
Db        413 TEAFKECPQLELLDLAFTRLKVKDAQSPFQNLHLLKVLNLSHSLLDISSEQLFDGLPALQ 472
```

```
Qy        473 TLKMAGNSFKDNTL--SNVFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNL 530
Db        473 HLNLQGNHFPKGNIQKTNSLQTLGRLEILVLSFCDLSSIDQHAFTSLKMMNHVDLSHNRL 532

Qy        531 LFLD---SSHYNQLYSLSTLDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKF 587
Db        533 TSSSIEALSHLKGIY----LNLASNHISIILPSLLPILSQQRTINLRQNPLDCTCSNIYF 588

Qy        588 LQWVKEQKQFLVNVEQMTCATPVEMN----TSLVLDFNNSTCYMYKTIISVSVVSVIVVS 643
Db        589 LEWYKENMQKLEDTEDTLCENPPLLRGVRLSDVTLSCSMAAVGIFFLIVFLLVFAILLIF 648

Qy        644 TVAFLIYHFYFHL 656
Db        649 AVKYFLRWKYQHI 661
```

RESULT 2
T08664
Toll protein-like receptor DKFZp547I0610.1 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08664
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16466
A;Accession: T08664
A;Molecule type: mRNA
A;Residues: 1-786 <POU>
A;Cross-references: UNIPROT:Q15399; EMBL:AL050262
A;Experimental source: fetal brain; clone DKFZp547I0610
C;Genetics:
A;Note: DKFZp547I0610.1

Query Match 10.5%; Score 457.5; DB 2; Length 786;
Best Local Similarity 23.7%; Pred. No. 1.6e-20;
Matches 194; Conservative 144; Mismatches 324; Indels 155; Gaps 31;

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Qy         88 EIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQ 147
Db         24 ESEFLVDRSKNGLIHV--------------PKDLSQKTTILNI--SQNYISELWTSDILS 67

Qy        148 LITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLS- 206
Db         68 LSKLRILIISHNRIQYLDISVFKFN-QELEYLDLSHNKLVKISC--------HPTVNLKH 118

Qy        207 LDMSLNPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKTCLQNLAGLHVHR--LILGEFKD 264
Db        119 LDLSFNAFDALPICKEFG-NMSQLKFLG-LSTTHLEKSSVLPIAHLNISKVLLVLGETYG 176

Qy        265 ERNLEIFEPSIMEGLCDVTIDEFRLTY-TNDFSDDIVKFHCLANVSAMSLAGVSIKYLED 323
Db        177 EKE----DPG---GLQDFNTESLHIVFPTNK------EFHFILDVSVKTVANLELSNIKC 223

Qy        324 VPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMN---------------------- 359
Db        224 VLEDSKCSYFLSILAKLQTNPKLSSLTLNNIETTWNSFIRILQLVWHTTVWYSSISNVKL 283

Qy        360 KGSISFKK-----VALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRH---------- 401
Db        284 QGQLDFRDFDYSGTSLKALSIHQVVSDVFGFPQSYIYEIFSNMNIKNFTVSGTRMVHMLC 343

Qy        402 -------LDLSFNGAIIMSANFMG---LEELQHLDFQHSTLKRVTEFSAFLS-LEKLLYL 450
Db        344 PSKISPFLHLDFSNNLLTDTVFENCGHLTELETLILQMNQLKELSKIAEMTTQMKSLQQL 403

Qy        451 DISYTNTKID-FDGIFLGLTSLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLSKCQLEQI 509
Db        404 DISQNSVSYDEKKGDCSWTKSLLSLNMSSNILTDTIFRCL---PPRIKVLDLHSNKIKSI 460

Qy        510 SWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIETSKGILQHFPKSLA 569
Db        461 PKQVV-KLEALQELNVAFNSL--TDLPGCGSFSSLSVLIIDHNSVSHPSADFFQSCQKMR 517

Qy        570 FFNLTNNSVACICEHQKFLQWVKEQKQFLVNVEQMT------------CATPVEMNTSLV 617
Db        518 SIKAGDNPFQCTCELGEFVK----------NIDQVSSEVLEGWPDSYKCDYPESYRGTLL 567

Qy        618 LDFN------NSTCYMYKTIISVSVVSVIVVSTVAFLIYHFYFHLILIAGC---KKYSRG 668
Db        568 KDFHMSELSCNITLLIVTIVATMLVLAVTVTSLCIYLDLPWYLRMV----CQWTQTRRRA 623

Qy        669 ESI----------YDAFVIYSSQNEDWVRNELVKNLE-EGVPRFHLCLHYRDFIPGVAIA 717
Db        624 RNIPLEELQRNLQFHAFISYSGHDSFWVKNELLPNLEKEGM---QICLHERNFVPGKSIV 680

Qy        718 ANIIQEGFHKSRKVIVVVSRHFIQSRWCIFEYEIAQTWQFLSSRSGIIFIVLEKV-EKSL 776
Db        681 ENII-TCIEKSYKSIFVLSPNFVQSEWCHYELYFAHHNLFHEGSNSLILILLEPIPQYSI 739

Qy        777 LRQQVELYRLLSRNTYLEWEDNPLGRHIFWRRLKNAL 813
Db        740 PSSYHKLKSLMARRTYLEWPKEKSKRGLFWANLRAAI 776
```

RESULT 3
A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A29943
R;Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A;Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, ap
A;Reference number: A29943; MUID:88135760; PMID:2449285
A;Accession: A29943
A;Molecule type: DNA
A;Residues: 1-1097 <HAS>
A;Cross-references: UNIPROT:P08953; GB:M19969; GB:J02682; NID:g158640; PIDN:AAA28941.1;
C;Genetics:
A;Gene: FlyBase:Tl
A;Cross-references: FlyBase:FBgn0003717
C;Keywords: transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-1097/Product: Toll protein #status predicted <MAT>

Query Match 9.3%; Score 406; DB 2; Length 1097;
Best Local Similarity 23.3%; Pred. No. 3.8e-17;
Matches 188; Conservative 135; Mismatches 263; Indels 220; Gaps 33;

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Qy         41 DQKLSKVPDDIPSSTKNID---LSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAW 97
Db        375 NNRLTHLPDSLFAHTTNLTDLRLEDNLLTGISGDIFSNLGNLVTLVMSRNRLRTIDSRAF 434

Qy         98 HGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVA 157
Db        435 VSTNGLRHLHLDHNDIDLQQP-------LLD--IMLQTQINS----PFGYMHGLLTLNLR 481

Qy        158 HN---FIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMSLNPI 214
Db        482 NNSIIFVYN----DWKNTMLQLRELDLSYNNISSLGYEDLAFLSQN---RLHVNMTHNKI 534

Qy        215 DFI--QDQAFQGIKLHELTLRGNFNSSNIMKTC-----LQNLAGLHVHRLILGEFKDERN 267
Db        535 RRIALPEDVHLGEGYNNNLVHVDLNDNPLVCDCTILWFIQLVRGVHKPQ-YSRQFKLRTD 593

Qy        268 -LEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSLAGVSIKYLEDVPK 326
Db        594 RLVCSQPNVLEGTPVRQIEPQTLICPLDFSDDPRERKC--------------------PR 633

Qy        327 HFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLSYLDLSRNALSFS 386
Db        634 G--------CNCHVRTYD-------KALVINCHSGNLTH----VPRLPNL---------- 664

Qy        387 GCCSYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEK 446
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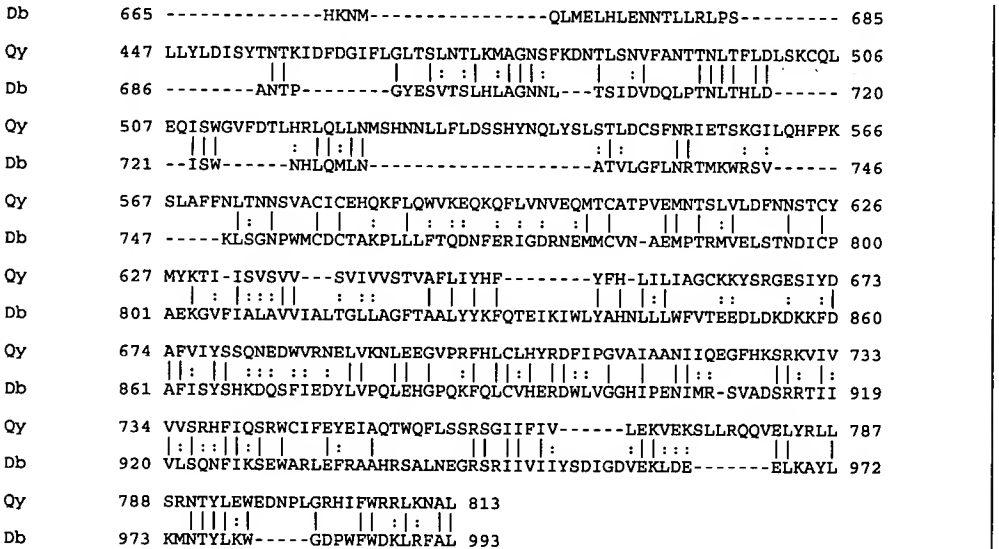
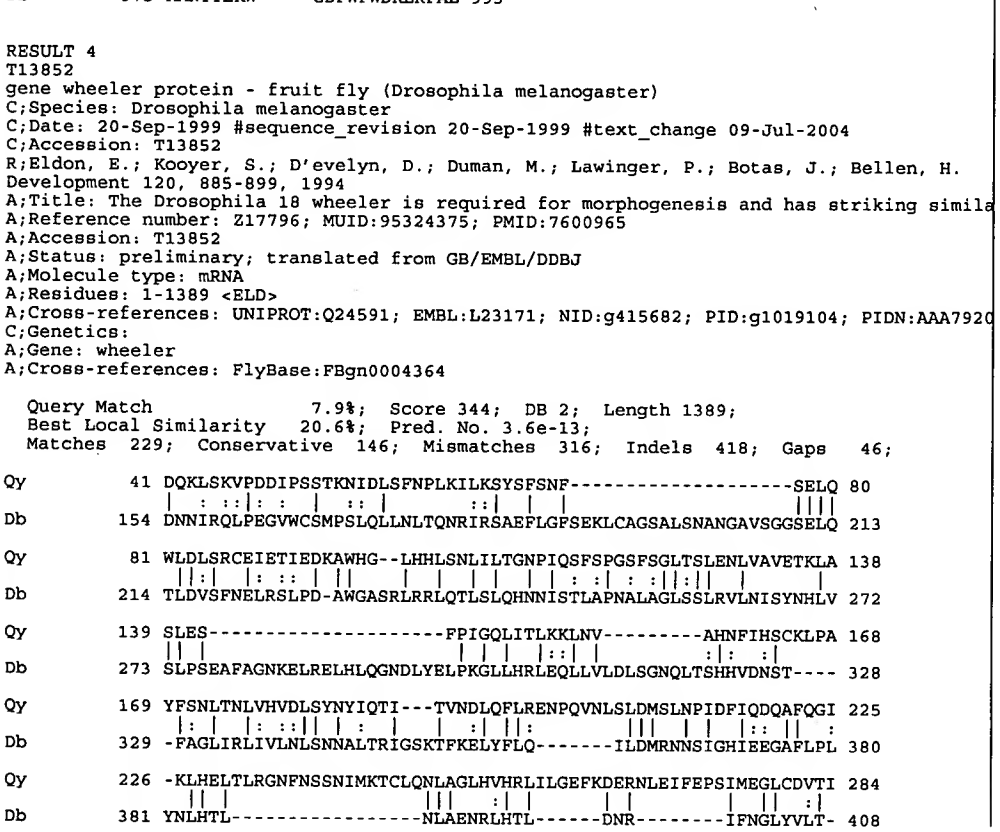
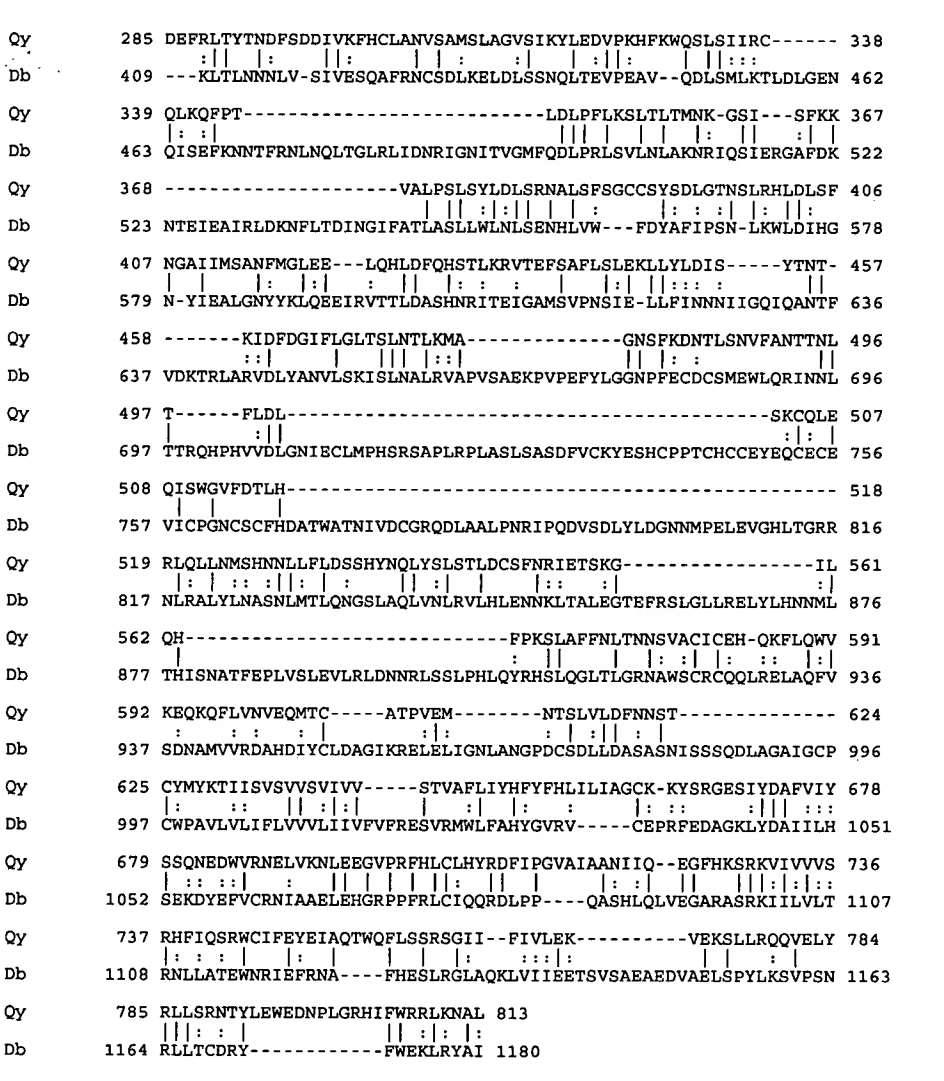


RESULT 4
T13852
gene wheeler protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13852
R;Eldon, E.; Kooyer, S.; D'evelyn, D.; Duman, M.; Lawinger, P.; Botas, J.; Bellen, H.
Development 120, 885-899, 1994
A;Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simila
A;Reference number: Z17796; MUID:95324375; PMID:7600965
A;Accession: T13852
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1389 <ELD>
A;Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:g415682; PID:g1019104; PIDN:AAA7920
C;Genetics:
A;Gene: wheeler
A;Cross-references: FlyBase:FBgn0004364

Query Match 7.9%; Score 344; DB 2; Length 1389;
Best Local Similarity 20.6%; Pred. No. 3.6e-13;
Matches 229; Conservative 146; Mismatches 316; Indels 418; Gaps 46;





RESULT 5
T13887
tlr protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13887
R;Chiang, C.; Beachy, P.A.
Mech. Dev. 47, 225-239, 1994
A;Title: Expression of a novel Toll-like gene spans the parasegment boundary and contribu
A;Reference number: Z17805; MUID:95151581; PMID:7848870
A;Accession: T13887
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1385 <CHI>
A;Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PIDN:AAB33383

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C;Genetics:
A;Cross-references: FlyBase:FBgn0004364
A;Note: tlr

  Query Match             7.9%;  Score 342;  DB 2;  Length 1385;
  Best Local Similarity   20.3%;  Pred. No. 4.8e-13;
  Matches  223;  Conservative  151;  Mismatches  325;  Indels  402;  Gaps   43;

Qy         41 DQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNF-------------------SELQ 80
              |  : ::|: :  |  :: |       ::|  |  |                     ||||
Db        154 DNNIRQLPEGVWCSMPSLQLLNLTQNRIRSAEFLGFSEKLCAGSALSNANGAVSGGSELQ 213

Qy         81 WLDLSRCEIETIEDKAWHG--LHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLA 138
               ||:|  |: :: | ||    |  |  | |  | | : :| : :||:|| |       |
Db        214 TLDVSFNELRSLPD-AWGASRLRRLQTLSLQHNNISTLAPNALAGLSSLRVLNISYNHLV 272

Qy        139 SLESFPIGQLITLKKLNVAHNFIHSCKLP--------------------------AYFS 171
              || |         |::|::  | ::  :||                         : |:
Db        273 SLPSEAFAGNKELRELHLQGNDLY--ELPKGLLHRLEQLLVLDLSGNQLTDHHVDNSTFA 330

Qy        172 NLTNLVHVDLSYNYIQTI---TVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGI-KL 227
              |  |: ::|| | :  |    |  :| ||:         |||  | |  |:: ||  :  |
Db        331 GLIRLIVLNLSNNALTRIGSKTFKELYFLQ-------ILDMRNNSIGHIEEGAFLPLYNL 383

Qy        228 HELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEF 287
              | |                  |||   :| |      | |       |  ||  :|
Db        384 HTL-----------------NLAENRLHTL------DNR--------IFNGLYVLT---- 408

Qy        288 RLTYTNDFSDDIVKFHCLANVSAMSLAGVSIKYLEDVPKHFKWQSLSIIRC------QLK 341
              :|| |:    ||:     | | :    :|   | :||:    | ||:::       |:
Db        409 KLTLNNNLV-SIVESQAFRNCSDLKELDLSSNQLTEVPE--AAQDLSMLKTLDLGENQIS 465

Qy        342 QFPT--------------------------LDLPFLKSLTLTMNK-GSI---SFKK--- 367
              :|                          |||  |  |  |:  ||   :| |
Db        466 EFKNNTFRNLNQLTGLRLIDNRIGNITVGMFQDLPRLSVLNLAKNRIQSIERGAFDKNTE 525

Qy        368 ------------------VALPSLSYLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGA 409
                               | || :|:|| | | :      |: : :| |: ||:  |
Db        526 IEAIRLDKKFLTDINGIFATLASLLWLNLSENHLVW---FDYAFIPSN-LKWLDIHGN-Y 580

Qy        410 IIMSANFMGLEE---LQHLDFQHSTLKRVTEFSAFLSLEKLLYLDIS-----YTNT---- 457
              |     |:  |:|    :  ||  |: :  :    |:| ||::: :          ||
Db        581 IEALGNYYKLQEEIRVTTLDASHNRITEIGAMSVPNSIE-LLFINNNIIGQIQANTFVDK 639

Qy        458 ----KIDFDGIFLGLTSLNTLKMA-------------GNSFKDNTLSNVFANTTNLT-- 497
                  ::|     |   ||| |::|               || |: :          |||
Db        640 TRLARVDLYANVLSKISLNALRVAPVSAEKPVPEFYLGGNPFECDCSMEWLQRINNLTTR 699

Qy        498 ----FLDL-------------------------------------------SKCQLEQIS 510
                  :||                                          :|: | |
Db        700 QHPHVVDLGNIECLMPHSRSAPLRPLASLSASDFVCKYESHCPPTCHCCEYEQCECEVIC 759

Qy        511 WGVFDTLH-------------------------------------------------RLQ 521
               |    |                                                  |:
Db        760 PGNCSCFHDATWATNIVDCGRQDLAALPNRIPQDVSDLYLDGNNMPELEVGHLTGRRNLR 819

Qy        522 LLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIETSKG-----------------ILQH- 563
              | :: :||: | :     || :|  |     |:   :|                  :| |
Db        820 ALYLNASNLMTLQNGSLAQLVNLRVLHLENNKLTALEGTEFRSLGLLRELYLHNNMLTHI 879

Qy        564 ---------------------------FPKSLAFFNLTNNSVACICEH-QKFLQWVKEQ 594
                                        :  ||    |  |: :| |:  ::   |:| :
Db        880 SNATFEPLVSLEVLRLDNNRLSSLPHLQYRHSLQGLTLGRNAWSCRCQQLRELAQFVSDN 939

Qy        595 KQFLVNVEQMTC-----ATPVEM--------NTSLVLDFNNSTCYM-------YKTIISV 634
                 : :   : |        :|:        : | :|| : |           |:  :
Db        940 AMVVRDAHDIYCLDAGIKRELELIGNLANGPDCSDLLDASASNISSSQDLAGGYRLPLLA 999

Qy        635 SVVSVIVVSTVAFLIYHF--------YFHLILIAGCKKYSRGESIYDAFVIYSSQNEDWV 686
              :|: :| :  |  ::: |        : |  :     ::     :||| :::| :: ::|
Db       1000 AVLVLIFLDVVLIIVFVFRESVRMWLFAHYGVRVCEPRPEDAGKLYDAIILHSEKDYEFV 1059

Qy        687 RNELVKNLEEGVPRFHLCLHYRDFIPGVAIAANIIQ--EGFHKSRKVIVVVSRHFIQSRW 744
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Db       1060 CRNIAAELEHGRPPFRLCIQQRDLPP----QASHLQLVEGARASRKIILVLTRNLLATEW 1115

Qy        745 CIFEYEIAQTWQFLSSRSGII--FIVLEK----------VEKSLLRQQVELYRLLSRNTY 792
                |:  |    |  |  |:    :::|:           | |   : |   |||: : |
Db       1116 NRIEFRNA----FHESLRGLAQKLVIIEETSVSAEAEDVAELSPYLKSVPSNRLLTCDRY 1171

Qy        793 LEWEDNPLGRHIFWRRLKNAL 813
                        || :|: |:
Db       1172 -----------FWEKLRYAI 1180


RESULT 6
JC6128
insulin-like growth factor binding complex acid labile chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: JC6128
R;Boisclair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T.
Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996
A;Title: Organization and chromosomal localization of the gene encoding the mouse acid la
A;Reference number: JC6128; MUID:96413591; PMID:8816745
A;Accession: JC6128
A;Molecule type: DNA
A;Residues: 1-603 <BOI>
A;Cross-references: UNIPROT:P70389; GB:U66900; NID:g1621612; PIDN:AAB17270.1; PID:g162161
C;Comment: This protein is a serum protein and it is of the ternary complex in the physic
C;Genetics:
A;Gene: als
A;Map position: 17

  Query Match             7.4%;  Score 319.5;  DB 2;  Length 603;
  Best Local Similarity   24.2%;  Pred. No. 3.7e-12;
  Matches  159;  Conservative   85;  Mismatches  228;  Indels  185;  Gaps   23;

Qy         39 CMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWH 98
              |  : |:::|| || ||: : |  | |  : | :| | | | :|:|    : ::| :|
Db         60 CSSRNLTQLPDGIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALL 119

Qy         99 GLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAH 158
              || :| :| |  | ::| : | |    || :|       |  ||          |  | ||:
Db        120 GLQNLYHLHLERNLLRSLAAGLFRHTPSLASLSLGNNLLGRLEEGLFRGLSHLWDLNLGW 179

Qy        159 NF--------------IHSCKL---------PAYFSNLTNLVHVDLSYNYIQTITVNDLQ 195
              |                :|   |          ||     |  |  :||| | :::: |
Db        180 NSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPALLCGLGELRELDLSRNALRSVKAN--V 237

Qy        196 FLRENPQVNLSLDMSLNPIDFIQDQAFQGIK-LHELTLRGNFNSSNIMKTCLQNLAGLHV 254
              |:       | || :|  |  :  :|| |:| |  | |  |   : :::      | ||||
Db        238 FIHLPRLQKLYLDRNL--ITAVAPRAFLGMKALRWLDLSHN-RVAGLLEDTFPGLLGLHV 294

Qy        255 HRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSLA 314
              |                                                ||: :  ||
Db        295 LR---------------------------------------------LAHNAITSLR 306

Qy        315 GVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNK----GSISFKKVAL 370
                    |: ||                  || ||: | |  |:    |  :|:   |
Db        307 ----------PRTFK----------------DLHFLEELQLGHNRIRQLGEKTFE--GL 337

Qy        371 PSLSYLDLSRNAL------SFSGCCSYS--DLGTNSLRHLDLSFNGAIIMSANFMGLEEL 422
              |  | |: | :        :| |  :  :  :|  | || |                | ||  |
Db        338 GQLEVLTLNDNQIHEVKVGAFFGLFNVAVMNLSGNCLRSLP---------EHVFQGLGRL 388

Qy        423 QHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFK 482
              |  :|| | |:   :                  | ||: | |  | :     :
Db        389 HSLHLEHSCLGRIRLHT-----------------------FAGLSGLRRLFL-----R 418

Qy        483 DNTLSNV----FANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSHY 538
              ||::|::      |  : |  |||:  ||  :   :|  | :|: | :|:| | |
Db        419 DNSISSIEEQSLAGLSELLELDLTANQLTHLPRQLFQGLGQLEYLLLSNNQLTMLSEDVL 478

Qy        539 NQLYSLSTLDCSFNRIET-SKGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQKQF 597
                  |  || | ||:|| ::|:     : | : || |||:       | |:     :: :
```

```
Db        479 GPLQRAFWLDLSHNRLETPAEGLFSSLGR-LRYLNLRNNSL------QTFVPQPGLERLW 531

Qy        598 LVNVEQMTCATPVE-------MNTSLVLDFNNSTC--------YMYKTIISVSVVSV 639
              |  :     |: |::         |  :|  |  : |         | |  |       :|
Db        532 L-DANPWDCSCPLKALRDFALQNPGVVPRFVQTVCEGDDCQPVYTYNNITCAGPANV 587


RESULT 7
JC1282
insulin-like growth factor-binding protein acid labile chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1282
R;Dai, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A;Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A;Reference number: JC1282; MUID:93038676; PMID:1384485
A;Accession: JC1282
A;Molecule type: mRNA
A;Residues: 1-603 <DAI>
A;Cross-references: UNIPROT:P35859; GB:S46785; NID:g258002; PIDN:AAB23770.2; PID:g570593
A;Experimental source: liver
A;Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

  Query Match             7.3%;  Score 317.5;  DB 2;  Length 603;
  Best Local Similarity   24.1%;  Pred. No. 4.9e-12;
  Matches  159;  Conservative   86;  Mismatches  223;  Indels  193;  Gaps   24;

Qy         39 CMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWH 98
              |  : |: :||||| ||: : |  | |  : | :| | | | :|:|    : ::| :|
Db         60 CSSKNLTHLPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPQALL 119

Qy         99 GLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAH 158
              || :|  | |  | ::: : | |:   || :|       | ||       |  | ||:
Db        120 GLQNLYYLHLERNRLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGW 179

Qy        159 NF--------------IHSCKL---------PAYFSNLTNLVHVDLSYNYIQTITVNDLQ 195
              |               :|  |          || |  |  |  :||| | ::::  |
Db        180 NSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPALFCGLGELRELDLSRNALRSVKANVFV 239

Qy        196 FLRENPQV-NLSLDMSLNPIDFIQDQAFQGIK-LHELTLRGNFNSSNIMKTCLQNLAGLH 253
              |   |::  | || :|  |  :   || |:| |  | |  |   : :|:     | |||
Db        240 HL---PRLQKLYLDRNL--ITAVAPGAFLGMKALRWLDLSHN-RVAGLMEDTFPGLLGLH 293

Qy        254 VHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSL 313
              | |                                              ||: :  ||
Db        294 VLR-------------------------------------------------LAHNAIASL 305

Qy        314 AGVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNK----GSISFKKVA 369
                    |: ||                 || ||: | |  |:    |  :|:
Db        306 R----------PRTFK----------------DLHFLEELQLGHNRIRQLGERTFE--G 336

Qy        370 LPSLSYLDLSRNAL------SFSGCCSYS--DLGTNSLRHLDLSFNGAIIMSANFMGLEE 421
              |  |  | |: | :       :|||  : :  :|  | || |             | ||::
Db        337 LGQLEVLTLNDNQITEVRVGAFSGLFNVAVMNLSGNCLRSLP---------ERVFQGLDK 387

Qy        422 LQHLDFQHSTLKRVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSF 481
              |  | :|| |  |   :                          | ||: |  | :
Db        388 LHSLHLEHSCLGHVRLHT-----------------------FAGLSGLRRLFL----- 417

Qy        482 KDNTLSNV----FANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSH 537
              :||::|::     |  : |  |||:  :|  :   :|  |  |: | :|:|  |  | :
Db        418 RDNSISSIEEQSLAGLSELLELDLTTNRLTHLPRQLFQGLGHLEYLLLSYNQLTTLSAEV 477

Qy        538 YNQLYSLSTLDCSFNRIET-SKGILQHFPKSLAFFNLTNNSVACICEHQKFLQWVKEQ-- 594
                |     || | | :|| ::|:     : : : :| |||           ||    |
Db        478 LGPLQRAFWLDISHNHLETLAEGLFSSLGR-VRYLSLRNNS----------LQTFSPQPG 526

Qy        595 -KQFLVNVEQMTCATPVE-------MNTSLVLDFNNSTC--------YMYKTIISVSVVS 638
               ::  ::      |: |::         |  :|  |  : |         | |  |      :
```

```
Db        527 LERLWLDANPWDCSCPLKALRDFALQNPGVVPRFVQTVCEGDDCQPVYTYNNITCAGPAN 586

Qy        639 V 639
              |
Db        587 V 587


RESULT 8
JC5239
insulin-like growth factor acid-labile chain - baboon
C;Species: Papio sp. (baboon)
C;Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C;Accession: JC5239
R;Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-lik
A;Reference number: JC5239; MUID:97040714; PMID:8886027
A;Contents: liver
A;Accession: JC5239
A;Molecule type: mRNA
A;Residues: 1-605 <DEL>
C;Comment: This factor is structurally related to proinsulin and have insuline-like meta

  Query Match             7.3%;  Score 316.5;  DB 2;  Length 605;
  Best Local Similarity   22.2%;  Pred. No. 5.7e-12;
  Matches  147;  Conservative   89;  Mismatches  238;  Indels  189;  Gaps   17;

Qy         32 VPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIET 91
              |  ::  |  : |:::|| ||  |: : |  | | :   :| | | | :|:|   :: :
Db         53 VNELSVFCSSRNLTRLPDGIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGS 112

Qy         92 IEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITL 151
              :| :|  || :| :|  |  | ::| : |:|:   :|  |      :|: ||
Db        113 LEPQALLGLENLCHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLED--------- 163

Qy        152 KKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMSL 211
                                    |  | ||  ::| :| :
Db        164 ---------------GLFEGLGNLWDLNLGWNSLAV---------------------- 184

Qy        212 NPIDFIQDQAFQGI-KLHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEI 270
                  : | ||:|:  | || | ||                              |
Db        185 -----LPDAAFRGLGGLRELVLAGN-----------------------------RLAY 208

Qy        271 FEPSIMEGLC-----DVTIDEFRLTYTNDFSD--DIVKFHCLANVSAMSLAGVSIKYLED 323
              :|::  ||       |:: :  |     | |:    : | :   |: |    |
Db        209 LQPALFSGLAELRELDLSRNALRAIKANVFAQLPRLQKLYLDRNLIAAVAPGA------- 261

Qy        324 VPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNK--GSISFKKVALPSLSYLDLSRN 381
                                  | |  |: | |: |:  | :       |  |  | || |
Db        262 --------------------FLGLKALRWLDLSHNRVAGLLEDTFPGLLGLRVLRLSHN 300

Qy        382 ALSFSGCCSYSD--------LGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLK 433
              |::      ::  |         || | :| |           :| || :|: |    |: |:
Db        301 AIASLRPRTFEDLHFLEELQLGHNRIRQL---------AERSFEGLGQLEVLTLDHNQLQ 351

Qy        434 RVTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNS------------- 480
              | :  ||| |  :  :::|     :   : :| ||  |::| : |:
Db        352 EV-KVGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFAGLS 410

Qy        481 ------FKDNTLSNVFANT----TNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNL 530
                   |||  |   :      |  |||:  ||  :   :|  | :|: | :||| |
Db        411 GLRRLFLKDNGLVGIEEQSLWGLAELLELDLTSNQLTHLPHQLFQGLGKLEYLLLSHNRL 470

Qy        531 LFLDSSHYNQLYSLSTLDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKFLQ- 589
                | :      |     || | ||:|   | |       | : || |||:          |:
Db        471 AELPADALGPLQRAFWLDVSHNRLEALPGSLLASLGRLRYLNLRNNSLRTFTPQPPGLER 530

Qy        590 -WVKEQKQFLVNVEQMTCATPVE-------MNTSLVLDFNNSTC---------YMYKTII 632
               |::              |: |::         | | |  |  : |         | | .|
Db        531 LWLEG--------NPWDCSCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPVYTYNNIT 582

Qy        633 SVS 635
                |
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Db        583 CAS 585


RESULT 9
T15864
hypothetical protein C56E6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15864
R;Fulton, L.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C56E6.
A;Reference number: S69019
A;Accession: T15864
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1066 <FUL>
A;Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:g1055114; PID:g1055120; PIDN:AAA810
C;Genetics:
A;Gene: CESP:C56E6.6
A;Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3; 9

  Query Match             7.3%;  Score 315.5;  DB 2;  Length 1066;
  Best Local Similarity   21.2%;  Pred. No. 1.4e-11;
  Matches  180;  Conservative  128;  Mismatches  217;  Indels  323;  Gaps   37;

Qy         56 KNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEI----------------ETIE------- 93
              : :|:|:| :: ::  ||     :| ||||  |                 :|::
Db        171 RELDISYNQIQTVEDSSFETVGHMQSLDLSYNRIAYLPRGMLKNFAKTLKTLKLAENMIH 230

Qy         94 --DKAWHGLHHLSNLILTGNP-------------------------IQSFSPGSFSGLTS 126
                :|    | :|::| | ||                         ::    |  ||:
Db        231 ATPEALRDLRNLTHLNLNGNKLNRIDGDVLKGCTDTLVELFIANNYLEHIPHGVLSGMKQ 290

Qy        127 LENLVAVETKLASLE------SFPIGQLITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVD 180
              ||:|   : |: ||:      |    :  |:::||:| | |::      | ::  | :||
Db        291 LEHLDISKNKIMSLKKPTSLLSITKEETSTVRRLNLAGNRINNMSDYLIFEHMPLLTYVD 350

Qy        181 LSYNYIQTIT------VNDLQ--FLREN-----PQV-------NLSLDMSLNPIDFIQDQ 220
              :|:| |: |:      : :|:  ||: |     | :       :| ||   | |  | :
Db        351 VSFNRIRFISPRVFEKLKNLESLFLQNNQLAHFPSLFRLDKLRHLMLDN--NQIQKIDNF 408

Qy        221 AFQGI-KLHELTLRGN---------FNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEI 270
              :   : ||  |:| ||         | ||:  :    |||   :| :    | |  ||:
Db        409 SLADLPKLQHLSLAGNQLDIITENMFGSSSSSELKSLNLAHNKIHSISSRSFSDLDNLQ- 467

Qy        271 FEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSLAGV-SIKYLEDVPKHFK 329
                       : ||:: |           :  :::|: : : :::|| |:  :
Db        468 --------------QLRLSHNN----------IRTITSMTFSNLRNLRYL-DLSHN-- 498

Qy        330 WQSLSIIRCQLKQFPTLDL------------------PFLKSLTLTMNK---------G 361
              : : |:   | | | ||:                  |:|| |: |          |
Db        499 -RIIKILPSALYQLPALDVLHLDHNNLNEIDRDAFRSFSDLQSLKLSHNAFRRFSCEFLG 557

Qy        362 SISFKKVALPSLSYLDLSRNALSFSG--CCSYS----DLGTNS-------------LRH 401
              |||         :  |||| | ::      | :       | :||             |
Db        558 SIS-------QVHQLDLSSNQINEIDIFCIARGIRKLSLASNSVEKINRKLLQDATELTS 610

Qy        402 LDLSFNGAI-IMSANFMGLEELQHLDFQHSTLK-------------RVTEFSAFLS--L 444
              :|:| || | :  |   :| |:   |: ::               :| |  |     |
Db        611 IDISHNGIIDVDSDAFCECRKLSHIKLSHNYIRNLWKGTRVCIPWISHLTTFCPFTKEHL 670

Qy        445 EKLLYLD----------------ISYTNTKIDF--DGIFLGLTSLNTLKMAGN------ 479
              |: :                  :|: | |:|   || |  | ||  | :: |
Db        671 ERTISFSYIIVDSSQLTSFGNLSILSFANNKVDSIEDGAFENLLSLKILDLSNNPVTSWS 730

Qy        480 --SFKD--NTLSNV-FANT---------------------------------TNLTFLD 500
                :|:|  :::|::  |||                                 | :  ||
Db        731 PTAFRDLSHSISSINMANTGLFSMPKFSHRSIQSLNISCNKIYELSEKDLAPLTKVVALD 790

Qy        501 LSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSL---------------- 544
              :|   |:|||   |: |  |: ||:| | :  | : |  |||
Db        791 ISHNNLKQISSMAFEPLIHLKQLNVSANPITHLTNEHIQQLYKLYNIPDMARPYQISSIL 850

Qy        545 ----------------STLDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKFLQ 589
                             | ||  |   :|   :|:|    :|  |||   |       : |
Db        851 SNLPPLHTIYVDIKESALDRQFYTADTR--LLRHL--VVAGRNLTKIEVGAFATIRGF-- 904

Qy        590 WVKEQKQFLVNVEQMTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVVSVIVV------- 642
                                     :|:: | : :| :    :: |:  :|::|: :
Db        905 -----------------RVRIEIHNSSIEEFPSR---IFDTLTGISILSLSLTDNKLTTF 944

Qy        643 ----STVA 646
                  ||||
Db        945 NPFQSTVA 952


RESULT 10
A29944
chaoptin precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: photoreceptor cell-specific membrane protein
C;Species: Drosophila melanogaster
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29944; A21123
R;Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
Cell 52, 291-301, 1988
A;Title: Chaoptin, a cell surface glycoprotein required for Drosophila photoreceptor cel
A;Reference number: A29944; MUID:88135762; PMID:3124963
A;Accession: A29944
A;Molecule type: DNA
A;Residues: 1-1134 <REI>
A;Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M1901
R;Zipursky, S.L.; Venkatesh, T.R.; Teplow, D.B.; Benzer, S.
Cell 36, 15-26, 1984
A;Title: Neuronal development in the Drosophila retina: monoclonal antibodies as molecul
A;Reference number: A21123; MUID:84106810; PMID:6420071
A;Accession: A21123
A;Molecule type: protein
A;Residues: 31-43,'HX',46-49,'H' <ZIP>
C;Genetics:
A;Gene: FlyBase:chp
A;Cross-references: FlyBase:FBgn0000313
A;Introns: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
C;Superfamily: chaoptin; leucine-rich alpha-2-glycoprotein repeat homology
C;Keywords: cell adhesion; glycoprotein; membrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-1134/Product: chaoptin #status predicted <MAT>
F;80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR
F;103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
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F;326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F;551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
F;577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
F;601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>
F;625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR23>
F;649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>
F;673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR25>
F;708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>
F;733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR27>
F;757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR28>
F;781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>
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F;805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR30>
F;828-851/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR31>
F;854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
F;879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
F;903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
F;928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F;949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
F;973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
F;996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
F;1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
F;1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Query Match 7.0%; Score 303.5; DB 1; Length 1134;
Best Local Similarity 20.8%; Pred. No. 8.6e-11;
Matches 169; Conservative 122; Mismatches 275; Indels 247; Gaps 31;

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Qy      44 LSKVPDD--------------------IPSST-------KNIDLSFNPLKILKSYSFSN 75
           |:::|||                    ||| :       :::|| :| :  ::  ||
Db     114 LTEIPDDAFTGLERSLWELILPQNDLVEIPSKSLRHLQKLRHLDLGYNHITHIQHDSFRG 173

Qy      76 FSE-LQWLDLSRCEIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSF-SGLTSLENLVAV 133
             : || | |    |  :   :: ||  |  | |:|| :    |  |  |:  |  |:
Db     174 LEDSLQTLILRENCISQLMSHSFSGLLILETLDLSGNNLFEIDPNVFVDGMPRLTRLLLT 233

Qy     134 ETKLASLESFPIGQLITLKKLNVAHNFIHSCKLPAYF----SNLTNLVHVDLSYNYIQTI 189
           :  |: :    :| | :|: |:::|| | |      :    |   || :: | ||:|: :
Db     234 DNILSEIPYDALGPLKSLRTLDISHNVIWSLSGNETYEIKASTKLNLDNLHLEYNHIEVL 293

Qy     190 TVNDLQFLRENPQVNLSLDMSLNPIDFIQDQAFQGIKLHELTLR------------GNF 236
             |  ::     || :     |||  ::: ||:  :: |: :|
Db     294 PPNSFKYF---DTVNRTF-FDGNPIHTLREDAFKPARIREIYMRYCGLTNISPVAFDSLV 349

Qy     237 NSSNIMKTCLQNLAGLHVHRLI-------LGEFKDERNLEIFEPSIMEGLCDVTIDEFRL 289
           ||  |:     ||  || |:|         :  :| : ::| :|:         |:  :|
Db     350 NSLQILDLSGNNLTKLH-HKLFNNFDVLRVISMRDNK-IKIQKPTETFNAVHYTL--LKL 405

Qy     290 TYTNDFSDDIVKFHCLANVSAM-SLAGVSIKYLEDV---PKHFK-----WQSLSIIRCQL 340
             : |  :|      | |:: | ::  :|| |      |: ||     : | | |  |
Db     406 DLSGD-RNDPTNLQTLRNMTRMRNMRSLSISRLGSSSVGPEDFKDFGVELEDLQITRASL 464

Qy     341 KQFPTLDLPFLKSL----------------------TLTMNKGSISFKKVALP------ 371
           :     :: |                        :|   | |  :   |||
Db     465 SGIQSHAFKHVRGLKRLDFSENGISSIENDAFHEIGHSLISLKMSHGYSGSALPAEPLRH 524

Qy     372 --SLSYLDLSRNALSFSGCCSYSDL------------------GT------NSLRHLDLS 405
             ||  || | | :|      |:  |                  ||      : |  | |
Db     525 LTSLQELDFSNNHISSMSDTSFHFLKNLRLLELHDNRIEQVLKGTFQGDIHSKLEEISLR 584

Qy     406 FNGAIIMSAN------------------------FMGLEELQHLDFQHSTLKRVTEFSA 440
           ||    :| :                       || |:||::|  : :  :  :  :
Db     585 FNHLTSISQHTFFDLEALRKLHLDDNKIDKIERRAFMNLDELEYLSLRGNKINNLAD-ES 643

Qy     441 FLSLEKL---------------------------------------------------- 447
           | :| ||
Db     644 FQNLPKLEILDMAFNQLPNFNFDYFDQVGTLSNLNVNVSHNQIRQLMYNSSWSGRNEHGG 703

Qy     448 LY------LDISYTNTKIDFDGIFL-GLTSLNTLKMAGNSFKDNTLSNVFANTTNLTFLD 500
           :|      ||:|: |  |  | |       ||  | :  ||   ||  :|| |  :| :||
Db     704 MYHSNIKILDLSHNNISIIHPGYFRPAEISLTHLHLGYNSLM-NTTRDVFGNMPHLQWLD 762

Qy     501 LSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFN-------- 552
           ||   : :: :  |    :|||:   || |  :   :  :  |  :| | |
Db     763 LSYNWIHELDFDAFKNTKQLQLVFFGHNYLSDIPQDIFKPVQGLRIVDFSHNHLRGLPDN 822

Qy     553 --------RIETSKGILQHFPKS---------LAFFNLTNNSVACICE---HQKF--LQW 590
                   ::: |  ::    | |         |   :|:|| :: |       ||  |::
Db     823 LFYNGGMEKLDVSHNMMLKIPSSSLSSLAALTLCELHLSNNFISTIHSMDLSNKFRSLRY 882

Qy     591 VKEQKQFLVNVEQMTCATPVEMNTSLVLDFNNS 623
           :     :|: ::    ||   |    ||| :::
Db     883 LDISYNYLLRIDDAVFAT---MPKLAVLDLSHN 912
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RESULT 11
A41915
insulin-like growth factor-binding complex acid-labile chain precursor - human
N;Alternate names: Acid-Labile Subunit (ALS)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A41915
R;Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
Mol. Endocrinol. 6, 870-876, 1992
A;Title: Structure and functional expression of the acid-labile subunit of the insulin-l
A;Reference number: A41915; MUID:92357025; PMID:1379671
A;Accession: A41915
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-605 <LEO>
A;Cross-references: UNIPROT:P35858; GB:M86826; NID:g184807; PIDN:AAA36047.1; PID:g184808
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:110171)
F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

Query Match 6.7%; Score 291.5; DB 2; Length 605;
Best Local Similarity 22.0%; Pred. No. 2e-10;
Matches 147; Conservative 86; Mismatches 233; Indels 201; Gaps 17;

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Qy      39 CMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWH 98
           |  : |:::|| :|  |: : |  | |  :  :| | | | :|:|   :: ::| :|
Db      60 CSSRNLTRLPDGVPGGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLEPQALL 119

Qy      99 GLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAH 158
           || :| :| |  | ::| : |:|:   :| :|     :|: ||      | :|  ||:
Db     120 GLENLCHLHLERNQLRSLALGTFAHTPALASLGLSNNRLSRLEDGLFEGLGSLWDLNLGW 179

Qy     159 NFIH----------------------SCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQ 195
           | :                      :   || || |  |  :||| | :: |  |
Db     180 NSLAVLPDAAFRGLGSLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKAN--V 237

Qy     196 FLRENPQVNLSLDMSLNPIDFIQDQAFQGIK-LHELTLRGNFNSSNIMKTCLQNLAGLHV 254
           |::      | || :|  |  :   || |:| |  | |  |   : :::     | || |
Db     238 FVQLPRLQKLYLDRNL--IAAVAPGAFLGLKALRWLDLSHN-RVAGLLEDTFPGLLGLRV 294

Qy     255 HRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSLA 314
           ||                                                  |  ::|
Db     295 LRL-------------------------------------------------SHNAIA 303

Qy     315 GVSIKYLEDVPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLS 374
             :       |: ||                 || ||: |
Db     304 SLR-------PRTFK-----------------DLHFLEEL-------------------- 319

Qy     375 YLDLSRNALSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKR 434
                               || | :| |           :| || :|: |   |: |:
Db     320 -----------------QLGHNRIRQL---------AERSFEGLGQLEVLTLDHNQLQE 352

Qy     435 VTEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNS-------------- 480
           | :  ||| |  :  :::|    :   : :| ||  |::| : |:
Db     353 V-KAGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLEGSCLGRIRPHTFTGLSG 411
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Qy        481 -----FKDNTLSNVFANT----TNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLL 531
Db        412 LRRLFLKDNGLVGIEEQSLWGLAELLELDLTSNQLTHLPHRLFQGLGKLEYLLLSRNRLA 471

Qy        532 FLDSSHYNQLYSLSTLDCSFNRIETSKGILQHFPKSLAFFNLTNNSVACICEHQKFLQ-- 589
Db        472 ELPADALGPLQRAFWLDVSHNRLEALPNSLLAPLGRLRYLSLRNNSLRTFTPQPPGLERL 531

Qy        590 WVKEQKQFLVNVEQMTCATPVE-------MNTSLVLDFNNSTC---------YMYKTIIS 633
Db        532 WLEG--------NPWDCGCPLKALRDFALQNPSAVPRFVQAICEGDDCQPPAYTYNNITC 583

Qy        634 VSVVSVI 640
Db        584 ASPPEVV 590
```

RESULT 12
T42218
slit-1 protein homolog - rat
N;Alternate names: MEGF4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42218
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T42218
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1531 <NAK>
A;Cross-references: UNIPROT:O88279; EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF4
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r

  Query Match 6.6%; Score 287.5; DB 2; Length 1531;
  Best Local Similarity 21.0%; Pred. No. 1.3e-09;
  Matches 161; Conservative 99; Mismatches 266; Indels 239; Gaps 26;

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Qy          5 WLLARTLIMALFFSCLTPGSLN--------------------------------PCIEV 31
Db        229 WLRQRPTI-GLFTQCSGPASLRGLNVAEVQKSEFSCSGQGEAAQVPACTLSSGSCPAMCS 287

Qy         32 VPNITYQCMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIET 91
Db        288 CSNGIVDCRGKGLTAIPANLPETMTEIRLELNGIKSIPPGAFSPYRKLRRIDLSNNQIAE 347

Qy         92 IEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITL 151
Db        348 IAPDAFQGLRSLNSLVLYGNKITDLPRGVFGGLYTLQLL----------------LLNA 390

Qy        152 KKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMSL 211
Db        391 NKIN--------CIRPDAFQDLQNLSLLSLYDNKIQSLAKGTFTSLR----AIQTLHLAQ 438

Qy        212 NPIDFIQDQAFQGIKLHELTLRGNFNSSNIMKT----CL--QNLAGLHVHRLILGEFKDE 265
Db        439 NP--FICD--------CNLKWLADFLRTNPIETTGARCASPRRLANKRIGQIKSKKFRCS 488

Qy        266 RNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDDIVKFH-CLANVSAMSLAGVSI-KYLED 323
Db        489 AKEQYFIPG---------TEDYHL--NSECTSDVACPHKCRCEASVVECSGLKLSKIPER 537

Qy        324 VPKHFKWQSLSIIRCQLKQFPTLDLPFLKSLTLTMNKGSISFKKVALPSLSYLDLSRNAL 383
Db        538 IP-----QSTTELRLNNNEISILEATGL-------------FKK--LSHLKKINLSNNKV 577

Qy        384 S------FSGCCSYSD--LGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRV 435
```

```
Db        578 SEIEDGTFEGATSVSELHLTANQLES---------VRSGMFRGLDGLRTLMLRNNRISCI 628

Qy        436 TEFSAFLSLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDN---------- 484
Db        629 HN-DSFTGLRNVRLLSLYDNHITTISPGAFDTLQALSTLNLLANPFNCNCQLAWLGDWLR 687

Qy        485 ------------------------------------------------------------TL 486
Db        688 KRKIVTGNPRCQNPDFLRQIPLQDVAFPDFRCEEGQEEVGCLPRPQCPQECACLDTVVRC 747

Qy        487 SN---------VFANTTNLTFLDLSKCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSH 537
Db        748 SNKHLQALPKGIPKNVTEL-YLDGNQFTLVP---GQLSTFKYLQLVDLSNNKISSLSNSS 803

Qy        538 YNQLYSLSTLDCSFNRIETSKGILQHFPKSLAFFNLTNNSVA---------------- 579
Db        804 FTNMSQLTTLILSYNALQCIPPLAFQGLRSLRLLSLHGNDVSTLQEGIFADVTSLSHLAI 863

Qy        580 ------CICEHQKFLQWVKEQKQFLVNVEQMTCATPVEMNTSLVL 618
Db        864 GANPLYCDCHLRWLSSWVKTGYK---EPGIARCAGPPEMEGKLLL 905
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RESULT 13
T10504
disease resistance protein Cf-2.1 - currant tomato
C;Species: Lycopersicon pimpinellifolium (currant tomato)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10504; T10515
R;Dixon, M.S.; Jones, D.A.; Keddie, J.S.; Thomas, C.M.; Harrison, K.; Jones, J.D.
Cell 84, 451-459, 1996
A;Title: The tomato Cf-2 disease resistance locus comprises two functional genes encodin
A;Reference number: Z17062; MUID:96190812; PMID:8608599
A;Accession: T10504
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1112 <DIX>
A;Cross-references: UNIPROT:Q41397; EMBL:U42444; NID:g1184074; PIDN:AAC15779.1; PID:g118
A;Experimental source: cultivar Cf 2
A;Accession: T10515
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1066,'I',1068-1085,'E',1087-1110,'R',1112 <DI2>
A;Cross-references: EMBL:U42445; NID:g1184076; PIDN:AAC15780.1; PID:g1184077
A;Experimental source: cultivar Cf 2

  Query Match 6.5%; Score 283.5; DB 2; Length 1112;
  Best Local Similarity 22.6%; Pred. No. 1.4e-09;
  Matches 182; Conservative 109; Mismatches 285; Indels 231; Gaps 32;

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Qy         11 LIMALFFSCLTPGSLNPCIEVVPNIT--YQCMDQKLSKVPDDIP--SSTKNIDLSFNPLK 66
Db        385 LSMLYLYNNQLSGSIPASLGNLNNLSRLYLYNNQLSGSIPEEIGYLSSLTYLDLSNNSIN 444

Qy         67 ILKSYSFSNFSELQWLDLSRCEIETIEDKAWHGLHHLSNLILTGNPIQSFSPGSFSGLTS 126
Db        445 GFIPASFGNMSNLAFLFLYENQLASSVPEEIGYLRSLNVLDLSENALNGSIPASFGNLNN 504

Qy        127 LENLVAVETKLASLESFPIGQLITLKKLNVAHNFIHSCKLPAYFSNLTNLVHVDLSYNYI 186
Db        505 LSRLNLVNNQLSGSIPEEIGYLRSLNVLDLSENALNG-SIPASFGNLNNLSRLNLVNNQL 563

Qy        187 QTITVNDLQFLRENPQVNLS----------------LDM---------------------- 209
Db        564 SGSIPEEIGYLRSLNDLGLSENALNGSIPASLGNLNNLSMLYLYNNQLSGSIPEEIGYLS 623

Qy        210 ----------SLN---PIDFIQDQAFQGIKLHELTLRGNFNSS--------------NIM 242
Db        624 SLTYLSLGNNSLNGLIPASFGNMRNLQALILNDNNLIGEIPSSVCNLTSLEVLYMPRNNL 683

Qy        243 K----TCLQNLAGLHVHRLILGEFKDERNLEIFEPSIMEGLCDVTIDEFRLTYTNDFSDD 298
Db        684 KGKVPQCLGNISNLQVLSMSSNSFSGEL------PSSISNLTSLQILDFG---RNNLEGA 734
```

```
Qy        299 IVKFHCLANVSAMSL-----------------AGVSIKYL--------EDVPKHF----K 329
Db        735 IPQ--CFGNISSLEVFDMQNNKLSGTLPTNFSIGCSLISLNLHGNELEDEIPRSLDNCKK 792

Qy        330 WQSLSIIRCQLKQ-FPTL--DLPFLKSLTLTMNK--GSI--SFKKVALPSLSYLDLSRNA 382
Db        793 LQVLDLGDNQLNDTFPMWLGTLPELRVLRLTSNKLHGPIRSSRAEIMFPDLRIIDLSRNA 852

Qy        383 LSFSGCCSYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFL 442
Db        853 FS-------QDLPTSLFEHL--------------KGMR----------TVDKTMEEPSYE 881

Qy        443 SLEKLLYLDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDNTLSNVFANTTNLTFLDLS 502
Db        882 S----YYDDSVVVVTK----GLELEIVRILSL--------------------YTVIDLS 912

Qy        503 KCQLEQISWGVFDTLHRLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIETSKGILQ 562
Db        913 SNKFEGHIPSVLGDLIAIRILNVSHNALQGYIPSSLGSLSILESLDLSFNQLS------G 966

Qy        563 HFPKSLA------FFNLTNNSV-ACICEHQKFLQW----------------------V 591
Db        967 EIPQQLASLTFLEFLNLSHNYLQGCIPQGPQFRTFESNSYEGNDGLRGYPVSKGCGKDPV 1026

Qy        592 KEQKQFLVNVEQMTCATPVEMNTSLVLDFNNSTCYMYKTIISVSVVSV-IVVST-----V 645
Db       1027 SEKNYTVSALEDQ------ESNSEFFNDFWKAALMGYGSGLCIGISMIYIILISTGNLRWL 1080

Qy        646 AFLIYHFYFHLILIAGCKKYSRGESIY 672
Db       1081 ARIIEKLEHKIIMQR--RKKQRGQRNY 1105
```

RESULT 14
B36665
slit protein 2 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
C;Accession: B36665
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and co
A;Reference number: A36665; MUID:91099665; PMID:2176636
A;Accession: B36665
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1469 <ROT>
A;Cross-references: GB:X53959
C;Genetics:
A;Gene: FlyBase:sli
A;Cross-references: FlyBase:FBgn0003425
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F;1028-1061/Domain: EGF homology <EGF>
F;1068-1099/Domain: EGF homology <EGF2>
F;1115-1148/Domain: EGF homology <EGF1>

Query Match 6.3%; Score 273; DB 2; Length 1469;
Best Local Similarity 21.6%; Pred. No. 9.4e-09;
Matches 150; Conservative 86; Mismatches 241; Indels 218; Gaps 23;

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Qy         39 CMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWH 98
Db        308 CREKSLTSVPVTLPDDTTDVRLEQNFITELPPKSFSSFRRLRRIDLSNNNISRIAHDALS 367

Qy         99 GLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAH 158
Db        368 GLKQLTTLVLYGNKIKDLPSGVFKGLGSLRLLLLNANEI---------------------- 406

Qy        159 NFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQ 218
Db        407 ----SCIRKDAFRDLHSLSLLSLYDNNIQSLANGTFDAMKSMKTVHL----AKNP--FIC 456

Qy        219 DQAFQGIK--LHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEIFEPSIM 276
Db        457 DCNLRWLADYLHKNPIETSGARCESPK---------RMHRRRIESLREE----------- 496

Qy        277 EGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSLAGVSIKYLEDVPK--HFKWQSLS 334
Db        497 -----------------------KFKCSWGELRMKLSG-ECRMDSDCPAMCHCEGTTVD 531

Qy        335 IIRCQLKQFPTLDLPFLKSLTLTMNK---GSISFKKV--ALPSLSYLDLSRNALSFSGCC 389
Db        532 CTGRRLKEIPR-DIP-LHTTELLLNDNELGRISSDGLFGRLPHLVKLELKRNQL------ 583

Qy        390 SYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLY 449
Db        584 --TGIEPNA----------------FEGASHIQELQLGENKIKEISN-KMFLGLHQLKT 623

Qy        450 LDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDNTLSNVFAN---------------- 492
Db        624 LNLYDNQISCVMPGSFEHLNSLTSLNLASNPFNCNCHLAWFAECVRKKSLNGGAARCGAP 683

Qy        493 -----------------------------------TTNLTFLDLSKCQLEQISWGV--- 513
Db        684 SKVRDVQIKDLPHSEFKCSSENSEGCLGDGYCPPSCTCTGTVVACSRNQLKEIPRGIPAE 743

Qy        514 ----------FDTLH--------RLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIE 555
Db        744 TSELYLESNEIEQIHYERIRHLRSLTRLDLSNNQITILSNYTFANLTKLSTLIISYNKLQ 803

Qy        556 -----TSKGI------------LQHFP-------KSLAFFNLTNNSVACICEHQKFLQWV 591
Db        804 CLQRHALSGLNNLRVVSLHGNRISMLPEGSFEDLKSLTHIALGSNPLYCDCGLKWFSDWI 863

Qy        592 KEQKQFLVNVEQ--MTCATPVEMNTSLVLDFNNST 624
Db        864 K-----LDYVEPGIARCAEPEQMKDKLILSTPSSS 893
```

RESULT 15
A36665
slit protein 1 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
C;Accession: A36665; A31640; S13523
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and co
A;Reference number: A36665; MUID:91099665; PMID:2176636
A;Accession: A36665
A;Status: preliminary

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A;Molecule type: mRNA
A;Residues: 1-1480 <ROT>
A;Cross-references: GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g8615
R;Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
Cell 55, 1047-1059, 1988
A;Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of
A;Reference number: A31640; MUID:89077533; PMID:3144436
A;Accession: A31640
A;Molecule type: DNA
A;Residues: 881-1182,'G',1185-1404,'GT',1463-1464,'YHA' <RO2>
A;Cross-references: GB:M23543; NID:g340939; PID:g514357
C;Genetics:
A;Gene: FlyBase:sli
A;Cross-references: FlyBase:FBgn0003425
A;Introns: 1351/3
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r
C;Keywords: alternative splicing; growth factor
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
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F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F;1028-1061/Domain: EGF homology <EGF>
F;1068-1099/Domain: EGF homology <EGF2>
F;1115-1148/Domain: EGF homology <EGF1>

  Query Match             6.3%;  Score 273;  DB 2;  Length 1480;
  Best Local Similarity   21.6%;  Pred. No. 9.5e-09;
  Matches  150;  Conservative   86;  Mismatches  241;  Indels  218;  Gaps   23;

Qy         39 CMDQKLSKVPDDIPSSTKNIDLSFNPLKILKSYSFSNFSELQWLDLSRCEIETIEDKAWH 98
              | :: |: ||  :|  | :: |  | :  |   |||:|  |: :|||   |  |   |
Db        308 CREKSLTSVPVTLPDDTTDVRLEQNFITELPPKSFSSFRRLRRIDLSNNNISRIAHDALS 367

Qy         99 GLHHLSNLILTGNPIQSFSPGSFSGLTSLENLVAVETKLASLESFPIGQLITLKKLNVAH 158
              ||  |: |:| || |:    | | || ||  |:   ::
Db        368 GLKQLTTLVLYGNKIKDLPSGVFKGLGSLRLLLLNANEI---------------------- 406

Qy        159 NFIHSCKLPAYFSNLTNLVHVDLSYNYIQTITVNDLQFLRENPQVNLSLDMSLNPIDFIQ 218
                ||     | :| :|  : |  | ||::       ::    |:|    : ||  ||
Db        407 ----SCIRKDAFRDLHSLSLLSLYDNNIQSLANGTFDAMKSMKTVHL----AKNP--FIC 456

Qy        219 DQAFQGIK--LHELTLRGNFNSSNIMKTCLQNLAGLHVHRLILGEFKDERNLEIFEPSIM 276
              |   : :   ||:  :  :       |          :||  :   ::|
Db        457 DCNLRWLADYLHKNPIETSGARCESPK---------RMHRRRIESLREE----------- 496

Qy        277 EGLCDVTIDEFRLTYTNDFSDDIVKFHCLANVSAMSLAGVSIKYLEDVPK--HFKWQSLS 334
                                  || |       | |:|   :   | |   | :  ::
Db        497 ----------------------KFKCSWGELRMKLSG-ECRMDSDCPAMCHCEGTTVD 531

Qy        335 IIRCQLKQFPTLDLPFLKSLTLTMNK---GSISFKKV--ALPSLSYLDLSRNALSFSGCC 389
                :||: |  |:| | :  | :|    | ||   :   || |  |:| || |

Db        532 CTGRRLKEIPR-DIP-LHTTELLLNDNELGRISSDGLFGRLPHLVKLELKRNQL------ 583

Qy        390 SYSDLGTNSLRHLDLSFNGAIIMSANFMGLEELQHLDFQHSTLKRVTEFSAFLSLEKLLY 449
                : :  |:                 | |   :| |     : :| ::    || | :|
Db        584 --TGIEPNA----------------FEGASHIQELQLGENKIKEISN-KMFLGLHQLKT 623

Qy        450 LDISYTNTKIDFDGIFLGLTSLNTLKMAGNSFKDNTLSNVFAN---------------- 492
                |::           | |  | || :| :| | |  |      ||
Db        624 LNLYDNQISCVMPGSFEHLNSLTSLNLASNPFNCNCHLAWFAECVRKKSLNGGAARCGAP 683

Qy        493 ---------------------------------TTNLTFLDLSKCQLEQISWGV--- 513
                                                |   | :  |: ||::|  |:
Db        684 SKVRDVQIKDLPHSEFKCSSENSEGCLGDGYCPPSCTCTGTVVACSRNQLKEIPRGIPAE 743

Qy        514 ----------FDTLH--------RLQLLNMSHNNLLFLDSSHYNQLYSLSTLDCSFNRIE 555
                       : :|         |  |::|:| :  | :  :  |  ||||  |:|:::
Db        744 TSELYLESNEIEQIHYERIRHLRSLTRLDLSNNQITILSNYTFANLTKLSTLIISYNKLQ 803

Qy        556 -----TSKGI-----------LQHFP-------KSLAFFNLTNNSVACICEHQKFLQWV 591
                     |:          :  |         |||    | :| : | |  : |  |:
Db        804 CLQRHALSGLNNLRVVSLHGNRISMLPEGSFEDLKSLTHIALGSNPLYCDCGLKWFSDWI 863

Qy        592 KEQKQFLVNVEQ--MTCATPVEMNTSLVLDFNNST 624
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Search completed: March 12, 2005, 19:57:16
Job time : 27.5445 secs
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